SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ĺ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	4	\=possible nucleotide insertion)
			ISDVERBOURDE VOLDCON VERBORDO
l	İ		ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
Ì		ŀ	DTEQLAQRGAGLCFTFVSAQQNSFSSTGSGNTEHSCSSQKQISI
			QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
	1		RQI\DEQQKMLEKYK\ERLNRCFDNEFRNFLIEKSKQEKMACRD
			KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
	1	}	REEIERORKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL
			TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL
			KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
	į.		RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
	1		YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
			IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
	1		KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEDDXTSNK
			VDVWSVGVIFYQCLYGRKPFGHNOSOODILOENTILKATEVORD
			PKPVVTPEAKAFIRRCLAYRKBDRIDVQQLACDPYLLPHIRKSV
5996	1612		STSSPAGAAIASTSGASNNSSSN
	7017	981	DQQACLLGLMLTLEPGILEFDPSWIGSWTQR/SWVSWRSRPGCE
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVI.
			AFLTCLLYLALDVYFPOISSVKDRKK\AVLSGHPVVSGFBUDAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGPPGPRG
5997	1612		FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAOP
333.	1012	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGUT.
İ			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGRPHDAA
i			FWAFLWFTGDSCYL\ANQWOVSKPKDNPLNEGTDASPGPDSDES
5998	1612		FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
	1012	981	DQQACLLGLMLTLEFGILEFDPSWIGSWIQR/SWVSWRSRPGCE
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
- 1			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
5999	2	1790	FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
	-	1,790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
,			GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
ł			ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
į	ļ		LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS
	i		QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
			ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
			FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
1			KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
Ī	1		QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
- 1	1	1	EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
-	J		LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL
İ	ı]	VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
1			LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP
6000	101	1561	TED COMMON THAT I TET SUSETE PPDEKP
- 1	·		TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
- 1	i	ŀ	DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
- f			KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
- 1	f		VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK
- 1			ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
	1		NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV
}	1	i	LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCOTGCCV
}	ì	İ	RAKVFQVMNLRBNGMYGKRKLLELIGHAVAHLKKADEANDNLFR
]		VCSILASLHALADQYEDAEYYFOKEFSKELTPVAKOLIHLRYGN
	!	1	FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL
1		i .	SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
		l I	
6001	176		SWNGE
6001	176	1038	SWINGE AFAHSPSRGHRETHIHTPRHTPRCTMAESHLOSSTTTASOPFET
6001	176	1038	SWNGE AFAHSPSRGHRETHIHTPRHTPRCTMAESHLQSSLITASQFFEI WLHFDADGSGYLEGKELONLIOELOOARKKAGLELSPEMKTEUD
6001	176	1038	SWINGE AFAHSPSRGHRETHIHTPRHTPRCTMAESHLOSSTTTASOPFET

	SEQ	Predicted	Predicted end	Amino poli
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	location	corresponding	H=H1Stldine, i=Isoleucine V-Tucine
	1	corresponding to first	to first	L=Leucine, M=Methionine N-Asparasina
	ŀ	amino acid	amino acid	P=Proline, O=Glutamine D-argining
		residue of	residue of amino acid	S-Serine, T-Threonine, V-Valine
		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	a o que ince	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LKLFDSNNDGKLELTEMARLLPVQENFLLKPQGIKMCGKEPNKA
			,	FELYDQDGNGYIDENELDALI,KDI,CEKNKODI,DINNITTEVYYYY
	6002	0.55		MALSUGGKLYRTDLALILCAGDN
	0002	977	81	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSDLDLDDADLUDUG
				SMAQKSDLLELDCQLTRDRVVVVSHDENLCROSCLMPDVCCI DE
- 1]		EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
- [EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSYMKKKAANP EMPLSPTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIINRT
-1			İ	I FFFSCSCLNQLLAVVSKWLIMRKSLIRHLEEPGVOOREWCI NE
ŀ	6003	140		ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
	0003	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRDSSAAGAEKUD
-		}	J	APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDPDDPTVA
				FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
1				SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACTTVA HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
-				RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
1				RHAAVLVETIKKGIHDADAEARVEARKTYMGIDNHEDGEARTTY
1				NSLEPSYQKSLQTYLKSSGSVASLPOSDRSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
1				KWSTANPSTVAGRVSAGSSKASSLPGSLOPSPSDTDUNA DACAV
1				AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQFGSRSGSPGRVLT
ı				TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
			•	ARSSKIPKPSVSQGCSREASRESSRDTSPVRSFODT.ASPUUCDG
ı		}		IGALIAPEVYGASGPGYGISOSSRIGSSVSAMDVINTGEDVERN
Ţ				VADALLLGDIRTKKKPARRRYESYGMHSDDDAMEDAGGAGGGGG
				ISSENGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGT.GLON
				LLKNORTLSRVELKRLCEIFTRMFADFHGKRVFSMFLETLVDFI OVEKDDI ODWLEVIL TOLL KYMEN IN TOLL KYMEN
		1	i	QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
]		*INSSETRLAVSRVITWTTEPKSSDVRKAAOSVITGI.ETI.NEDE
		ļ		FIMILGALPKTFQDGATKLLHNHLRNTGNGTQGGMGGDI TEDDE
				RSPANWSSPLTSPTNTSONTLSPSAFDYDTENMMSEDIVERIDG
1] [i	VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
l		1		GGDATDSSQTAL\DNKASLLHSMTTHSSPRSRDYNPYNYSDIS PFNKSALKEAMFDDDADQFPDDLSLDHSDLVABLLKELSNIHER
			i	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
			İ	TRALALKVLREILRHOPARFKNYARI, TVMKTI FAUVIDUVERE
			1	SAEEAASV (LATSI (SPECCTKVT.CPT TOTADVD TMT. NA TUMOR
				KVIERVSKETLNLLLPEIMPGLIOGYDNSESSVPKACVECT VALL
L				HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GOS
	6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEBSVDGNRFSSAASAFKVP
			1	APKISGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDPIVA
		j		FIDVPSIQIYSSRELEETLNKIREILSDDKHDWDODANAT.VVID
			1	SLLVAGAAQYDCFFQHLRLLDGALKI.SAKDI.DSOUUDBACTTILA
			ļ:	HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
				RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLOEWOTHSLE RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
	- 1		1	NSLEPSYQKSLOTYLKSSGSVASI.POSDPSSESSOPET NDDBGG
	- 1	1	-	KNSTANPSTVAGRVSAGSSKASSLPGST.OPSPSDTDVATA ADGREE
	1	ĺ	1 4	AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKT.DCTAGEDCDxx
	İ		1 2	KAKLSAPLAGMGNAKADSRGRSRTKMVSOSODGGDGGDGGDGDTT m
	ļ		;	TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
	- 1			RGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVERA
	1		1 \	ADALLEGDIRTKKKPARRRYESYGMHSDDDANSDASSACCEDS
	1	1	1 7	SSRNGSIPTYMRQT\EDV\ABVLNRCASSNWSERKEGI.CT.ON
			11	LKNORTLSRVELKRLCEIFTRMFADPHGKRVFGMFLFTIVDBT
	- 1		9	VHKDDLQDWLFVLLTQLLKKMGADLLGSVOAKVOKALDVTPPc
			1 1	PNDLQFNILMRFTVDQTOTPSLKVKVAILKYIFTLAYOMDDOD
				INSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
				•

SEQ	Predicted	Predicted end	Amino agid cognost contribute discontinuity
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 20.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
			RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
ļ		[VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
j	i		PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
	1		VEERKIALYELMKLTQEESFSVWDEHFKTILLLLETLGDKEPT
l l			IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR
			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
	1		KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
1	i		HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
			GOS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL
1			NNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKPRDPKIPKS
	i		KRQKKERMLLCRQLGDSSGEGPEFVEEREEVALRSDSEGSDYTP
			GKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAQLL
			BDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
	1		KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
	i		TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKPK
1 1	1		PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
1			SDGSTSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV
1 1	l i		CQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI
1			QWEAKEDNSEGEEILBEVGGDLEEEDDHHMEFCRVCKDGGELLC
	ļ		CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI
1 1			WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS
1			YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK
ł 1] [S\RKRKNKDPKFAEMEERFYRYGIKPEW\MMIHRILNHSVDKKG
1 1	1		HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG
	1		EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
1 1	i j		
1 1			TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYSL
1 .			YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
1 1			DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
1 1	l l		LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
1 1			LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED
1 1			QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
1 1			KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
]			LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH
1 1			RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR
1 }	·		FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
]		APSRAHRIGONKKVMIYRFVTRASVEERITOVAKKKMMLTHLVV
1 1			RPGLGSKTGSMSKQELDDILKFGTRELFKDEATDGGGDNKEGED
1]		SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQYVV
	}		REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQOORDLAR
] [NIGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE
] 1	l		DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR
1 1			
1 !	·		QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
1 1	-	1	MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ
] }	}	1	EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP
] }		į	NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT
1 1			QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
1		l	AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
			DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTKKT
1 1			YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
	ļ		NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
			PSMALNTRFAEVECLAESHOHLSKESMAGNKPANAVLHKVLKOL
, 1		,	EELLSDMKADVTRLPATIARIPPVAVRLOMSERNILSRLANRAP
1		•	EPTPQQVAQQQ
6006	1	965	DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
"""	-	703	GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS
[İ	1	
) [}	1	ERIHEQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKVGV
[[CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF
			LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<u> </u>	amino acid	sequence	Codon, /-possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKMB
ĺ			EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG
			SLAPRPCDVPTCPTL
6007	3	2351	HELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE
	1		GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPBNETELIK
ſ	1		EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSQLEYYAS
j			SPDEKALVBAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
ł	J		FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
			HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E
			EKLAAVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV
1			WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSECAEQLR
1			QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
1			LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
	ł		GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
			VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICFT
1			SLPILIYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT
			ILGFSHAFIFFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM
			VITVTVKMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
1			LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
1			HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
6008	4554	1000	GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
8008	4554	1089	AGVRRAGARRGPGRALPAGATAVPPPSARRRRCPAPEHAGPAR
			ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE
			DFKQFEPNDFYLKNTTWEDVGLWDPSLTKNQDYRTKPFCCSACP FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
			IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
1			KCTYRDPLYEIVRKHIYREHFQHVAAPYIAKAGEKSLNGAVPLG
			SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG
1			HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
			SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV
1			GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ
1			APARYSLOSANASSLSSGOLKSPSLSQSQASRVLGQSSSKPAAA
1 1			ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP
			AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS
			TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH
!			LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
]			SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
1 1			TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN
1 1			GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
			SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
1 1			TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
1			LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
i 1			LGKEDDSSSDSFENLEEESNESGSPFDPVFEVERKISNDNPEEH
j			VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS
,			EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE
1 1			SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
1			QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP
6009	4272	7624	MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC
1 5003	74/4	1534	
		ļ	HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG
		İ	RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL
1			NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG
j	1	ļ	NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
1			VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
1	1	İ	FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
, 1	ł		I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN
1 1	Ì		AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG
1 1	Í		DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP
1 1	1		RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT
	ĺ	Ī	RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDELLWFGGR*LIIIG

SEQ Predicted Predicted end Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly location location corresponding II=IIistidine, I=Isoleucine, K=Lysine,	
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G=Gly	'' A B'-
	CTITE!
	٠.
1	••
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine,	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown,	*-Ston
	-
	• •
sequence \=possible nucleotide insertion\ 1**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQG	nurui cc
AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDG	
GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWC	
CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQR	
R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVY	
GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRW	
TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACT	
LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD	Or Ograni
	KUT CERM
6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENS AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAA	
1 1 1	
PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSE	
TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEV	
VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFA TRAOTCCPCCOAORDII.UGAVDMLEGGSVLIPTAPGI	
IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSI PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYS	
1 1	
IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQB	
IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKI TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAIT	
TVDDQTKTEABSALQMDTAAKEGGGNPKAQHTADATT	
1	
TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGI	4
YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIF	,
ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGN	
TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHR	
KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAE	
SIGSDDPETQVVLINAIKDVAKALSDLISATKGAASK	
YQLKGAAKVMVTRVTSLLKTVKAVEDEATRGTRALEA	
ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAA	
DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRA	
TLGYLDLLEHVLVII_QKPTPELKQQLAAFSKRVAGAV	
EAMKGTEWVDPEDPTVIAETELLGAAASIEAAKKLE	_
PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQR	
VGSTPANAADDGQWSQGLISAARMVAAATSSLCEAAN	
SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRI	
KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQI	IMAQUEN
LKKERELEEARKKLAQIRQQQYKFLPTELREDEG 6011 446 1835 LLOPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQ	DET.KDMT
6011 446 1835 LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLG TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTS	
DMEYTIDVFFROSWKDERLKFKGPMTVLRLNNLMASK	
FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\	
GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPAR	
GSRLNOYDLLGOTVDSGIVQSSTGEYVVMTTHFHLKR	
QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLT	
ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY	
WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLA	
TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSR	
GIFNLVYWATYLNREPQLKAPTPHQ	THE PUR
	T.FCTVCP
EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQAC	
CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSG	
QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQAR	
REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDI	
EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQV	
PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFE	
QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQ	
IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCT	
QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFK	
NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGD	
ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVAC	
CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGE	
NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSS	
NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPE	TAKECTT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion, -possible nucleotide insertion)
<u></u>	sequence		PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLFAN
1			GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
Į	ļ		VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
-			PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
1			KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
			VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
1	Ì		EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1 :			GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
1			NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
1	1		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
			GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
'			KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ
	}		LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
			KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
1			DDFSKVVDREFCADIBLIIDGNKNMVLEESCSQPCPGDCYLKDW
			SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
1			SOPDADRSCNPPCSOPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
			CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
1			PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
		i	NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
1			SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
•			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
			ARPESNDQPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
			RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
			DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
1			KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
1			LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
!			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
			EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
1			TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
1			RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
			EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
1			IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
			ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
			ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
j			SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
]			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
į į	į		QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATALQ
6015	13	2322	P PECAEDOCEPONIEI CMCMECCACOCI CECCMDI UMCANVCVO
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
; l			RITYWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
}			GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
			HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
j			EGIBEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK
j i			GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
1 1			KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
, ,		,	FEQLAALQIEYEENVOLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
	•		ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
			SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
			F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
]			KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
	ŀ		EKEVLPDQVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
			QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
, ,			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
	r		
6016.	13	2237	\scgvgs\cncsnssssnfrgafileargslh\gl\ktglqlf AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	1
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
J	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence		\=possible nucleotide insertion)
			VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
1			RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
}	ł		GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1	1		HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
1	i		EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
			GSEEVDSHCKKALSHKELYBRARELLVSYEEEQFTVLEKFRYLP
1			KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
!	l		FEOLAALOIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSONFTQ
			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
			SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
	i		F\KAMGQGLQDE\BQEKLLRICSIYTQSGENSLVQEGSEASPIG
	Í		KSPYTLDSLYWSVKPASSSFGSEAKACQQEEQGSVNDVKEEEKE
			RKEVLPDQVEEEERNDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
			QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
1			\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLF
6017	203	3469	SHOEIEONSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRNDS
8017	203	2402	NFALQTMEPALPMPPVEELDVMFSELVDELDLTDKHREAMFALP
1			AEKKWOIYCSKKKDOEENKGATSWPEFYIDOLNSMAARKSLLAL
ì			EKEEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK
			TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQ
			SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER
1			TREOTLINDLDXSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL
1			DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE
1			DELEFAKRFELVHIDTKSATOMFELTRKRLTHSEAYPHFMSILH
1			HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN
1			
			FNIKNVVRMLVNENEVKQWKEQAEKMRKEHNELQQKLBKKEREC
1			DAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE
			LSRRAVCASIPGGPSPGAPGGPFPSSVPGSLLPPPPPPPPPPLPGGM
			LPPPPPPLPPGGPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ
			PTNALKSFNWSKLPENKLEGTVWTEIDDTKVFKILDLEDLERTF
ļ			SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA
}			QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE
			KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK
	1		KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN
			KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP
1			SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ
			KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV
			KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE
1			RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
		25-2	FDKDLSKLKRNRKRITNOMTDSSRERPITKLNF
6018	13	2510	TISOSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
1			ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
			GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV
	i		TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD
ł]		GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT
I			AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW
1]		ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF
1			WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG
1			LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
i			PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK
			LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS
1	!		HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL
1			ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED
			QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQLLRNVTHHVSV
1	,		TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG
1	i		MVDFALBSGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
1			VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL
1			SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF
			QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK
6019	2	1066	TPNDREPPPORPPSSRRASHLAQEITSAASLGDQTQILGSLTTA

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i		sequence	
	sequence		\=possible nucleotide insertion)
1	i	ŀ	PVITSAIRSMPGISSQILTNAQGQVIGTLPWVVNSASVAAPAPA
1		Î	QSLQVQAVTPQLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES
j	j	l	LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET
1	1	į	PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTQT
	1	ļ	QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN
ŀ		l	1
i	}		EAELRNQEGQQNLMEFVGGEPSKKRKRRTSFTPQAIEALNAYFE
1	1	1	KNPLPTGQBITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF
ì			QIP
6020	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
	i	J	AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
J	1	!	•
1	1		QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
1	1		RKLRSRSLSQIHEAAVRMRSBATDVKSTLAEIEDWLDKLMQLTE
1	}		EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
1	l		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
1			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
	}		FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
!	1		
1	1		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
1	l		AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1	İ		LTQTASSTAGAMEELQDQEGWEYASLIGWKFHNKQRSSDTFRRR
Į	ĺ		RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOKHSA
1			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1	l		YAHICFLHRSKTTEIIHSTLNPTWDOTIIFDEVEIYGEPOTVLO
	<u>.</u>		
	Ì		NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
1			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
1	ļ		QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVBCGGERV
1]		ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
	i '		DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEERIV
	i	i	•
			DWWSKFYASSGEHEKCGQYIQKGYSKLKTYNCELENVARFEGLT
1 .			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
			ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
	1		KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
1	[TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
j .			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
1			
	l i		FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
(NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
	l		NKOKTOVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
]		SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
1			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
1			LFVAVLLYSLPNYLSMKIVKPNV
6021	4052		
6021	4953	549	EAIQFEVSIGNYGNKFDTTCXPLASTTQYSRAVFDGNYYYYLPW
1			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
1			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
		•	RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
i			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
1			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
]			l '' ''
1			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
]			FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
1 1			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
1	ļ		AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
1 1			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1	! !	ı	TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1	1		YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
1			NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
1			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
]		OGIRPVVQLTAIEILAWGLRNMKNFOMASITSPSLVVECGGERV
]			
			ESVVIKNLKKTPNFPSSVLFMKVFLPKEBLYMPPLVIKVIDHRQ
			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR

SEQ	Predicted	Predicted end	Amino and a
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-2ton
İ	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKERETT
			DWWSKFYASSGEHEKCGOYIOKGYSKLKIYNCELENDAR FECT TO
1			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRTVDI.DDDGVDADD
İ			ROFRELPDSVPQECTVRIYIVRGLELOPODNNGLCDBVIKTTLC
i			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
-	ł		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
ł	1		PEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
ĺ	1	1	NIS RYYLRVIIWATKDVILDEKSITGEEMSDIYVKGWIPGNEE
- 1		1	NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
	ł		PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
1		[KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
6022			LFVAVLLYSLPNYLSMKIVKPNV
0022	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTOYSRAVFDCNVVVVLDW
ı			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERIOTNIEALKGGI
1			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANUTVI.DTOT
1			RKLRSRSLSQIHEAAVRMRSEATDVKSTLAFTEDWIDKIMOLTE
1	1		EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
I	1		GKTOTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
i i	i		FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYONSSRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
ł			AVDEKGWEYGITIPPDHKPKSWVAABKMYHTHRRRRLVRKRKKD
			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
		1	RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
	1		YAHICFLHRSKTTEIIHSTLNPTWDOTIIFDEVETYGEPOTVAO
	1		NPPKVIMELFONDQVGKDEFLGRSIFSPVVKINSEMDITDKIJM
ŀ	1 1	!	HPVMNGDKACGDVLVTAELILRGKDGSNI,PTI,DDODADNI,VMVD
1	İ		QGIRPVVQLTAIEILAWGLRNMKNFOMASITSPSLVVECCGPPV
1			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPDI.VIKVITDUDA
	1		FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEBEIV
1			DWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
	1 1		DFSDTFKLYRGKSDENEDPSVVGEPKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1	1		KKVIE DRDHYI PNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
	1.		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
		i	RDSLR\PTQ\LLQNVARFKGFPOPILSEDGSRTRVGGPDVGLDF
ļ	1 1		FEANKILHQHLGAPEERLALHILRTOGLVPEHVETPTLUGTEOD
1]	l I	NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIVVKGWIPGNED
		1.	NKQKTDVHYRSLDGEGNFNWRFVFPFDVI.DAFOLCTVAVVENTU
	1	·	SIDUIEFRIPPR\LIIOIW\DNDKFS\IDDVI.GEDDTI.TCDUTT
		1.	HFLQKSPGGNC/RGLDMIPDLKAMNPIKAKTASI.FFOKSMVCWW
1	[]		PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
] ;	KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SOFI CMEVEL NOT A NOTICE DE LA COMPANSION DE LA COMPANSIO
ĺ			SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL
			SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGQLVF LEGL/IVCSGR\VFQAQKEPHPLQPLREANAGNLKPLFEFVREA
		! 1	LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT
Ì	1	17	/CWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL
	1		ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
6655		F	AKGMSPAVL
6024	3	3260 F	PLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEEAE
ŀ		-	PAELFORKVVASFPRTVLSTGMDNRYLVLAVNTVONKEGNGER
İ		J R	LVITASQSLENKELCILRNDWCSVPVEPGDITHTEGDCTSDTW
		(±	IDEOFGYLILYPDMLISGTSIASSIRCMRRAVISETERSSIDA
			RQMLIGTVLHEVFQKAINNSFAPEKLQELAFQTIQBIRHLKEM
			. 10

SEC	Predicted	Predicted end	
ID		nucleotide	Amino acid segment containing signal peptide
NO:		location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Ì	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPQMQLSL
ļ		ļ	PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKIDVTVGVKI
		Į	HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSQERRADP
	Ī		EAGLLLYLKTGQMYPVPANHLDKRELLKLRNQMAFSLFHRISKS
ļ			ATROKTQLASLPQI IEEEKTCKYCSQIGNCALYSRAVEQQMDCS
- 1			SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKN
l	1	ļ	HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGQYLHNFQCKH
i	1	1	GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
1	1		RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKLMENTFVSKKLR
- 1			DLIIDFREPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
	1		VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
1	ı		AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI
J			KS\LALLEELYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ
İ			ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF
1	i		KRLEONKSAVVOLTVOYRMNSKIMSLSNKLTYEGKLECGSDKVA
1			NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD
1	1		KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIIAP
			YRQQLKIINDLLARSIGMVEVNTVDKYOD\RDKSTVLVSEVDSN
1	•		KDGTVGELLKDWRRI NVAITRAKHKLILLGCVPSLNCVPDI EKT.
6005			LNHLNSEKLIIDLPSREHESLCHILGDFORE
6025	3977	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
1.	1		ARYGEAGEGPGWGGAHPRICLOPPPTSRTSFPPPRI,PALEOGPG
1			GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVOOWVSYADTELTD
1			AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWIRI,HTVI.A
ļ	1		GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVPO
			PEFRAVLGEVVLYSGARPLSHQPGPEAPALPKTAAQLKKEAKKR
			EKLEKFQQKQKIQQQQPPPGEKKPKPEKREKRDPGVTTVDI.DTD
	1		PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
1	}		AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE
	1		TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW
	1		KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR
1	1 1	i	LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG
	Į į		YKEKVEFGVLVSFAYKVQGSDSDEBVVVATTRIETMLGDVAVAV HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT
1	1		PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR
ļ	İ		KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR
1	1		CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
			KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE
			KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED
j	1		LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
1	!	i	IVRDAHGRKMSKSLGNVIDPLDVIYGISLOGLHNOLLNSNIDDS
ł	1	ŀ	EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSOGRDINI,DVN
	1		RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSOPGGHESLVDP
1	1	ł	WIRSRLTEAVRLSNOGFOAYDFPAVTTAOYSFWLVELCDUVLEC
i			LKPVLNGVDQVAAECAROTLYTCLDVGLRLLSPFMPFVTERLEO
j	1	Į.	RLPRRMPQAPPSLCVTPYFEPSECSWKDPEARAALELALSTTPA
	1		VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVOGDG
	1	Į.	QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLOLOG\LLDP
		1.	ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPI.\F
6026	2674		VQEADEAKLQQTEAELRKVDEAIALFQKML
0025	20/4	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC
	1	1 '	TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTOTILLO
	1		TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
			YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN
	}	1 .	
		1 3	LLRLHLNSNRLOMINSKWFDALPNLEILMIGENPIIRIKDMNFK
			PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKUPH
			PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMDET.
			PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIMI
			PLINLRSLVIAGINLTEIPDMALVGLENLESISPYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAPFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMNKTN
			PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIMI.

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Truntophon V managing,
İ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
Į.	sequence		\=possible nucleotide insertion)
		 	KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
1	- 1		SEPODNINGSINIKIPDIOANSKI ISKWA SOWIE AND AND AND AND AND AND AND AND AND AND
1	1		SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
	1		TENSHAAQSARIPSDVKVYNLTHLNESTEYKICIDIPTIYQKNR KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
	1	ł	CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS
			TSLKVKATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK
- 1		· ·	PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSQRPRT
Į.	1		LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV
Ī			TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
- 1		1	QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
1	1	İ	TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGF
[ļ	FTNYNWREEHLERMLGQAGERRADVYVGVDVFARGNVVGGRFDT
	1		DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
			DPVALRNRCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
	i i		LNVHMEVCAAFEAKEETYKSLMQKGQQMLARCPKSAETNIDQDI
1	į –		NNLKEKWESVETKLNER\KT\KLBEALNLA\MEFHNSL\QDFIN
Í			WLTQAEQTLNVASRPSLILDTVLFOTDEHKUPANEUNGUPBOTT
			ELDKIGTHLKYFSOKODVVLIKNLJ.TSVOSPWEKTROPLUEDOD
1	j i		SLDDARKRAKQFHEAWSKLMEWLRESEKSI,DSELETANDDDVIV
1	1		TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDMLVID
	1 ']		DMLSSLRDKWDTICGKSVERONKLEEA\II.FSGOETDALOALID
i	1		WLIRVEPQLAEDQPVHGDIDLVMNI.IDNHKAFOKELGKBTGGVO
			ALKKSAKELLEGSRDDSSWVKVOMOELSTRWETVCALCICVOMP
1	1		LEAADKQAEEFHSVVHALLEWLAFAFOTLDFUCITEDDEDAIDE
1	1		LIDQHKEFMKKLEEKRAELNKATTMGDTVI.ATCHDDGTTVIII
1	1 1		ITALKAKEEVLAWAKOHOORLASALAGI.TAKOPIT.PAITAKEO
}	}	i	WAETTITIDEDKEVIPOEIEEVKALTAEHOTEMEEMTPKODDITOK
1	1 1		VTKTYKRRAADPSSLOSHIPVLDKGRAGRKREPASSLVDSCSOT
ļ	1		QIETKNPRVNLLVSKWOOVWLLALERRRKT.NDAI.DRI.BRI.DRBN
ļ	1		NEDEDIWRKKYMRWMNHKKSRVMDFFRRIDKDODGKTTPOFFID
[1		GILSSKFPTSRLEMSAVADIFDRDGDGYTDYVEFVAALUDNING
1	1		YKPITDADKIEDEVTROVAKCKCAKRFOVEQIGDNKYRFFLGNO
1	l l	1	FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
]	ŀ		NMBLREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
í .			SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
l i	i i		ECSDFPVPSAEGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA
1 1	1	1	ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
		1	IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
1	1	Í	AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
1 1			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
			TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
!	1		VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
1 1			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
i I	1		PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
1	1	j	IRDIEQASLAAVSOSLATRODISVEALOFOLTSWOFTGHT TOD
	ŀ	i	TATAARGEAAQLGHKGTOLASYFEPI.II.AAVGVASKII.DUOOOM
			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
i i	i		EAVDDIMVTLNEAASEVGLVGGMVDAIAEAM9KI.DEGTDDEDVG
1		į '	TFVDYQTTVVKYSKAIAVTAOEMMTKSVTNPEELGGLASOMTED
·]	l	1	YGHLAFQGQMAAATAEPEEIGFOIRTRVODI.GHGCIFI.VOKAG\
}		1.4	ALQVCPTDSYTKRELIECARAVTEKVSLVI.SALOAGNKGTORGT
1		{ ·	TAATAVSGIIADLDTTIMFATAGTINARNSETEADHDENTI POR
		1 3	KALVEDTKLLVSGAASTPDKLAOAAOSSAATITOLAEVVKLGDA
J		1 2	SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDDSM
ŀ		1.3	YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALRATIECIVO
J		j 1	ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNGCBOR
		I	DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
· }	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
			EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
1	ļ		PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
1			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
. I .	}	İ	SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
L			LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
i			APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF
			TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
1	Ì		SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT
1			IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
			VERYREAIIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
1			AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
			MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
			BTLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
			RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
			AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
i			VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
		1	IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
			QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSREGLEDAVEGADEALQKAIKS
1			DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
·			DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
1			IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQBAENGAL
1 1			DISKLAEFIIGMMGTLCAPARDEBVKKLKDIKEIVPLFREIFSV
			LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
1 1			FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
1	i		YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
1			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
1 1			TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
1 1			IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
6032	39	2415	KFARLVNYNKMVFCPYYDAILSKILVRS
		2123	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1 1			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
i	1		QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
1. 1	İ		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
] }			SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
	1		SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
1	1	İ	ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTFTPRTDAPTPGS
1	l		NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
	Į		MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
1	İ	ļ	PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
]	ļ		IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
]]			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
	1		AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
] [ŀ	i	W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
1		[EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
1 1			W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
			RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
]	1		SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1	1	1	YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
1		l l	QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
	į.		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
]	ł		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
] [i	ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan V museine V V
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence] -	\=possible nucleotide insertion)
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD
- 1		1	PHHIMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
·			IGPGIPRHAPOTNELNUGBIAGANET CATEGORIA CONTROL CO
			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
	1		DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
	i		AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
	1		EVLHUTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
1			W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDXYIVTGS\GDK\
Ĺ	1	1	RATVYEVIY
6034	2683	714	
Į.		1	ESGRRRLKRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
1	1		EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR
	Ī		VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
i			RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR
1			LOFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
1	1		RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
	1		LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ
1			DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEQRKGL
1			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
1	1		RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
	1		DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE
1	1		TOKALLAEIONGCKRNLVLAREREEKEOPPOLSASMPETTATEP OPDDEPAAGVONGAPSPAPSPDSDSDSDSDGEEEEEEEGERDET
i			PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP
			PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASQESGQETL
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
	. 1		YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
			LENASTLALPDSSQPF\SLHTARVQGCVVEILTQGLGPLPV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN
1	1 1		SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
1			VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD
i	}		SSTSLDAIIEFLNYHNEVDIVGNIOATSPCLHPTDLOKUAEMTP
	1	i	EEGYDSVFSVVRRHQFRWSEIQKGVREVTEDININDAKDDDDOD
			WDGELYENGSFYFAKRHLIEMGYLOGGKMAYYEMRAFHSVDTDV
1		1	DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGGLTNGUTVVG
		İ	GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKOTI.CCI.V
			LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAVLGNEVSDEEGLE
1 1		}	RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFARHIC\I.I.
6037	2936		MEKGLINFMPKNRNLAVNIGEKK
000.	2336	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA
1 1	!		GGGFPRRHSVTLPSSKFRONOLLSSLKGEPAPALSSPRSPRDDD /
!		[SFSEGGERLLPTQKOPGGGOVNSSRYKT\ELCPPFFFNGACVVC
	1	1	DRCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCDVGDDCUET
	ŀ	1	HNAEERRALAGARDLSADRPRLOHSFSFAGFPSAAATDAATGTT
1			DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA
ĺ		1	PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
6038	1450	436	SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD
	-130	426	SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
1		1	YKGTKHAKKLKALEAMKNKOKSVTAKDSAKTTFTSTTTNTTNTS
1		1.	SDKTDGTAGTPAISTTTTVEIRKSSVMTTETTSKVEKSDT#DAMO
1		1 1	NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASOLEAHYSCTUUV
	İ	'	TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLONKTFHCRTCD
1	ļ	/	VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKT.OKTAHBT.
- 1	1	10	GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPEST.DTAD
6039	4073		AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY
	4073	1000 [7	LDEYEARLTLANLDDFEEDNEDDDENRVNOERKAAKTTELTNEL
		1 1	NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
1		1 1	RKTEDSFYNNSYNPFKEVOTPOYLNPFDEPEAFVTIKDSPROGT
1		} P	KKKNIRPVDMSKYLYADSSKTEEEEIDESNPEVERKSTDDDNNI
			/NPVQELETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS

SEC	Predicted	Predicted end	
ID		nucleotide	work bedinent containing signal
NO:		location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	
l	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Truntophan V.Tunneine,
l	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
<u>L</u>	sequence	1	\=possible nucleotide insertion)
			PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSW
			RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI
1	1	1	SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN
- 1		ļ	SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
			VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
İ	1		SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
			BTLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
	1		LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
1	İ	ľ	SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL
i		1	LBQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER
f	1		ARQLIAEARSGGKMSELPSYGERAAEKLKERSKASGDENDNIEI
1	ı	İ	DTNEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLB
ļ			VQPQVANSPSSAAQKAVTESSEODMKSGTEDLRTERLOKTTERE
1	İ	ļ	RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
- [1		EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEQKQ
	ĺ]	IDTRAALVEKRLRYLMDTGRNTREEEAMMOEWEMIJNIKKWAAL TD
	f		RENQUESILE KEHDLERRYELLNREI RAMTA I EDWOKTEN OKERE
i	1		QUILLES VALVNKRDALVRDI DAQEKQAEEBDEHLERTLEONKG
6040	475	1000	MAKKEEKCVLO
1	1/3	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
Ì			LSSNQ-TMVINVSVEVVNTLYEDIOYMOVPVADSPNSRICDEED
1	ŀ	ĺ	PLADHIHSVEMKOGR\TLLHCAAGVSRSAAT.CLAVI.MVVIIAMOT
}			LDARTWIKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV
6041	2	3886	GMIPDIYEKEVRLMIPL
1		3000	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
	1		NLLCVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
ł	1		EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
1	1		VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
1	ı		IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
ł	1		DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTFWL KGDIIGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
1	1		HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC
1	1		DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
			CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
1	1	i	DINSLOVLLSAVDDLLNTLLESEDSYLMCVYIGSVMPNDSEWEK
l	1		MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIXTLPSHLCT
1	1		SALLSKMVLIALRKETVLENNELEKIIAELLYSLOWCERLDNER
	1		IFLIGFCEILQKMNITYDNLRVLGNMSGLLOLLFNRSREHGTLW
J	1		SLITAKLILSRSISSDEVKPHYKRKESFFPLTEGNIHTTOSLCP
	1	ļ	FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLO
	1		TKSIDDGELLHGILKIIISWKKEHEDIFIFSCHISEASDFULGV
1	1	1	NIELLRELSLELKYCSSPLAESEWDETMCGMI.AUT.PPTGENAAT
1	1		YSIPLVQLFACVSCDLACDI,SAFFDSTTI,DTIGNI,DVNI TERRIY
	[EFFSQGIRSLLDPILVTVTGENKDVSETSFONAMT.XDMCDTTTTX
1	l I		ISKEQUUSHKUPARLVADOKTNUPEYIOTIJINTIADIJI.
]	1 1		VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS
}		ľ	LISIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
!	1	.	LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR
			TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT
	1	1	STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
	[IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
]	1	VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA/CLY
			KWFTSSNKSTCSLCRETFF
6042	1306	253	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
			GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
		1 (GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSST.AAGGVE
		1 3	LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHODWFY
i		1 9	QYQQDTPVAPRFDVNAPDLYIPAMAFITYVT,VAGI,AI,GTODDEG
1	1	[]	PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDI.TTDI.VA PI
			GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK
			The state of the s

SEQ	Predicted	Predicted end	I mino and a
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
· · ·	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
6043	403	599	LCLFFPFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
			PLPPLONKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV
	i		DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
L			AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRPQPPPPPPG
		j	AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSL
i	ĺ	İ	SNAVKOTTAAAAATFSEQVGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1	1	ļ	DWAKYFKGKKIHGBIDIKVEQAEFSDLNLVAHANGGFSVDMEVL
	1		RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
- }	ļ		VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
j	i i		EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
ĺ			KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
	1		MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
1	j		VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR
1			GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP
ľ	1		QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP
ł	1		ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
ĺ			ATRQTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
4	! !		AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
1	j ļ		AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
<u> </u>			LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
1	i 1		SLIMDSPRAGTHOGPLDAETEVGADRCTSTAYOFORDOVEOVCV
			QAPLS PGLPAMGGPGPGPCEDPAGAGGAGAGGGPDT.VTVTVCCA
1	}		FTVALRARRGADLSSLRALLGOALPHO\ AOT.GOT.SVT.A DCEDGU
	1		WVP1PEEESLQRAWODAAACPRGLOLOCRGAGGPPVI.VOVIDOU
			SYSAQGPEDLGFRQGDTVDVLCEVDOAWLEGHCDGRTGTFDKCF
6047	49		VVPAGPRMSGAPGRLPRSQOGDOP
""	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
			KGGRVVIFQREPESKNAPHSOGEYDVYSTFOSHEPEEDVLKGLE
1 1	'		LEBKINKIKWLPOONAAHSLISTNDKTIKIWKITEDDKDDDGUNI
!			LKDBEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
1			INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
1 1			NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
1 1			HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
·	1		TVKVWDL\NMBARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
1 1	1		WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV LKPRRVCVGGKRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
	1	İ	TNNLYIFQDKVNSDMH
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
		l l	KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS
1	ļ		ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
1			EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
1 1			SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT
ł i	j	1	PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
1	ı	1	DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
	i		SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
1	1		NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKDKKKKESSKE
	1	1.	LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLINGSSDPHOSP
		1	LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTOPI.TPI.HTT/
		1 '	TONGARASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAROLVK
		1 3	EGAKKTLFPPQPQSKDSPYYOGFESYYSPSYAOSSPGALNDSSO
i	!	1:	AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
		4	IQQRPNMYMQSLYYNQYAYVPPYGYSDOSYHTHIJSTNTAYROO
- 1	ł	1 3	YEEQQKRQSLEQQORGVDKKAEMGLKEREAALKEEWKOKPSIDD
}		1.3	TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGO
1		1 2	APEGLKVKLSDASHLSKEASEAKTGAECGROAEMDPILWYROEA
		1	EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK

SEC	Q Predicted		
ID		Predicted end	
NO		nucleotide location	I WE CALCULATE CELVSTEINE DENOMARE LE RELA RELA
	location	corresponding	Grandic Acid, Faphentialanian C. Clausia
1	corresponding	to first	n=nistidine, l=1solencine v_r
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1		<u> </u>	EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
1		1	IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP
	İ		YGSKVSGGEDADKARASPSVTCKSSSESKALDILQQHASHYKSK
			SPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRT
	į.		SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQQG
201			STPSLYPPPRR
6049	215	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
- [DSDYYSPTGGAPHGYCSPTSASYG\ KAT.NDVOVOVUGURIGA OG
			IPAKAIADISYASSYHOYGGAYNRVPSATNOPEKEVTEDETTAT
			I NGKPKKVKKPRTIYSSFOLAALOPPFOKTOVLALDEDA DE NA GE
	1		GLTQTQVKIWFQNKRSKIKKIMKNGEMDDEUGDGGGDDWAGNGD
			LAPANWAPQGSSKSLSHHPHAHPDTSNACDACGVI ENGA CUMPO
6050	566		MASSINSHLPPPGSLOHPLALASCTI.V
	300	1718	KGLERTCCAMEESDSEKTTEKENLGPPMDBBLGERG GOVERN
}	i		PNIAMARAVULMGKSGSGKTSMRSTTFANVTADDTDDTCARTTT
1	1		RIDDLY INSSLISTIST OF THE PROPERTY OF THE PROP
			DUGGEDIFMENYFTSORDNIFRNVEVT.TVVFDVECDET.EPDMTV
		1	YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
ļ	l l		RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
	L		FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6051	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
		1	PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVBHSHVRFIGNLVLNLW
1	1		DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
1	ĺ		YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
	[[RESEPTECSCERTSINDETLYKAWSSTUVOLIDATION TO THE PART OF
			FARTICADEVILLEERATFLVISHYOCKEORDAHDERVICKT ****
	1		FALSCSALAASFOSMEVRNSNFAAFIDTETCNTVINGERICED CT
6052	566		FORM TELEVISION AND FOR THE PROPERTY OF THE PR
1 0002	266	1718	KGLERTCCAMEESDSEKTTEKENI.GPRMDDDLGEDGLCGLGGUE
	1		PNIAMAAAVLLMGKSGSGKTSMRSIIFANVIADDTDDIGATTA
	ļ		KIRSLQINSSLSTYSLVDSVGNTKTFNVFHSINDELGATATATA
1			DCGGQDTFMENYFTSORDNIFRNVEVI.TVIPDIFECER EVENT
i			IQSCLEAILQNSPDAKIFCLVHKMDI.VORDODDI.TRVBBEDDY D
ĺ		}	RESEPTECS CERTS I WDETLY KAWSS TO VOLT DATE OF THE PARTY DATE.
l	1		FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
		j	FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
6053	201	1704	PSAATLINIRNARKHFEKLERVDGPKQCLLMR
	1		KGTEMNKSRWQSRRRHGRRSHQQNFWFRLRDSEDRSDSRAAQPA HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG
	1	1	HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
	1	i i	THE STATE OF THE PROPERTY OF T
		1	RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM
	1	1	ABNULETNIKKV\NSVCWASLNHLDSHILLCLMGLAREDGGARLE
]	i	PASEFVNSHPAGIDRPG\MLCSFRTDCAWCCAWCTMTCANDIONO
	1	1	TGUSKKVLLTNVVTGHROSFGTNSDVI.ACCEALMADIL ENCORG
	1	j '	GELFALDURCGNOGKGWKATRLFHDSAVTSUPTIONFOUT MAGE
		1 :	PAGKIKLWULRTTKCVROYEGHVNEVAVI.DI.HVHEEDGII INNIG
]	1.	WDC1TR1WSDHDARDDRTIPSPYPASKADTPSVAFSSPI CCSPC
6054	1		APGLLMAVGQDLYCYSYS
	-	1054	PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH
		1 '	NUSSSQUEENFFFRRORDISHSIVI,PAAVSQAHDUDVUTVUDDV
		į '	VITGIVPDWGDSIEVKNEDOIOGIHOACOLAPHULLI ACCET 101
		J 1	DMTTEETDALVHRETISHNAYPSPLGYGGFPKSVCTSVNNUT CIL
		1 0	#I PUSKPLQDGDIINIDVTVYYNGYHGDTSETELUGNUDECCVV
,] 1	VEVARRCRDEAIAACRAGAPFSVIGNTISHITHONGFOUGDUE
		įv	GAGIGS FRIGHPEIWHHANDSDI, DMREGMAFTTEDTTTECCOR
	·	F	KVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA
			•

SEQ	Predicted	Predicted end	Amino acid coment as being
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
6055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISOSAGPPPGTLOCSALHHDD
1		Í	GCANCSRFCRDCSPPACQCHTHVFPGNALNGVOPPELSRTLALT
1		ľ	SSREPPRKKKKSQTETGKERERTSFLTOGGKRFELOHGLAGICM
1	1		TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNKDW
ļ			WWGQIDDEEGWFPASFVRLWVNHEDEVEEGPSDVONGHLDPNSD
ļ			CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKOC
İ			RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKOYNNDDPHT.
1			SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYOHFF
1			EACRLLQQMIDIA\IDGFLLTPVQKICKYPLOLAELLKYTAODH
]			SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAOWOASVLDWE
	1		GEDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK
ŀ	1		KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFKLH
			NKETEEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFEISE
ľ			NOKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYLVP
6056			\DGIAQSQVFEFTEPKRSQSPFWQNFSRLTPFKK
0030	43	3358	SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLSSLPPPPSRA
			LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK
			YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPIQQ
1			MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYEDL
			ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE
1		•	EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGEP
			KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISPSV
ì			LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT
1			VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP
			KADEEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNTEA
			SSEBESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA
	1		YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS
. •			SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS
			IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI
1 1	i		EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHCAI
			CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF
1 1			IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH
	1		EICDGWLCARCKRNAWTAECCLCNLRGGALKOTKNNKWAHVMCA
1 !			VAVPBVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA
1		i	CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV
1			NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV
			MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG
1 1	1	i	AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF
			VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKXSQCNIF
6057	1	853	LSGTY
1 1	-	0.53	FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ
1 1	ļ	j	GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS
1	[}	RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS
1		Į	ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR
1 1	1	i	TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR
1			LVQKVCPDYNYHSDTPYYPSG
6058	i	986	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLFKRRARVGSP
1 1			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
		ļ	VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
		ĺ	ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
			PTPLTHHNTGLSEALE I LAEAAGFEGSEGRLLTFCRAASVLKAL
	1		PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/
1	j		RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP
<u> </u>			SREAGPWASLNCTLDPSASTP
6059	2	3650	QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT
1 1	1		QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH
			SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS
		İ	RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK
		1	ehlaksekbakkddfmcdycedtfsqteelekhvltrhpqlsek

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV
	İ		\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
1	1		BRGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
1			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
			SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
			VOPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
i			KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
i			FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH YMTTSTHYVCESCDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L
			CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
			VHVKHSHLGNPAKAHKCIFCGETFSTEVBLQCHITTHSKKYNCK
			FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
}	1		PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME
1	ł		VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE
			NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
	1		TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMQTVT
ł			STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR
1			SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV
			PRKKTYQCIKCQMTFENEREIQIHVANHMIBEGINHECKLCNQM
1			FDSPAKLLCHLIEHSFBGMGGTFKCPVCFTVFVQANKLQQHIFA VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
6060	2145	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
1			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
			DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
i			LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
			GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
-			HHGFDHFYGMPFSLMGDCARWELSBKRVNLEQKLNFLFQVLATV
1			ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
Í	ļ		DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV
	•		SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
1			EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIPRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
			QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR
1 .			GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
1 :			LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
			LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ
6061	110	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN
			VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK
1 1			ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS
	ì		VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
]			HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNBTGSTALSIA
1 1			RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRORTVLN
1 1			PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
1 1			KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
1			LALHRRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
	ľ		LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
			TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1 1			EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
	1		LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
;		İ	EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
1 !			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
	1		LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
1 1	i i		TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
]]		ł	EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
<u> </u>			LRICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	1	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-		residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	1	\=possible nucleotide insertion)
1			EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
ł	1		INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
L	1		YPYCYQGGRVICRVIMPCNWWVARMLGRV
6064	913	311	NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG
1			TTCCVPINATION TO THE TEMPT TO T
[TTSGKRVVYVDGKEEIRKEWMFKLVGKBTFYVGAAKTKATINID
į.			AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV
1			LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
6065	1153		SSG\KRKEGIIHTLIVDNREIPEIAS
0003	1153	641	MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLRDATG
}			AEEEAPWAATERRMPGQCSVLLFPGOGSOVVGMGRGLLNVDDVD
1	[1	BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAV
			EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
6066	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
	i l		EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG
1	1		VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
	i i		CONTERGUDARU SI SERDUDI DI SA CERCENTIANI DI CONTERGUDARU SI SERDUDI DI SA CERCENTIANI DI CONTERGUDI
l	i		QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDQTCA
]]		ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR
			ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV
1			ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV
			CDPSGXTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP
1 .			SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDISMLKT
1			GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQKPFQS
	į		GSTPLHLTHRFMVWNSIGIIRCYNDEODNAIDVEFHDTSTHHAT
	i i		HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK
			EWIIDLPQNEDIEAICLGOGWAAAATSALJJRLFTTGGVOKEVE
1	1		SLAGPVVSMAGHGEQLFIVYHRGTGFDGDOCLGVOLLELGKKKK
1	I		QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMINPGLG
			NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP
1			TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
1 1	į		KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL
1 1	1		MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE
1 1	1		EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE
1			KPEIHKPGONSFSKSTNSSDVSAKSGAVTFSSOGRVNPFKVSAS
Ì	í		SKEDAMSMNEADCTNITE DYMCKGGWARDEN SOURCE
1	1		SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
1	į.		LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI
1 1	1		CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM
			IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN
6067	858	333	QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE
	336	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF
1			PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL
[GAGNIGPELIKESNANPIFMRKDTKMSFOWRIRNI, PYPKDUVSV
, l			SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T
6060			PTAP
6068	13	1730	GSKMADLANEEKPATAPPVFVFQKDKGQKSPAEQKNLSDSGEEP
	1	1	RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL
1	ŀ		PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ
	1	J	FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR
	,		PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW
	ĺ		RSPSEAADEVCALEEKEPQKNESSNASEBEACEKKDPATQQAFV
i		l	FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS
l l			STENSING DESCRIPTION OF THE OWNER OWNER OF THE OWNER OW
Ţ			SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA
İ			AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT
	ļ		GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
1	ļ		TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM
ſ	ſ	1	DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEOFOFAK
ŀ			MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGOTTGS
6060			T
6069	583	27	PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
}	į		RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMDDETN
		[IDELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR
			The same same same same same same same sam

SEO	Predicted	Predicted end	Dmino poid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
-	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
'		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
			RPALLCVLSCI
6070	478	858	IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
1	1		TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
			RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
			VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
	ľ		ARLTLGRWERAPLASQGWKSRRARRDHFSIERAQQEAPAVRKLS
1			SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
1	}		GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
1	1		VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS
Ì			ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
			FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
	1	ľ	LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
	1		ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
			QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
			YDFPPTLQDYIHRAGRYGRYGSEVPGTVISFVTHPWDVSLVQKI
	-		ELAARRRSLPGLASSVKEPLPQAT
6072	1	742	
''-	_	774	KMERTEMMPTINSQLEPKSKPFPLVSSSRWLVKRGELTAYVEDT
			VLFSRRTSKQQVYFFLFNDVLIITKKKSEESYNVNDYSLRDQLL
	1		VESCONEELNSSPGKNSSTMLYSRQSSASHLPTLTVLSNHANEK
			VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
1			AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
6073	620	0.60	CAKEITCOATIDKNVERMGRLLGLETNV
00/3	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
6074	168	12.0	LVEAIKKVKDHRGIIPNKGFLRQLLALDRRLRQGLEA
0074	100	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
			GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
1	ł		DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
			DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE
1 1			GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
1 1			QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
1 1	ļ		VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
6075	320		QKYFGTD
1 60/5	320	1091	P?TCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
1	1		KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
1 1	Ī		LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
1 1	į.		NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
	1		VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
6076	1703		QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
] """	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
į į	ļ		KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
	į		GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
Į			HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
1 1			LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
į i		İ	SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
j í			PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
[[ľ	TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
; [AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
1	ŀ		GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
			A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
			BVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ
			AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
	ł	}	GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
]		į	QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
	1		EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
	1	ļ	PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA
	l	į	VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL
		<u>-</u>	The state of the s

SEQ	Predicted	Predicted end	Design
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	Watrontonhan Varancias Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ENNMYTMENTYDYOCIANTION OFFICIAL
			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE
j	ſ		LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
- 1			GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
1			CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
l l		į.	EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ
1	ľ	1	FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS
			NGLICEGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQIC
			NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA
ı			FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD
1	1		VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
1	1		IVLIGLALLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
6078	1426	180	KSAVTTVVNPKYEGK
1		100	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
1]		GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLQVNYSLKGIVEKY
1	1		NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
			GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
Ì			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
	1 1		LAVMQAYDPEINKLNTILQEQRMAFNIABAFKDVSEPIVFLQQM
1]]		QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
1	1		LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
1			FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDICGARRIDONANTGEROOF
1 .	1	~~~	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
İ]		GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
ŀ	l J		LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
1			NLRIALLGGGKAWSDDTSQLGPDKHARDVFSLDKYAEERWEVVL HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQFL
1 1			LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSFSTLGKD
			YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL
1			SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
			MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
1 1	1		VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
		ĺ	ELL\LAHAPKLGVLVFB/NTPAKRLMVVTPAGHSDVKRFWKRQK
			HSS
6080	1	1199	IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
1	1		TLRQQCLDSGVLFKDPEFPACPSALGYKDLGPGSPQTQGIIWKR
l i	.		PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
i i	i		YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
i I		i	LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
, ,	j	ļ	EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
	ļ	j	SAAEAEAITSQKLVKSHAYSVTGVEEVNFQGHPEKLIRLRNPWG
l l]	EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR
۱.		į	QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
	<u> </u>	ļ	PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
1	1		SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
	ł		TOGREHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRIKFSY
İ	İ	1	KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT
ĺ	ļ	Ì	PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
		İ	GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLLCLCLI
		[ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1288	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
- 1		ľ	PESVGQPEEASPEEQPEEASAEEERPEDOOEERAAAAA\V\TDE
ļ		!:	LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
1]		LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
ļ		1	EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
J	j	1 3	KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
1	1	1	KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
			FVRFEHGGQDSVYWKGWFGARVTNSSVWVEP
6083	1865	309	COWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE
			ATACAGA TO CONTRACT OF THE PARTY OF THE PART

SEO	Predicted	1 2000 21 25 2	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	Wantautic, CECVSCEINE Delenantic laid n
i -	location	location	Grucamic Acid, Febbeny alanina d di
	corresponding	corresponding	n=nistidine, i=Isoleucine V-Ismina
1	to first	to first	L=Leucine, M=Methionine, N-Asparacine
į.	amino acid	amino acid	P=Proline, O=Glutamine R=Argining
}	residue of	residue of	S=Serine, T=Threonine, V=Valine
		amino acid	W=Tryptophan, Y=Tvrosine, X=Upknown +=ster
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
	1		FPELESLVPNALDYIRTVKBLGNSLDKCKNNENLQQILTNATIM
1	i		VVSVTASTTOGOOLGEREN ED TOTOGOOLGEREN EN T
		ĺ	VVSVTASTTOGOOLSEEELERLEEACDMALELNASKHRIYEYVE
	1		SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
1	1		AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
	Ţ	1	RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
-	·		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
1	1		ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
1	1		RISALLORIUS AND CONTROL OF THE CONTROL OF THE
6084	1865	200	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
	1 2003	309	KQWCAERRGLGMSLADELLADI.EEAAEEEECGCVCEREEEDA
1			DVQESTQLDLSGDSVKTIAKLWDSKMFARTMMKTERVICVONVN
1	1 1		SEVINGPVEAAPEYRVIVDANNLTVEIENRINTTUKETEDVVCVD
	i .		FPELESLVPNALDYIRTVKELGNSLDKCKNNENT.OOTLENAGEN
	1		VVSVTASTTQGQQLSEEELERI, REACDMAI, RI, MA CRUD TYPEN I
I	ł		SKMSFIAPNLSIIIGASTAAKIMGVAGGITNI.GKMDACNIMITG
	i i		AURKILSGESSTSVLPHTGYIYHSDIVOSI, PDTDDDDGVAD \ DT
1	j		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
]		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
	1		ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
Į –			RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI
			VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
1 1		,	GVARVKPGNPWKPGPATOVPP
! !	ľ		GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
1	' _j		DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT
1 1	7		QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEEEEEEDEEDEEER
1 1	[KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFALR
1	1		RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR
]	1		VIGREETGDCQKNIHLWTPTDGGSWHVDORPRYGUTPGVEDION
1 1			SPIENTVEASCSADASIRIWDIRAADSKACMITTATATATOONATT
1	l		ISWSKKEPFLLSGGDDGALKIWDLROFKSGSDVATEVOURA DIE
!		I	SVEWHPQDSGVFAASGADHOITOWDLG/IVERDDEAGDUEADDG
1 1		į	DADDPQQLLFVHQGETELKELHWHPOCPGLLVSTALSGETTEDT
6086	2419		150
1	2413	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
1 1	1	ĺ	INTOPLKEKEKQEFLEGGVGHVEMI.FRCNVI.ALVGGGVVDVVDD
[[1		NKVMIWDDLKKKTVIEIEFSTEVKAVKI.RR\ DKIMAH DOMINA
1	1		FTFTHNP\HQLHVFE\TCYNPKGLCVI.CPNSNNSI.I.A PROTEIRG
1	j		HVQLVDLASTEKPPVDIPAHEGVLSCTALNI.OCTPTATAERVON
1 1	1	J	DIRIFOTSSGHLIQELRRGSOAANIYCINFNODASI.TOVCODUO
	1	1	TVITTAALDPKRNKOSSLASASFI.PKVFSSKWSFSVFOVDCCGD
		1	CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
6087	456		DDKI
0007	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCENMPCTCTWRNWRQWIRP
1		i .	LVAVIYLVSIVVAVPLCVWBLOKLEVGTHTKAWRTAGTELLIME
	I	1:	PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSNIALKYP
ſ	1] (GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVLILEAKD
		10	QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
- 1	ĺ	1 8	CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
İ	!	1 1	EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
1		1;	EWOTUEAVATGIODELICIEMELA 3 7 7 1
)	j	12	EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEABE
1		1 -	SCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
	l	[]	DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP
6088	1684	12	TTAKISDEILSDTIGEKKEPSDKSVDS
. 1		689	ASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE
1	1	J 1	ERQRLLRCPPPPVRRSEKPNWDYHAETOAFGHPLOPWEGIDIT
- 1	1	(K	TAFVNSCYIKSEEAKROOLGIEKEAUTINI.KENOELEEOGRAD
- 1		S	QTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVAPNIAUR
I		ĮΨ	LTLSEEFPVPPAVLQQTFFAVIGALLOSSGPERTAT.PTDDETT
		T	QMTGKELFEMWKIINPMGLLVEELKKRNVSAPESRLTRQSG\A
			A) DOGMITMOD (A

SEQ	Predicted	Predicted end	
ID	beginning	nuclectide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Ī	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ŀ			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
			TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
			PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK
- 1			LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
}			PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAKKTFD
		ļ	QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKAT DCCEDIUW
1	İ		LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
-]	VSDREKIDQLQEELLHTQLKYORILERLEKENKELEKIMIOKDD
ĺ			RGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTODHI, PPIANAC
1		}	DQSAGKTSVLEMIAQARIFPRGSGEMMTRSDVKITTLSPGDULVA
ł		l	LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSDETTS
ļ	i		LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETTEGTGVAVMO
1 .	1		DPNAILLCIQDGSVDAERSIVTDLVSOMDPHGPRTTRUITEVIT
i	1		AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNGGPGTPAT
		•	REYEEEFFQNSKLLKTSMLKAHOVTTRNLSLAVSDCBWKMUDDS
			VEQUADSFRATRENLETEWKNNYPRLRELDRNETERAKNETTE
1			EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSG
1			TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
1	í i		EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI
1			SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
j	1		KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE SRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH
			FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
i			KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE
L			ALHOEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQACKIPELPVQASIL
	! !		FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
			FNLLMVTTIVLGRRFIGSIVKEASORGKVST.RPSIT.LRITTERT
	1		LTATGWSLCRSLIHLFRTYSFLNIJ./FPIJ.SVWDVHSVDART D
ļ	İ		VARISHENHMASMGPREAVSGLAKSRDVIJTIP\ PPGGGTODG
	,		CHARTPUP/PHACCLSPSLIRSEVRFT.KMDPNWpMxpvrtvccwr
i		.9.	SALIVA: VPVWFVKNTHYYDKRWSCELFIJ VSISTSVTI MOULT
			FASICULLINKAAAHLGCWOKVDPALCSNVIOHPWFFFCWWDOGV
l i]		LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSVDIDTIMIT.II
	1	,	DEGAVIVYQLYSLMSSEXWHOTISLALTI.FSNVVAPEVYIPDDI
6091	3279	412	VLGKAYSYSASPQRDLDHRFS
		7**	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG
	į		WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG
			PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
		j	VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
l			PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPO
		,	LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
	f	İ	TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
j			KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS
1	1	į	SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
ļ	1		TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSULGIB
ı	-		RRQALRGKSSPVLKKTPNKGLVOVTTHRLCRLDDSDAULDTVD3
	i	1	SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPI,SI,DChip.
}		i i	RRLSLSRSLVLNRLRPVASGGGKAOPGSPWWPSKGVPCTGGIR v
	j	i	KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSPSLASDAVO
		i	KSLALIRQARQRREKRKEYCMYYNRFGRCNRGRRCDYTHDDEWY
1		1.	AVCTREVRGTCKKTDGTCPFSHHVSKEKMPVCSYFT.KGTCSNSN
		1	CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTIJ.CPDFAPDC
i	1		ACPRGAQCQLLHRTOKRHSRRAATSPAPGPSDATAPSPYCASUG
	1	Į,	PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS
	1	i i	SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS
6092	143	3190	SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
			AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ
		1	EVPKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKVYYE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
•	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
<u></u>	sequence		VIQLIKTNKKHIHSRSTLECAYRTHLVAGIGFYQHLLLYIQSHY
			OLELOCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
1	İ		LGDLSRYONELAGVDTELLAERFYYOALSVAPOIGMPFNQLGTL
}			AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
j			_
		1	LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
ľ	į		TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL
· l	\$		LIFQMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
	l		RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
ļ	Î		PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
ł	ł		SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
Į.	İ		EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
ŀ	ł		MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
			PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
· }			LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
	ł		LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
	[DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
	i		VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
ļ	1		SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
-	İ		VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE
	İ		VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
	}	ľ	MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
I			KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
1			PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\
i	Í	,	PAAGAGAAAEAPGGOWGPASTPSLYENPWTIPNMLSMTRIGLAP
	ł		VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
j	ĺ		ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
1	ļ		YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
1	į		ASLAAPVFNYADSIYLOILWCFTAFTTAASAYSYYHYGRKTVQV
}	}		IKD
6094	23	1010	PFLRCLRGDOKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
}			VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
1	1		FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
1			RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
1			QAHVDFEAMLRQHRLSEEERRRQQQEEDEQETAALLEEARKRRL
1			LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
1			GSLGSRPPLSRLVVVKKAKADPDCSNGOPQA/APHPRSPAEQEG
1			GOPYTPDAWRVLPEPTGCIPGO
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
6035	7	1933	
			GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
1			YTIRCRPLQFQPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
ł			STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
L			EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

SEQ Predicted predicted end nucleotide nucleotide location corresponding to first amino acid segment containing signal per (A=Alanine, C=Cysteine, D=Aspartic Acid, Glutamic Acid, F=Phenylalanine, G=Glycir H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,	R-
NO: nucleotide location corresponding to first lacetion, nucleotide location corresponding to first lacetion, nucleotide location corresponding to first lacetion, nucleotide location corresponding location location corresponding to first lacetion, nucleotide location corresponding location location location location corresponding location loca	E≕ e,
location corresponding to first L=Leucine, M=Methionine, N=Asparagine	e,
corresponding to first L=Leucine, M=Methionine, N=Asparagine	
() The content of th	
LO IIISC Amino acid P=Proline, O=Glutamina D_Awrining	
amino acid residue of SeSerine TeThroprine, W. Walling	
i and the second of the second	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown, *=S	top
sequence Codon, /=possible nucleotide deletion	_
\=possible nucleotide insertion)	
VKVHTVPKPGKGADLSKPPCRKAKEIRKERKRLKLMOONF	AGEL
EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHK	EVR
VVRSSPPSSQFKATLLESYOVYKRYOMVIHKNPPDTPTES	אידים
FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVID	T.PN
CVSSVYLYYDPDYSFLSLGVYSALREIAFTRQLHEKTSQL	SYYY
MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSL	NSK
YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQ	mpe
BEAAVLOYASLVGOKCSERMIJ.FRN	WF3
6096 2277 575 QRVRAALLSSAMEDSEALGFEHMGLDPRLLQAVTDLGWSR	יייד. ד
QEKAIPLALEGKDLLARARTGSGKTAAYAIPMLQLLLHRK	ACD
VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVAN	ATOL
EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLE	TITT
DEADLLFSFGFEEELKSLLCHLPRIYQAFLMSATFNEDVQ.	T A A
LILHNPVTLKLQESQLPGPDQLQQFQVVCETKEDKFLLLY.	LIV
LSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELP	DO"
CHIISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDK	KOK CDD
EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANN	SDP
LTFVLPTEQFHLGKIEBLLSGENRGPILLPYQFRMEEIEG.	GIV
CRDAMRSVTKQAIREARLKEIKEBLLHSEKLKTYFEDNPR'	RIR
LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\Gi	CCT
PLVGRPREOSPRTHCAASSTKEDNEDDODGDDEURGDI WO	SCD
6097 1673 192 APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPQPPT	CDD
PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGI	CED
YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLI	CDI
ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGG	SKL TCO
LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPI	DOT.
RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPF	T.De
RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAIS	CUT.
DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLK	POT
RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LG	DDY TOT
PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFF	21/2
VQALSNGPWSPGPLPHLLIIPSLDGGGGGFRTGRQQGAPFG	mas
QPPPSLPGTPOO	55T
6098 168 1074 NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALK	
EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQ	חתי
RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRS	WK
NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPR	COL
\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKV	WIT
TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERF	VK
ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD	עויי
6099 168 1074 NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALK	
EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQ	מתי
RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRS	QK
NI.CDGECUI.COMPONDENTI DA NOTO	KE
NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPR	:QL
\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKV	VR
TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERF	\D
ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD	
- FVEVSGIRSKADPEPRGREIMTIAYEFRYIIIGDTGVGKSC	LL
QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQI	SF
RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDAROHSS	NM
VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKT	CN
VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTS	GP
SASQRNSRDIGSNSGCC 5101 1 1399 FEGRAMPLREVSHWLGCPDVCSWSASWCDV DALCARY CONTROL	
- PROKAMPLIKEVSHWLGCKKVCSWSASWGRLPALSARLSPLLI	FR
GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDH	PY
AELWMGTHPRGDAKILDNRISQKTLSQWIAKNQDSLGSKVKI	TF

SEQ Predicted Predicted and Inclostide location nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence s	
NO: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequenc	
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Paperline, Q=Glutamine, X=Daparagine, N=Dap	
Corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence Sescine, T-Threonine, V-Valine, residue of amino acid sequence Codon, /=possible nucleotide deletion, \	
to first amino acid residue of amino acid residue of amino acid sequence W-Tryptophan, Y-Tyrosine, X-Enknown, *-Ste Codon, /=possible nucleotide deletion,	
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto Codon, /=possible nucleotide deletion, _possible nucleotide insertion) NGNLPPIFKVLVSETPLESTQAHPNKELAEKLHLQAPQHYPDM KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFGFLIGDEAR LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRE; AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTI MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\E G\SVTEYKDLALDSASILLMVQGTVLASTPTTQTPIPLQRGG G\SVTEYKDLALDSASILLMVQGTVLASTPTTQTPIPLQRGG G\SVTEYKDLALDSASILLMVQGTVLASTPTTQTPIPLQRGG G\SVTEYKDLALDSASILLMVQGTVLASSPAPACCSESGDER KGFLNQFLEGETHLFSALNSHLLTTQFMMDDLGTMISGIESI LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGND SIKKLDKLIEGRTVSKMQLEEQVLTITSSEIFKRIKSALKNABE KGFLNQFLEGETHLFSALNSHLLTTQFMMDDLGTMISGIESI HHAYLKWISGIEBESDNIQQVLMTNNVPEAASTLVSMBELDI QESSCTHLLGFMRATVKFMULLERQVLICKTGSFEELHAUPBF PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLITER HSQKNTLFLPPLLSS/WPIQVMLTPLCKRFRYHFRGRQTTMV KPEWYLAQVLMWIGNHTTEKTQTPLDKVGSLVNARLEFS LMMLVLEKLATDIPCLLYDDNLFCHLUDEVLLFREELHSVEG GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAWV YKDITDVDEMKVPDCASTFFMTLLLVITDRYKNLPTASRKLOF LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILMAVMYISTV DADADVFFIGLOQAALEVFREQOFFSIEKTFMQMLVEK VYITQEILLANHFNEGGAAQLQFDMTNNLFPLFSHYCKRPEN KHIKBACTVLMLNVGSALTAGKDVLPQLCGSLFSHTFMQMLVEK VYITQEILLANHFNEGGAAQLGFDMTNNLFPLFSHYCKRPEN KHIKBACTVLMLNVGSALTAGKDVLPQLQGSFPAT 6103 207 2523 SENSTMTYLERFIQONEERERGVRFSWNWWSSRLEAPTRWVVF PLIFIYVVDTCMEDEDLQALKESNOMALSLLPPTSHTQLLTF MVQVHELGCEGISKSYVFRGTKDLSARQLCGMLGLSKVPVTO, RGPGVQODPPSNRGLDVSKLDMNTTDLLKQLGRDPMVPQG RGPGVQODPPSNRFLDVSKLDKNDTNLTLKLGLGLGRDPMVPQG RGPGVQODPPSNRFLDVSKLDKNDTNLTLKLGLGLGRDPMVPQG PLRSSGVALSTAVGLLECTFPNTGARIMMFIGGPATQGPGMV DELKTPSKWDDLDKDRAKVVKKKKTHFFEALANRAATTGNVI VACALDQTGLLEKKCCPNLTGGVWMGDSSTTTSLFKCTFTGVKV	
residue of amino acid sequence Codon, /=possible nuclectide deletion,	
amino acid sequence Codon, /=possible nucleotide deletion, \possible nucleotide insertion) NGMLPPIFRVLSVETPLSIQAHPNKELAEKLHLQAPGHYPDA KPEMAIALTPPQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAR LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRI QAAAGNNEDLIGEELLQLLQQYPGDIGCFAIYFINLLTLKK AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTI MLSYTPSSKDRLFLPTRSQEDPVLSITDPVPDPTIMKA\B G\SVTEYKDLALDSASILLMVQGTVIASTPYTOTPIPQRGG FIGAMESVSLKLTEPKDLLIFRACCLL QTPQATLAANGAEDSRGGEMEMPAGSIGASPAAPCCSESGDER LEEKSDINVTVLIGSKQVSEGTDNGDLSYVSAFIEKEVGND SIKKLLDKLIEGRTVSKMQLEEQVITISSEIPKRIRSALKNAR KOPLNOFLEGETHLFSAINSHLLTAQPHMDDLGTMISQIEFI HLAYLKWISQIEELSDNIQQXLMTNNVPEAASTLVSMAELDI QESSCTHLIGFMRATVKFWHKILDKLTSPEFEILAQLHWPF PPOSOTVGLISPRSAPRIFYLSTLTFCQLKLKQTSHELLITEP HSQKNTLFLPPLLSS/WPIQVMLTFLQKRFRYHFRGRRQTTN KPEWYLAQVLMWIGNHTEFLDEKIQPTLDKVGSLVARLEES LMMLVLEKLADTIPCLLYDDLFCCHLDEVVLJFPRELHSVHG GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWV YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLOF LQKDLVDDFRIFIRTQVMKEEFTRASLGFRYCALIMAVWYISTV DWADNVFFLQUQQAALEVFASNNTLSKLQLGOLASMESSVPD HNLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQS AVNSLSSSACPLLLTLRDHLLQLEQQCCFSLFKXFMQMLVEK VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLSHPYCRPPD KHKEACTVLNLNVGSALTAGKUJLPVOLQGSPPAT 6103 207 2523 ESNSTMTTYLEFTQQNEERDGVRFSNNVWESSRLEATMVVF ALFTPLKERPDLPPIQYEPVLCGSTFTCRAVLNPLCQUDYRAK ACNFCYGROPPSYAGISELNOPBELDPSSEYSVLRGP PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITF MVQVHELGCEGISKSVYFGTKDLSAGLQEMGLSKVPTO, RGPQVQOPPSPSNRGLDEVGVLDNNLTDLLGELGRNPPTOG RGPGVQOPPSPSRRFLQPVGVLDNNLTDLLGELGRNPPTOG RGPGVQOPPSPSRRFLQPVGVLDNNLTDLLGELGRNPPTOG RGPGVQOPPSPRRFLQPVGVLDNNLTDLLGELGRNPPTOG RGPGVQOPPSRRFRLDVGVLDNNLTDLLGELGRNPPTOG RGPGVQOPPSRRFRLDVGVLDNNLTDLLGELGRNPPTOG RGPGVQOPPSRRFRLDVGVLDNNLTDLLGELGRNPPTOG PLRSSGVLSIAVGLLEKCFRULDRIDLGVRVPTOG PLRSSGVLSIAVGLLEKCFRULDRIDLGVRLDRIDGRNPTOGLFRCTVGVL	
sequence spossible nucleotide insertion	μ
NONLPFLFKVLSVETPLSTQAHPNKELAEKLHLQAPQHYPDA KPEMAIALTPFQGLCGFRPVEELYTFLKKVPEFGFLIGDERA LKQTMSHDSQAVSSLQSCSSHLMKSEKKVVEGQLNLUKKRI QAAAGNNMEDIPGELLLQLHQQYPGDIGCFAIYFLNLLTLKE AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTI MISYTFSSSKDRIFLFBTGDEPVLSTYDPVPDPTTIKAN G\SVTFSKDLALDSASILLMVQGTVLASTPTTQTPIPLQRGG FIGANESVSLKLTEFKDLLIFRACCLL 70 2415 QTPQATLAANGABEDSEGDEPVLSTYDPVPDPTTIKAN E\G\SVTFYKDLALDSASILLMVQGTVLASTPTTQTPIPLQRGG FIGANESVSLKLTEFKDLLIFRACCLL 70 2415 QTPQATLAANGABEDSEGDEPVLSTYDPVPDPTTIKAN E\GKELDINTVLLIGSKQVSEGTDNGDLPSYVSAFIEKEVGND SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAB KOPLNQFLBQETHLFSAINSHLLTAQPMMDDLGTMISGIEEI HLAYLKWISQIEELSDNIQQYLMTNNVPBAASTLVSMAELDI QESSCTHLLGFMRATVKFWHKILKDKLTSDFBEILACDHWFF PPQSGTVGLSRPASAPEINSYLLTCQLLKLGTSHEILTEP HSQKNTLFLDPLLLS/WPIQVMLTDTLQKKRTRYHFRGRNQTTNV KPEWYLAQVLMNIGNTEFFLDEKIQPILDKVGSLVNARLEFS LMMLVLEKLATDIPCLLYDDNIFCHLVDZVLLFERELHSVHG GTFASCMHILSEBTCFQRWLTVERKPALQKMDSMLSSEAAWV YKDITDVDEMKVPDCAETFMTLLVVITDRYKNLPTASRKLQF LQKDLVDDFRIRLTQVMKSETRASLGFRYCALINAVNYISTV DWADNVFFLQLQQAALEVFAENNTLSKLQLGGLASMESSVFD INLLERLKHDMLTRQCUPREVKDAAKLYKKEERWLSLPSQS AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFMQMLVEK VYIYQEIILANHFINSGGAAQLQFDMTRNLFPLFSHYCKREEN HIKBACTVINLNVSGSITAGKDVLPVQLGGSFPAT 6103 207 2523 ESNSTMTTYLEFIQQNEERDGVRFSNNVWESSRLEATRMVVF ALFTPLKERPDLPPIQTSPVLCSRTTCRAVLMPLCQUDYFAK ACNFCYQRNOFPPSVAGTELNQFABLPQFSSIEYVVLRGP PLIFLYVUDTCMEDBDLQALKESMQMSLSLLPPTALVGLITF MVQVHELGCEGISKSYVFRGTKOLSAKQLQBHLGLSKVPTVV RGPQVQQPPPSNRFLQPVGKIDMNITDLLGELQRDPWPVPQG PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMV DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVI VACALDQTGLEMKCCNNLTGGYMVMODSFNTSLFKQTFQRV	
KPEMATALTPPQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAA LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNILVKRI QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIVFINLITLKK AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTI MLSYTPSSKORDFIPTRSQBDYLSIYDPPVPDFTIMKA\B G\SVTFYKDLALDSASILLMVQGTVLASTPTTQTPIPLQRGG G\SVTSYKDLALDSASILLMVQGTVLASTPTTQTPIPLQRGG FIGANESVSLKLTEPKDLLIFRACCLL 6102 70 2415 QPPQATLAANGAEDSRGGEMPJAGSTGAS PAAPCCSESGDER LEEKSDINTVPLIGSKQVSEGTDNGGLPSYVSAFIEKEVGND SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAE KOFLNOFLBGETHLFSAINSHLTAQPHNDDLGTMTISQIEEI HLAYLKKISQIEELSDNIQQVLMTNNVPEAASTLVSMAELDI QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPF PPQSQTVGLSRPASAPRIYSVLETLFCQLLKLGTSHELLTEP HSQKNTLFLPPLLISSYPIQVMLTTPLCKKFRYHPRGNRQTNV KPEWYLAQVLMWIGNHTEFLDEKCQPILDKVGSLVXARLEFS LMMLVLEKLATDIPCLLYDDNLFCHLVDSVLLFERELHSVHG GTFASCMHILSEETCFQWLTVERKFALQKMDSMLSSEAAWV YKDITDVDEMKVPDCAETFFMTLLLVITDRYKNLPTASRKLOF LQKDLVDDFRIRITQVMKEETRASLGFRYCATLNAVNYISTV DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFD INLLBELKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQS AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLEKIFMQMLVEK VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPEN KHIKBACTULNLNVGSALTAGKDVLPVQLQGSFPAT 6103 207 2523 ESNSTMTTYLEFIQONEERDSVRFSMNWFSSRLEATRMVVF ALMFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAK ACNFCYQRNGFPSYAGISELNQPAELLPQFSSIEVVLRGP PLIFLYVVDTCMEDEDLQALKESNQMSISLLPPTALVGLITF MVQVHELGCEGISKSYVFRGTKDLSAKQLQBMLGLSKVPVTQ RGPQVQQPPSNRFLQPVQXIDMLIDLLGELQRDPWPYQGI PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMV DELKCFPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVII VACALDQTGLEBMKCCFNLTGGYMVMGDSFNTSLFKQTTQRV	NTLT
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HLRKATCLIGRS IGLAYEGKCIKASCEDIOCTGGKKCLMDFKV CRGRCSLCDLCDDSSBEPVCASDNATYASCAMKERACSGY LLEVKHSGSCNS ISEDTEEBEBEDDONSPPISSILBW SRCSSFRFEFGGGGK/LSPSEHRKWVEVFKACDEDHKGYLSRE DFKTAVVHLEGYKPSKIEVDSWMSSIMPNTSGILLEGFLNIVKK KKEAGRYKNEVRHIPTAFDTYYRGFLTLEDFKKARGVAPKLEE FTALEVFERV\DDSS\DGUSSBEPFMSASRFQSPTTPN 6108 3 1348 GSSLRFSPFRVPSGSKYFCPVPPGGGGLFSPFMSASRFQSPTTPN CLPRKYMKHRKDDGPFSKGDEADVTPVMTCVFVVMCCSMIVLL YYEYDLLVYVVIGIFCLASATGLYSCLAPCVRELP\SASAGESA LLAPTIPNSLPFHKRKDDGPFSKGDEADVTPVMTCVFVVMCCSMIVLL YYEYDLLVYVVIGIFCLASATGLYSCLAPCVRELP\SASAGESA LLAPTIPNSLPFHKRDGSFMEXPGAPRLLLALDWAVNVMGVPHNSDL MAWVLQDALGIAFCLVMLKTIRLPTFKACTLLLLUFLYDIFFV FITYPLTKGGSIMVEXPGPSANTLALDWAVNVMGVPHNSDL ALCDRPPSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI AYGVGLLUTFVALALMQRGQPALLYLVPCTLUTSCAVALMERREL GVFWTGSGFAKVLPPSFWAPAPDADGPPGNSATPLSEGPSEE PATSWPARGSPJSKRTSEEMGAGAPMREPGSFATSLSEGPDSAGPS PYUTQFGASA 6109 1 1381 CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVFSALRAAMLY LETYLEMIEQLJPMDLLBDRTFEMERBULQVQNAMDGLEGRVSEFF MNAKINKPENRESQMSIKKDYKALEDADEKVGLANOIYDLUD RHIRKLDGBLAKKYMBLEADMAGTET LERSILEDTPSQDVSN HHAHSHTPVEKRKYNFTSHHTTUTHIPEKKFKSFALLSTTJFSNA SKENTIGCRNNSTASSNAYNVNSSOPLGSVNIGSLSGGTGAG GI\TMAAAQAVQATAQMKEGGRTSSKASYEAFRNNNFGLGKFF SMARRTVCYSSSSALMTTITONASSNADSRSGKEKNNNKSSS QQSSSSSSSSSSSSSSSSTVORSISGOTTVVPESDISNGQVOVT YDPNSFRYCICNOVSYGENVGCDTQDCPIEWHYGCVGLTEAPK GKWYCPQCTYAAMKKRGSRHK ACKSWSCPQCTYAAMKRGSRHK ACKSWSTTISSGSGGFSPSPLALIAATCSRTESINENSINS QGPSGGGTGELDLTATGLSGGANGWGINGGGNGGGNGGGNGGGNGGGNGGGNGGGSSSFTMSNNSSSSSTMGGBSGSPSPLALIAATCSRTESINENSINS QGPSGGGTGELDLTATGLSGGANGWGGNGGGNGGGOPTS VARNATLTPSSAGVTISSGGQEGSPYTS GTTISSASLVSGASSSSSFFTNNNSYSTTTTSNMGIMNFTTIG SSGTMGGNGSSSSNTRYNSSSSPFTNNNSYSTTTTSNMGIMNFTTIG SSGTMGGNGGSSSSSTMGGNGGSSSSFTTMSSTAGAGGTAFTQAGUVOUPT VINADLSSMGGGSTFTTQA 1SQGLTGHAGGGGTHTATVATAGGTYGVYTNVP VALNANITLTLPFWSVCKKRFGGGSASALNTGMGVSWOTLOLOQULO VONPGAGTITARMGGUSGASSSSFFTNNNSYSTTTTSNMGIMNFTTIG SGGTMGGNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		Ì		
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QGPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG SSTNGSNGSESSKNRTVSGGQYVVAAAPNLQNQQVI-TGLPGVMP NIQYQVIPQFQTVDGQQLQFAATGAQVQDGSGQIQIIPGANQQ IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSESGSQPVTS GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNFTTSG SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKEGE Q\NQCTQAAPKSLSRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA ISQETLQNLQLQAVPNSGPIIRTPTVGPNGQVSWQTLQLQNLQ VONPQAQTITLAPMGQVSLGQTSSSNTTLTPIASAASIPAGTVT VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH GAQLGLHGAGGDGIHDDTAGGEEGENSPDAQPQAGRRTREFACT CPYCKDSEGRGSGDPGKKKQHICHLQGCGKVYGKTSHLRAHLRW HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK RFMRSHLISKHIKTHQNKKGGPGVALSVGTLPLDSGAGSEGSGT ATPSALITTNMVAMBAICPEGIARLANSGINVKEGGQFCSPINT				
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VONPOACTITLAPMOGVSLGOTSSSNTTLTPIASAASIPAGTVT VNAACLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH GAQLGLHCAGGGGGHDDTAGGEEGENSPDAQPQAGRRTRREACT CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK RFMRSHLLSKHIKTHQNKKGGPGVALSVGTLPLDSGAGSEGSGT ATPSALITTNMVAMBAICPEGIARLANSGINVKEGGQFCSPINT				
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atpsalittnmvameaicpegiarlansginvkeggqfcspint	 			
				<u>-</u>
SANGF		1		
	l			SANGF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
6111	1637	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG
1 0111	103/	/9/	
į,			SVEAVARLKRSRLKVRFCTNESQKSRAELVGQLQRLGFDISEQE
			VTAPAPAACQILKERGLRPYLLIHDGV\ASEFDQIDTS/STPNC
			VVIADAGESFSYQNMNNAFQVLMELEKPVLISLGKGRYYKETSG
			LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHQ
1			AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDEHHPEVKADG
			YVDNLAEAVDLLLQHADK
6112	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK
6113	1779	567	WEGRSWAACGVNLQGAWGERSGVRASEAESPGKRADVSWWSRQL
			ETMVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVL
f l			TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSQHIIPLEEVT
			LELLPETLQAKNRWMIKTAKKSFVVSAASATERQEWISHIEECV
			RRQLRATGRPA\STEHAAPWIPDKATDICMRCTQTRFSALTRRH
1			HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRELAAQQRK
1			EEAEEQGAGVPRAASHLARPICGRPVEMIMTPTRTRRAAGTATG
1 1			PAAWSSTPRGWPGLPSTADPRPAEHLSPSQLHCPGPQEGSSRSC
			PGLRDPIPWWQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPFR
<u> </u>			KPQNTHRSW
6114	818	245	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
1			RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAEOVOC
1 1			GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP
			HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSQVT
			GRPQWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
			SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
6116	595	1430	TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKEBEDESYTPVO
]			AARPOTLNRPGOELFROLFROLRYHESSGPLETLSRLRELCRWN
) [I		LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L
	,		WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL
			ASPLRSSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE
1 1			GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN
L			LYRDVMLENYRNMASLGK
6117	1433	222	VGVPSPAPPCSWBVGPGGGWTPGILKEGQGGRRTPLLLLATRTR
			GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA
<u> </u>		i	SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV
1			NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM
1	ļ	i	VWNSEEIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN
[TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK
1 1			\EQLKQI\PTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY
[HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDR
į į			GEPROHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL
			SPPSSPVILV
6118	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK
			KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK
1 1	1	ł	EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK
]	1	ĺ	NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
, !	1	ļ	DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKODSOP
] [į	[ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA
]	1]	II
6119	1217	462	DPRFVTENTTKAPAOERTTOPRSSREGTLRSTMEYLSALNPSDL
			LRSVSNISSEFGRRVWTSAPPPORPFRVCDHKRTIRKGLTAATR
1	ĺ	Ĭ	QELLAKALETLLINGVLTLVLEEDGTAVDSRDFFOLLEDDTCLM
	I		
l i		4	VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR
	1	i	DI MOOI MILLIAMENTA VANCONDOCA LABORATANI PROPERTO !
	Ì		DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence	Bequence	\=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVEAVR
8120	763	1,3	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR
	1	İ	SSRAGLOFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
}	1		
ĺ			ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQG
		L	G\VLPNIQAVLLPKKTESQKDEGANDP
6121	1612	107	FVRAQARGSROPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
1	1	ĺ	
			KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS
1	}		VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
-	ļ		QLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAE
	1		MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE
1	1		ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
	1		TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
1	{		PDINIYOLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPG
l .	ł		SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH SLIEDLILLE/AMRROHOSILRERSQREIRRVSLLNALLRSHT
i		ŀ	LCFVSCVNLSYWKFCSVFV
		2324	<u> </u>
6122	2	2324	RFRKMADGGAASQDESSAAAAAADSRMNNPSETSKPSMESGDG NTGTOTNGLDFOKOPVPVGGAISTAOAQAFLGHLHOVQLAGTSL
1			
į			QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA
,			GGQITGLTLTPAQQQLLLQQAQAQAQLLAAAVQQHSASQQHSAA GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV
1			LVHPTTNLQPA\OFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN
ŀ			
ŀ		1	LLQSQPRI\TLTSQPATFTCTIAATPIQTLPQSQSTPKRIDTPS LEEP\SDLEELEOFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
		ŀ	FSPTTIFRFRALNLSFKNMCKLKPLLEKWLNDAENLSSDSSLSS
1		1	PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\QKPTS
1	}	ł	EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP
Į.	1		IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS
ĺ		İ	VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA
ł		1	SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG
l			AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
1			GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA
	1		PNIVTAPLFLNPONLSLLTSNPVSLVSAAAASAGNSAPVASLHA
1	}		TSTSAESIQNSLFTVASASGAASTTTTASKAQ
6100		2944	HILHRWFGTDMOMINFTTGEFQLTEACPYLGTHSEESRFGILHL
6123	3	4344	HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
1	1		ARELLKYGGRLPGAGGSLRFKYPESTLMDCRRQLKDSKQILSIT
1	1	1	KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT
		l	SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL
ŀ			PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM
	1		EFMKTRORONASSSSOONNGPMDVISPHSYKSNCKNFLDTYGPS
1		1	DKGRGKNCLPVNTPOSRIONAAKRSPATYGHSQKKHKCSVYYSK
1	1		HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI
			SLRYASGINVNLOKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
			MKEGIOTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL
	1		PRNSPQYHOPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK
1	1		PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
1	1		ONLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
1			SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK
1	l		KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
1			VDAOHFLPAGDSVSONDFPSEAPISLNLSHNICNPMTGNSLPQY
1]		AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE
i			NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAPP
I			EENMYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
1			QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN
	L	L .———	ALEGGME THE LEMONICH OF THE LAGORATING CETT

SEQ Predicted Predicte	d end Amino acid segment containing signal peptide
ID beginning nucleoti	de (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO: nucleotide location	
location correspo	
corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
to first amino ac	
	, , , , , , , , , , , , , , , , , , , ,
1	
amino acid sequence	
sequence	\=possible nucleotide insertion)
	PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTT\A
	NRNANFPLSRDSSYCGNV
6124 1573 236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
	GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK
	GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF
	SKDHKCSLVFYILSPLNLNSIPDIBOPNVASATKKFSYKLVKTG
	SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV
1 1	SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPQSAL
	PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPCPSEPPA
	RPGAASWGPTPGG\PSAPPQEEAEAAAAGGPHFLDPVFLSTKS
1 1	HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV
1 '	
	PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVE
6125 1 904	PSLTPES
6125 1 904	The state of the s
	EARHSYHRSHYDPPPSRQAGGLSRFFGARSHRGALMDSQQASGT
	IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
	TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEEL
	PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKIALETERPPQV
	EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI
	FTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
6126 1224 389	RLLSEAPCPRSRRRFQMNPEWGQAFVHVAVAGGLCAVAVFTGIF
	DSVSVQVGYEHYAEAPVAGLPAFLAMPYNSLVNMAYTLLGLSWL
	HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRRAAVLDQ
	WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH
	PQGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS
	CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL
	THENTHPREHPSGGKTR
6127 1335 463	
	IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD
	GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQIWRKYDA
]	DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR
	NKDGRLDLNDLARILALQENFLLQFKMDACSTEKRKGDFEKIFA
1	YYDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKFREILL
	RHCDVNKDGKIQKSELALCLGLKINP
6128 2511 843	
543	The state of the s
	SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSRRAPPSEGTRR
	GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA
	MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
	TRCLPGHKEEEDGEGAGPGEQGGGKLVLSSLPKRLCLVCGDVAS
	GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKAC
	QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
	FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD
	GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS
	VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGLGELG\
1 1	AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS
	SCEKLLHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAG
	KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD
6129 1764 771	
	HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM
]	KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA
]	CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
	CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKOEKG
1 1	KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA
	YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS
6130 3 577	

Dogiming nucleotide location corresponding to first amino acid acid acid acid acid acid acid acid	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cocation Corresponding	ID	beginning		(A=Alanine, C=Custeine, D=Acrostic A-id
corresponding to first a mino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence seque	NO:	nucleotide	1	Glutamic Acid. F-Phenylolomine o cluster
Leucine, MeMethionine, MeApparagine, Pervoline, Ocelutamine, Rehryinine, amino acid amino acid amino acid amino acid sequence Secrine, Tethreonine, Vevaline, weight of amino acid sequence Secrine, Tethreonine, Vevaline, Merrypeophan, Tethreonine, New York, Secrine, Tethreonine, Vevaline, Secrine, Tethreonine, New York, Secrine, Tethreonine, Vevaline, Merrypeophan, Tethreonine, Vevaline, Secrine, Tethreonine, Vevaline, Secrine, Tethreonine, Vevaline, Secrine, Tethreonine, Vevaline, Secrine, Tethreonine, Vevaline, Secrine, Secrine, Tethreonine, Vevaline, Secrine, Tethreonine, Vevaline, Secrine, Secrine, Tethreonine, Vevaline, Secrine, Secrine, Secrine, Tethreonine, Vevaline, Secrine, Secrine, Tethreonine, Vevaline, Secrine, Sec	İ	location	3	Halistidine Telsoleusine Vermein
to first amino acid residue of amino acid amino acid sequence Serine, T-Threonine, V-Valine, Waltherm, *-Stop Codo, /-possible nucleotide deletion, Walthylophan, Y-Tyrosine, X-Bucknown, *-Stop Codo, /-possible nucleotide insertion) PPYRKSIEV\PSSSSPANGISWTOGOTEO_VASMEDUTYKROGOT LIVYSLVNOQSPQ\DIKMEDGITRVKYSEKUPUT\LUCK\SVD\ LESSENVSSSSGRALAEBMOGPHETSAKSKTWVDELFABIUTO MWYAAQPYKDDPCCSACNIQ SPERKTISDNSHPSSWAFIFEREVOGSFPSILVENGGLOVF FRSISANRILPLAPGRIRRSSPRILFSCSSPALLLUVLGGCLOVF GVAACTRRPNVULLITUDQDEVLGMFTSKYCCHPSRPVGG FRSISANRILPLAPGRIRRSSPRILFSCSSFALLLUVLGGCLOVF GVAACTRRPNVULLITUDQDEVLGMFTSKYCHPSGRWFTS SAVVBALCCPSKASILITKKYPHHHVVNNTLECKCSSKSWKKI CENTYPALIKSKCYOTYPIAGKYNTYLTSUNGARKGENYDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENYSVDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENYSVDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENYSVDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENYSVDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENYSVDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENYSVDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENYSVDYLTDVLANVSL DFLVKSKSFEPFFMATDVAAPSHTAADVOKASHPUJG SYWALBKNSKYYNTISINGKARKGENTISTOONATOPPERLS SYNALEKANASHPUJG SYMALEKANASHPUJAGGGCIKNTYSKMUANTDJGTILDLAPOJDLANVSL STOPPERLSTAND SYWALEKANASHPUJG SYWALEKANASHPUJAGGGCIKNTYSKMUANTDJGTSCSSFACK KARTINITATATATATATATATATATATATATATATATATATA	ł	corresponding		L=Leucine, M=Methionine W=Acrossine,
sequence sequen	i		amino acid	P=Proline. O=Glutamine P-Arginine
### ### ### ### ### ### ### ### ### ##		amino acid	1	S=Serine. T=Threonine V-Valina
sequence Codon		residue of		W=Tryptophan Y=Tyrosine Y=Unlength
Apossible nucleotide insertion	İ	amino acid		Codon. /=possible nucleotide deletide
DPYRKELEV\DSSPSVAGISHTQQGTGDF\ABMRDINITKGGGC LIVYSIVNQQSG\DIRMEDGIERVKYSEKVPVI\LVGN\SVD LESSREVSSEGRALABEMGCPFMSTSAKSKTMVDELFAEIVRQ MYNAGPENDDFCSACHIQ SSPERKTSDSSHRPSHGFIFLELVGLSPFSYLCVPPSREVGGS PRISAMRLEDLAFGELRGSPFHLECVGLSPFSYLCVPSFSRVGGS SPERKTSDSSHRPSHGFIFLELVGLSPFSYLCVPSFSRVGGS GRYWALENSKYPHNITVSITGLAGFTELKYGLSPFSYLCVPSFSRVGGS GRYWALENSKYPHNITVSITGLAGFTELKYGLSPFSYLCVPSFSRVGGS SAVPSALCCSSCRSILIGEVFHNIHVVNTLAUGGLGVP GRANTPFAILSMCGVOFFF\AGKYLREYGADAGGLEUFLJGM SYWALENSKYTNYTLSINGKRHGGENYDVJUTDYLANVGL GENTFPAILSMCGVOFFF\AGKYLREYGADAGGLEUFLJGM SYWALENSKYNYTYLSINGKRHGGGNYDVJUTDYLANVGL DFLDYKSHYEPFMMTAPQ\APRISWTAPQOKAPONVFABRN KNPNIGTIKKMLIFOATGMARHGGENYDVJUTDYLANVGL DFLOYKSHYEPFMMTAPQ\APRISWTAPQOKAPONVFABRN KNPNIGTIKKMLIFOATGMARHGTAPQOKAPONVFABRN KNPNIGTIKKMLIFOATGMARHGTAPQOKAPONVFABRN KNPNIGTIKKMLIFOATGMARHGTAPQOKAPONVFABRN KNPNIGTIKKMLIFOATGMARHTAPTAPAGNAFONYDLLAFYDIKAGL BFDLOYKSHYEPFMMTAPQOKARTAPYDRIFTAPAGNAFONYDLLAFYDLAFONY GRYDGYRPDYDRYBPSHAPAGNAFTAPSOKARTAPYDRIFTAPAGNAFT		sequence	1 -	\=possible nucleotide incertion)
6131 3 1811 SPERTINSSERRALBEBREGFPRITSARKENTUNDELFABIURG MYNAAPPKUDPCCSACTIQ MYNAAPPKUDPCCSACTIQ FRISARRILLELAGGLERGSPRILLECGLEPSTYCCYPSTEPVEGS PRESISSARRILLELAGGLERGSPRILLECGLEVE GVAACTRERNVLLILTDOOGVIGMTPLEKKLIGEMATPS SAYVPSALCCESRASILIGKYPNIHHVVNINTLEGNCSSINGKI QEPHTPPALISKNOGVOTFP-VAGKVLEWYSACDLEWPLGW SYWKALEKNSKYYNYTISINGKARHGENSVDVILTDVLANUGL DPLDYKSNYEDPPRIMTARY DANSWAKLAGVENDERDVFABRU KNPHIGTUKHMITGAKTOWINSIGPLINAFRKOOTHEVARM KNPHIGTUKHMITGAKTOWINSIGPLINAFRKOOTLESUS BEDIKVPLLVRGGGIKEPOTSKILVANITYTOGSSIPIOKALIV ROWGOSLIPITAGRANITYTETODOVITIOLAGVINA TOMOGNSLIPITAGRANITYTETODOVITIOLAGVINA TOMOGNSLIPITAGRANITYTETODOVITIOLAGVINA TOMOGNSLIPITAGRANITYTETODOVITIOLAGVINA TOMOGNSLIPITAGRANITYTETODOVITIOLAGVINA TOMOGNSLIPITAGRANITYTETODOVITIOLAGVINA TOMOGNSLIPITAGRANITYTETODOVITIOLAGVINA TOMOGNSLIPITAGRANITYTETODOVITIOLAGVINA POVEDOPPOVATOPPOVATOPPOVATORITORIAGVINA ARGAMEPERITYTOLACTIOLAGRANITYTETODOVITIOLAGVINA POVEDOPPOVATOPPOVATOPPOVATORIAGVINATULOGUSEPPALESS FREELGRAQVIMBUNINATLEPETOOPPALSSEPPETOSVESGW ARGANITYTOLAGORITORIAGVINATULOGUSEPPALSES FREELGRAQVIMBUNINATLEPETOOPPALSEPPARSELSGENGENTY FREELGRAQVIMBUNINATLEPETOOPPALSEPPARSELSGENGENTY FREELGRAQVIMBUNINATLEPETOOPPALSEPPARSELSGENGENTY FREELGRAQVIMBUNINATLEPETOOPPARSENTY VARATUNVONGLIDELGSVOLDITOPPARACVILLIGGLEGFF LHLKEFYLTIPASPAMHUNITALLELLI/IGGEBFPANNISOVENTY VARATUNVONGLIDELGSVOLDITOPPARACVILLIGGLEGFF LHLKEFYLTIPASPAMHUNITALLELLI/IGGEBFPANNISOVENTY TUNVOGGOTUPPERGEEEEEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNVOGGOTUPPERGEEPPROKESPUTSSVOLDYSOMTY TUNDOGGOT			· · · · · · · · · · · · · · · · · · ·	DEVEKETEV DSSPSVAGTSWTOOGTEOF ASMEDIT VIVEOGG
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GVAAGTRENVULLITDODEVLIGHTPLKKTKALIGEMGMTFES SANYDSALCCESRASILITELENCSSKSNOKI QENTTPATLASMOGYGTEP AGKYLNEYGAPDAGGELEVULGW SYWALEKNSKYNYTYTESINGKARKIGHSYVYDYLTDVLANVSL DFLDYKSNEEPFMWTATE VAPHSHYVDYDYLTDVLANVSL DFLDYKSNEEPFMWTATE VAPHSHYDYDYCKAPONYPAEN KNPHIGITKKWLITGOKITHNISADDYCKAPONYPAEN KNPHIGITKKWLITGOKITHNISADDYCKAPONYPAEN KNPHIGITKKWLITGOKITHNISADDYCKAPONYPAEN KNPHIGITKKWLITGOKITHNISADDYCKAPONYPAEN EPIKVPLLVAGGGIENDYSKWLANTDLOPTILDIAGYDLNK TOMOGMSLLPILAGGANLTWSDULUEYQGEGNVUTDPTCESLS POVSQCPPOCVCEDAYNTYACVITNSALMNLLYCEPDOGEVEY EVYNLTADPDQITTIAKTIDEELIGMMYYRIMMLGGCSGPTCKT POVPDGITRPPRIMFSNRGSVETTRFSKHLL ARGLLEPELIVDLLQDPKGVYEPPAEEELSKGGKKKLIPTSKO PREBELQKAQ VIMEWINATLEPELVOGEDBETTERSEDWFDGLIHHL FORLAALKLEAEDIALTATSOKIKLITVLEAVYRS COSMSGRE SGA/WSSITHNOLISTLHLUALAKREPDLAPTNUVGVETIT ESTKSGLKSEKLIVEQLTEYSTDKDEPPKDVFDELIFLLABENVAA VKRALVNEYNOKLDRIGISGVONIDTOPPADLEPTNUVGVETIT ESTKSGLKSEKLIVEQLTEYSTDKDEPPKDVFDELIFLLABENVAA VKRALVNEYNOKLDRIGISGVONIDTOPPADLEPTNUVGVETIT ESTKSGLKSEKLIVEGLTEYSTDKDEPPKDVFDELIFLALBENVAA VKRALVNEYNOKLDRIGISGVONIDTOPPADLEPTNUVGVETIT ESTKSGLKSEKLIVEGLTEYSTDKDEPPKDVFDELIFLALBENVAA VKRALVNEYNOKLDRIGISGVONIDTOPPADLEPTNUVGVETIT ESTKSGLKSEKLIVEGLTEYSTDKDEPPKDVFDELIFLALBENVAT VKRALVNEYNOKLDRIGISGVONIDTOPPADRIJTNUVGVETIT ESTKSGLKSEKLIVEGLTEYSTDKDEPPKDVFDENVETYNSTOKT TOVSVSQOPASPVPLANARVAGHLSTTVSSGAONSDETK KTUVTLIANNAANPLVQOGGCPLILTONPAPGLIGTMUTQPVLR PVOYMONANHVTSSPVASQPIPTTTQGFPVRNVRVRVNAMNOVG IVLNVQCQGTVRFITITPATTTTGFFVRNVRVRVRNAMNOVG IVLNVQCQGTVRFITITPATTTTGFFVRNVRVRVRNAMNOVG IVLNVQCQGTVRFITITPATTTTGFFVRNVRVRVRNAMNOVG STMPYRFTTNIFTTUFATTTTRSTTYPOSGSGOTITSTTTTT TATQFTSLGGLAVQSFGGSWATNSKLAPSFPSPAVSIASPVT VKREGVTGESSMEVSSSTPFDLQGGGRKACKLENVTSLIMILDDFFY GRDGSKVAGLINTPRVATSRCCHCTKLLKINIRRMMKHHYE LDQOMSEVDGHOHTCHCHCTGFFFFFFORGERVLTGLENGT KLCEMAFSSEPLILOMMATHLICHTURFFFFFFTOK KLCEMAFSSEPLILOMMATHLICHTURFFFFFTOKALLOPSTTYC KLCEMAFSSEPLILOMMATHLICHTURFFFFFTOKALLOPTURFTTYTC KLCEMAFSSEPLILOMMATHLICHTURFFFFFTOKALLOPTURFTYTCH CKCKGVOPANNYGVROCHTCHCCHCTGAGACHTURTURFTYTCH CKCCGRAPANHYMNINTPRISSKVALAFINSVTSLIKECTOT	ł		}	PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLAU GGCT CVP
SAVVPSALCCEPSRASILTGKY PRINHHWUNITLEGINCS SKSHOKI QENTTPA LIRBMCCYDTFP\ASKIRCH QADPAGGLERUPLGW SYWYALEKNSKYYNYTIS INGKARHGENYSUVITDVLANVEL DFLDYKKNSKYNYTYTS INGKARHGENYSUVITDVLANVEL DFLDYKKNEPEPPMTATPQ APRISHMAPQYCKAPGONYPAPRN KNFNIHGTNKHALIRQAKTPMTNSIGPLDNAPRKHWOTLLSUD DLUVKLVKUKLEPTGELHNYTI SYTDANTAQOFSLPIDKRQLY EFDIKVPLLVRGPGIKENOYSKHLVANIDLGPTILDIAGYDLMK TOMDOMSLLPILRGASNLTWRSDVLVSYQGEGRUNTDFTCESLS PGVSQCPPDCVCEDAYMNYTACVETMSSLMNLQYCEPDDGDEVEV EVYNLTADPDGTTNTAKTIDPELIGKMYNYELMINGSCSGPTCAT PGVPDGVAFPDPRMFRNRSUVTRAFSLMNLQYCEPDDGDEVEV EVYNLTADPDGTTNTAKTIDPELIGKMYNYELMINGSCSGPTCAT PGVPDGVAFPDPRMFRNRSUVTRAFSLMSLOYCESGM AWEAMPSEPLYDLLQD KGVEPPPAEELSKGGKKKYLPPTSRCD PKFEELQKBA\UNEMINATLIPEHIVVRSLEEDHFDGLILHHI FORLAALKLEABDTALTATSQKHKLIVEANNS\CYRRSGRP SGA\WESISNKOLLSTHLLVALAKRFOPDLSLPTNQVSEVITI ESTYSGLKSEKLVSQLICTSTSKOREPPERVOPDELFKLAPERVOA VKRAIVNFWNGKLDRIGLSVGRUDTQFADGVILLLIGQLEGFF LHLEFYLLPPNSPAEHHUVTLALELL/TGGRPAQLDC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHADTFHGAPN VKRGAIVNFWNGKLDRIGLSVGRUDTQFADGVILLLIGQLEGFF LHLEFYLLPPNSPAEHHUVTLALELL/TGGRPAQLDC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHADTFHGAPN VKRGAIVNFWNGKLDRIGLSVGRUDTQFADGVVEDYNSVEDYN TVUSVQQPVSAPVPLAARSVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNAGNFLVQGGGGFLILTONPAGGIGTHVTOPVLR PVQVMONANNTYSSFVASOPIFTTTGGFPVRNVRPVONMNOVG IVLNVQGGTVRPITLVPAPGGGGFPLINTONPAPGISTTP TATQPTSLGQLAVOSPGOSNGTTTPKLADSPFSTYDT TATQPTSLGQLAVOSPGOSNGTTTPKLADSPFSTYDT TATQPTSLGQLAVOSPGOSNGTTTPKLADSPFSTYDT TATQPTSLGQLAVOSPGOSNGTTTPKLADSPFSTYDT TATQPTSLGQLAVOSPGOSNGTTTPKLADSPFSTYDT TATQPTSLGQLAVOSPGOSNGTTTPKLADSPFSTYDT GROGKVAQLINTPKVATSFRCHCKKKKINLADSPFSTYCT KKEGMTYCCCPENVEYNGKYGKSLDSEPSVPSAAKVPSPKATKPMAK GGGRTTGGESSMKVTSSITVPDLDDGGRKICPRCNAQPRVTBAL GGGRCYACCPENVEYNGKYGKSLDSEPSVPSAAKVPSFKXTLAVSA /THPSSTPIPALSPPY/TRVEPNREWODAVCTRLIMLUDDTYY GRDGGKVAQLINTPKVATSFRCHCTKKRIKNINFHMKKHNUZ LDQGMGEVTPVSSMDTTPSAALGAAGATAPSEPLLTPTLAPSTYC KLCEMAFSSEPLLCHMKNTHKTPEKRYROGHENGKYNYNYN CKKCRVQPLPAKKKEHLUNHALTTFRKKRYNYNS IQGAMAKHUNTHPSHRSSSILPRERPQGHTMEHGKR NYNYNYN POSPPNHAMATUNSSYGIKLACTSCTVT SVGDAMAKHUNTHPSHRSSSILPRERPUTCOVCYNSTILT	1	1 .		GVAAGTRRPNVVLLLTDDODEVLGGMTPLYKTYAL TGEMGMTPG
QEPNTFPAILSMCYQTFFYAGRUAGDAGGLEHVPLGW SYMYALSKNSKYNYTLSINGKARHGNYSVDYLTDYLANVEL DFLDYKSNFEPFMMTATP\APPKSVDYLTDYLANVEL DFLDYKSNFEPFMMTATP\APPKSVDYLTDYLANVEL DFLDYKSNFEPFMMTATP\APPKSVDYLTDYLANVEL DFDYKWYLKLEFTGELNNTYLFYTSDNOYHTGQFSLFTDKRQLY BFDIKWYLLVRGEFIKPROTSKMLVANIDLGFTILDIAGYDLNA TQMDGMSLLPILRGASNLIWRSDVLVSYQGEGRNVTDPTCPSLS PGVSQCFPDCVCEDAYMNTYACVRTMSALMNLQYCFEDDDGWFW EVYNLTADPDQITTIALTIDFELIGKNYNYLMMLQSCSGPTCAT PGVVDGVRFPDRLMFSNRGSVRTRRFSKHLL AGGLEPGLVPEDDRFRFNLDFPGTGSFALSFELFSCVSSGN AWEAMEPEFLYDLLQLFKGVEPPALEELSKGGKKKYLPPTSRKD PKFFELGKAA\UMBENTALTLPEHLIGKNYLEMDLFGCLIHHL FQRLAALKLEABDTALTATSQKHKLTVULEAVMRS\CSWRSGRF SGA\WSSJTNKDLLSTLHLVALAKRFQPDLSLFPHVQVSWITT ESTKSGLKSEKLVSQLTEYSTDKDEFPKOVPEDFFKLABFKVAA VKRAATVNFVNGKDRIGLSVQNLDTQFADCUTLLHIGOLEGFF LHLKEFYLTPNSPABEMHAWTLALELL\TGRCAPAQLEC\LALK\ TIVNKDAKSTLRVLYCLFCKHTQXAHRDTPHEARAN VKRAATVNFVNGKDRIGLSVQNLDTQFADCUTLLLIGOLEGFF LHKKEFYLTPNSPABEMHAWTLALELL\TGRCAPAQLEC\LALK\ TIVNKDAKSTLRVLYCLFCKHTQXAHRDTPHEARAN VKRATVNFVNGKDRIGLSVQNLDTQFADCUTLLLIGOLEGFF PVGGMADTDLFMGEEBELBFWQKTSDYVEDSVEDVNSVDKT TVSVSQQPVSAPVPIAARASVACHLSTSTTVSSGQNSDSTK KTLVTLIANNAGNFPLVQGGGGPLLITONPAGGGGTWATPSTSTTP PVQVMQNANNHYTSSPVASQPFFTTTQFPVRVRVPQNAMNQVC IVLNVQGGTVRPITLVPAGTGTPVRVRVPQNAMNQVC IVLNVQGGTVRPITLVPAGTGTPVRVRVPQSSGQNTKSTPSTSTTP TATQPTSLGGLAVQSSGGSNGTTNPKLASFSFTDPSTSTTP TATQPTSLGGLAVQSSGGSNGTTNPKLASFSFTDPSTSTTP TATQPTSLGGLAVQSSGGSNGTTNPKLASFSFTSTTP TATQPTSLGGLAVQSSGGSNGTTNPKLASFSFTSTTP TATQPTSLGGLAVQSSGGSNGTTNPKLASFSFTSTTP TATQPTSLGGLAVQSSGGSNGTTNPKLASFSFTSTTP TATQPTSLGGLAVQSSGGSNGTTNPKLASFSFTSTP TATQPTSLFGRESSMKVTSSTTVPDLQDGGRKICFCRAAFFWSAL GSGRTSGPESSMKVTSSTTVPDLQDGGRKICFCRAAFFWSAL VKREWTVEGNSTVPSNSCHTSFFCPCTKELKNNIRFMMHHKHUZ LDQGNGEVDGHTTCOHCVRGPSTPPOLOCHLENVHSPYSSTYRC KTCEMAFFSFPLFLGMKOTKKPGEMYDOVQVQYRSSLYSEVD VHFRMTHEDTRHLLCPYCLKVPRXGGARQFBFFKKTVTTAA SKOGRTTYPVSSNCHTFSALQEAVENNIRFMHHKHKHUZ LDQGNAFKHUNTHYPSFKYLALFKNSSGIKLACTTSCTVT SKGDAMAKHLVPNFSHRSSSILPGRAUCHTGRAGAFTFVTUSSCCRYST CCSRAYANHINNHVPRSFKYLALFKNSVSGIKLACTTSCTVT SKGDAMAKHLVFNFSHRSSSILPGLAGAFTLYTHGSLCFRYDG CCSRAYANHINNHVPRSF	ĺ			SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNOSSKSHOVI
SYNYALEKISKYYNYTISINGKARHGENYSUPUITDULANVEL DFLDYKKNEPEPPHMITP PAHENDRYCKARGONYPAPEN KNPHIGTNKHALIRQAKTPMINSIOPLDNAPKRHOCTLISUD DLUVEKLVKALEFTGELHNYTI YTSDHYTGOPSIPIDKRQLY BFDIKVPLLVRGGGIKPNOTSKALVANIDLGPTILDIAGYDIAK TOMDGMSLIPILRGASNLTWRSDVIVEYQGGGRUNTDFTCBLS PGVSQCFPDCVCEDAYMNTYACVRIMSALMNLQYCEPDDGUVEV EVYNLTADPDQITNIAKTIDPELIGKMYYRLMALQSCSGPTCRT PGVPDGVKPPPRLMSPROSUPTRERSKALL 6132 96 1241 ARGLEPGGLVPBDRRFTRNLLSPGGOFPALSR LJFSCVSGK AWEAMPEPELVDLLQIB KGVEPPAERSKAUL FORLAALKLEABDIAITATSKHKLITVULEAVMRS\CSWGKKYLDPTSRKD PKFBELQKDA\UMBWINNTLDEHIVVRSLEEDMFDGLILHHL FORLAALKLEABDIAITATSKHKLITVULEAVMRS\CSWGKKYLDPTSRKD RKFBELGKDA\UMBWINNTLDEHIVVRSLEEDMFDGLILHHL FORLAALKLEABDIAITATSKHKLITVULEAVMRS\CSWGKKYLDPTSRKD WKRAI'NFVNOKLDRIGLSVUNLDTGAVULLLLIGGGEF LHLKEFYLIPNSPAEMHHNUTLALELL/IGRGPAGLDC/LALK/ TUNKDAKSTIRVULGICKGUNDATHGHADPHICLEGFF LHLKEFYLIPNSPAEMHHNUTLALELL/IGRGPAGLDC/LALK/ TUNKDAKSTIRVUNGICKGUNDATHGHADN 6133 2 4256 FURGGRADTDLFMBCGEEELEPWGKISDVIEDSVVEDYNSVDKT TTYSVSQQVSAPVPIAAHASVAGHLSTSTTVSSSGANDSDKT KTIVTLIANNRAGNEDVQGGGGLILTOMPAGGIGTWVTDPVLR PVQVMQNANHTTSSPVASGPIFITTGGFPVRNVRPVQNAMNOVG IVLNVQGGGTVBITILVAPAFGGYEVEVQVFVGNTFVRGR STHPVRPTTNTFTVIFARTITISTVPOSGSGOTKSTPSTSTTP TANGPTSLGGLAVOSSGOSONOTTSPHLASPFSPAMYSTSSTYV VKRPGVTGENSNEVAKLUNTLUNTIPSLGGSPGPVVVSNNSSAH\ GSGRTSGBSSMKVTSSIPVFDLQDGRKICPRCNAPFRVTBAL RGHMCYCCPENVEYQKKKKSLDSEPSYSPANAPSFEKTPVAS /HHBSSTPIPALSPFP/TKVPENNENVGDAVCTIKINLUDDFYY GROGKVAGUNTPFKVATSFECHCIKKRIKNIFFMHKKHVE LDQGMGEVDGHTICOHCVRGPSTFFOLQCHLENVHSPTSSTTKC KICCMAFFSEPILFICAMKUNTKYBERFYLLBLUNDDFYY GROGKVAGUNTPFKVATSFECHCIKKRINIFFMHKKHVE LDQGMGEVDGHTICOHCVRGPSTFFOLGCHLENVHSPTSSTTKC KICCMAFFSEPILFICAMKHVERY CKRCAVQFLFAKKIEKHLQHHTETPRKVSGKIKLACTSCTTVT SVGDAMAKHUVFNSHRSSSILPRGLTHIABSRGGTEDRVHDR NVKMYTPPSHFSFYLLALEKNSVSGKIKLACTSCTTVT SVGDAMAKHUVFNSHRSSSILPRGLTHIABSRGSGTERVHDR PKIRWLBRPGARAGGERUKKLRVULFRENSVSGIKLACTSCTTVT SVGDAMAKHUVFNSHRSSSILPRGRTKNAVSGGTERRVHDR PKIRWLBRPGARAGGERUKKLRVULFRENSVSGIKLACTSCTTVT SVGDAMAKHUVFNSHRSSSILPRATTANSAGGTERRVHD RKMNYNYPPSHRSSSILPRATTANGSGGTERVHDR PKIRWLBRPGARAG	j			QEPNTFPAILRSMCGYOTFF\AGKYINEYGA DDAGGI, FUIDI GW
DFLDYKSNEEPFMWTATP\ADPISSWTAADQYOKAFQNVFAPRN KNFNIKTKKHLIRGAKTPWINSSIGDLDNAPRKRWGUTLISUD DLVSKLVKRLEFTGELNNTYIFYTDDNGYHTGGPSLPIDKRGLY BFDIKWPLLVRGGGIKFONGYSKULVAUIGGFILD AGYDLNK TQMGMSLLPILRGASNLTWRSDVLVEYQGGGRNYDDTCCSLS PGVSQCPPDCVCEDAYNNTYACVRTMSALWRLQYCFEDDGEVEV EVINLITADPDGITRIAKTIDPELIGKNYKLMMLQSCSGTCAT PGVPDGVSRFDPRLMFSNRGSVRTRRFSKHLL AGGLEPGLVPEDPRRFSRLLDFGIGGOFPALISRELFSCVSGW AWEAMSPEPLYDLLQLPKGVEPPABEELSKGKKKYLPPTSRKD PKFSELGKAAVLMEANDTATPSQKHKLTVULEAVNRS\CSWRSGEP SGA\WESITNKDLISTIALLUVALAKREVDPLSLFDHYDGLILHHL FORLAALKLEABDIALTATSQKHKLTVULEAVNRS\CSWRSGEP SGA\WESITNKDLISTIALLUVALAKREVDPLSLFDHYDQLILHHL FORLAALKLEABDIALTATSQKHKLTVULEAVNRS\CSWRSGEP SGA\WESITNKDLISTIALLUVALAKREVDPLSLFPNVQVEVITI ESTKSGLKSEKLVEQLIEYSTDKDEPPKDVFDEIFKLAPSKVNA VKRALVNFUNKLDRIGLSVONLDTGYSADGVILLLIGQLEGFF HIRKEFYLLFNSPABEHHNVTLALELL/TGRGPAQLEC/LALK/ TIVNKDAKSTLRVLYGLFCKHTOKAHBDTFHBAPA 6133 2 4256 FVIGGMADTDLFMSCEEELEPWGKISTGSVESVEDPINSVDKT TVSVSQQPVSAPVPLAARASVACHLSTSTTVSSSGAONSDTK KTLVTLIANNAGNEPLVOQGGGGELLITOPPABGGIGTWYTDPVLR PVOVMONANHYTSSPVASQPFFTTTOGFPVRNVRPVQNMANNQVG LIVLNVQGGGVERFITUNDPABGGIGTWYTDPVLR PVOVMONANHYTSSPVASQPFFTTTOGFPVRNVRPVQNMANNQVG LIVLNVQGGGVFRFTTUNDPABGGGSVKTSTSTSTTP TANGPTSLGGLAVQSSGGSNGTTTSPKLAFSFSTSTTP TANGPTSLGGLAVQSSGGSNGTTTSPKLAFSFSTSTTP TANGPTSLGGLAVQSSGGSNGTTTSPKLAFSFSTSTTP TANGPTSLGGLAVQSSGGSNGTTSPKLAFSFSTSTTP TANGPTSLGGLAVQSSGGSNGTTSPKLAFSFSTSTTP TANGPTSLGGLAVQSSGGSNGTTSPKLAFSFSTSTTP TANGPTSLGGLAVQSSGGSNGTTSPKLAGSGPFDVVSNNSSAH\ GSGRTSGPESSMKVTSSIFVPDLQDGGRRICPCCNAGFKVTEAL RGMGYCCPCPENVEYGKGKSLDSSEPSARAPPSFEKTAPVAS /THESSTFIPALSFPY/TKVPENSENGDAVGTKLINLUDDFYY GROGKVAQCINFPKVATKFFFCHCTKRNIFFRMKHRIVE LDQONGEVDGHTICOHCYRGFSTPPOLOCHLENVHSPYSSTYKC KICCHAFFSFPPLGIMKHNIFFKHRKNIFFRMKHRIVE LDQONGEVDGHTICOHCYRGFSPPDLOCHLENVHSPYSSTYKC KICCHAFFSFPPLFLGMKHRIPGKRKNVTH CNKKNYEPSSRDTTFSSALGAAPATSRKKHVTGSGGTRCVHDR RKMKNYPPSHRSSSILPGRITMIAHSRRGGTRCRVHDR PSFTYNKAATNINNHVPRSKYRSAGLARDSUGTROPHDR RKMKNYPPSHRSSSILFRACHTSTANGSGTRDFUDDE LASGGGGGGWGKKSLOLCKKLRVVFLAGLCCTTROABEHFRNPQ GRAFKFURDARDGIGHTANDSSTYLERGTROWLDFLOGLIP				SYWYALEKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVST.
RNPNIHGTNIKHLIRQAKTPWTNISTQFLDNAFRKRWGTLLSUD DLVSKLVKREFTGELNNTYIFTROKYHTUGGSLP DIKRQLY BFDIKVPLLVRGGEIKPNOTTSKMLVANIDLGFTILDIAGVDIAK TOMGSMSLIP BILGSANITWESPUTYGGEGRIVTDFTCPSLS PGVSQCFPDCVCEDAYNNTYACVRTMSALMILQVCEPDDQDVV EVINLTADDPGITNTAKTIDPELLGKMNYRUMMLQSCGGTTCH PGVFDPGYRFDPRIMFSNRGSVBTRFFSKHLL 6132 96 1241 AAGLLPPGLVPEDPRFTRILLPFGIGGPFFALSRPLFGCVSGW AWEAMPEPLYDLLQLPKGVEPFABERLSKGKKKYLPPTSRXD PKFEELQKPA,VIMMINAATLLPEHLVVBSLEEDMFDGLLIHHL FORLAALKLEABDIALTATSQKKLTVVULAVNRS\CSWRSGRP SGA/WESIFNKDLLSTLHLLVALAKFFDFDLSLFTNVQVEVTIT ESTKSGLKSEKLVEQLTEYSTDKDEFPKDVPELFKLAPEKVNA VRABIVNFVNOKLDRGLSVQNLDTPFADGVILLLIGOLEGFF LHLKEFYLFPNSPARMHNVTLALELL/IGGPAQLEC/LALK/ TIVKNOAKSTLEVLYGLFCKHTGKARFDRTHGAPN FVGGAMADTDLFMCEESEBLEFFQKTSDVIEDSVEDYNSVDKT TTVSVSQCPVSAPVPLAARSVAGHLSTSTTVSSCGANSDSTK KTLVTLLANNNAGNPLVQGGQELLITONPAPGLGFMVTDPLR PVCVMQNANHVTSSFVASOPIFTTTQGFFVURNVEPVCNAMNOVG ILVLNVQGGTVPETITVPAPGTGFVEPVRVEPVQFVOFSGMTVVRPG STMPVRPTTNTFTTVIPATLTRSTVPGSOSOGTKSTDSTSTTP TAQOFTSLGQLAVSGGOSONTTNLPSFGSFSTSTSTTP TAQOFTSLGQLAVSGGOSONTSTNLPSFSFSPSVLASFYT VKRFGVTGENSNEVAKLVNTLNTIBLGCBGFPVVSNNSSAH\ GSGRTSGPSSMKVTSSIPPFLQGGKICPRCNAQFRVTEAL RGGMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFSTTSTC GROGKVAQLTNTPFKVATSIPPFLQGGKICPRCNAQFRVTEAL RGGMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFSTYTKC KICEMAFSSFLIFGDEKKLQHKKTRPKDKLGLGLKSFLYSTS GROGSCAVAQLTNTPKVATSIPPFLQGGKICPRCNAQFRVTEAL SKGOGPTTPVSSNDTPSSALQRAPLTSSMDPLPVFLYPFVQRS IQKRAVKRSVMGROTCLECSFEIPDF PNHFPTYVICSLCKRYST CCSRAYAHHINNHVPRKSFRYLLGKLGCTTFOTAL SKGOPRTVPVSSNDTPSSALQRAPLTSSMDPLPVFLYPFVQRS STATPPPPTHTHQALALPSFRSSSILPRGLWIAHSSHGGTRDRVHDR NVKNYMYPDFSFFNKAATVKSAGATPEELTPLIAPALPSPS STATPPPPTHTHQALALPFRSFRKSSILPRGLTNVDDDESSPYTOEPE LASGGGGGGGGGGGGGGKGLGSVKLTSTRUKGHTRHLTTPHARRR VKANTYPPSFFTRKAATVKSAGTERELCTTPTOAGHFRHYD RRIKRWBRRGAGGGGGGGGGGKTSTRUKHDR RRIKRWBRRGAGGGGGGGGGKTSTRUKHDR RRIKRWBRRGAGGGGGGGGGGKTSTRUKHDR RRIKRWBRRGAGGGGGGGGGGGKTSTRUKHDR RRIKRWBRRGAGGGGGGGGGGGKTGFRCHUDD RRIKRWBRRGAGGGGGGGGGGGGKTSTRUKHDR RRIKRWBRRGAGGGGGGGGGGGKTGFRCHUDD RRIKRWBRRGAGGGGGGGGGGGGGKTGTGCHUDDDLESMIVATICPTUFUT VAHTLPKOVAENBGLIF DF	1			DFLDYKSNFEPFFMMTATP\APHSPWTAAPOYOKAFONUFAPRN
BEDIKVPLLVRGEGIKPNOTSKHUNANIDLGFILDIAGVIDIAK TOMDGMSLLPILRGASNLTMRSDVLVEYGGEGRAVTDFTCPSLS PGVSQCPPOCVEDAYMNTYACVRTMSALMINLGVCEPDDGDEVV EVYNLTADPDQITNTAKTIDPELLGKMNYRIMMLQYCEPDDGDEVV EVYNLTADPDQITNTAKTIDPELLGKMNYRIMMLQYCESGGFTCRT PGVFDGCYRPDFLMFSNRGSVRTRFSKHLP GSGFTCRT AAGALLPGGLYPDFLMFSNRGSVRTRFSKHLP PGREACKPA,VUMSKINGTLLEBELGKGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLLEBELGKGGKKKYLPPTSRKD PKFEELGKPA,VUMSKINATLATGFGBLSLFINVQVSVITI ESTKSGLKSEKLVEGLTEYSTDKDEPPKOVEDELFKLAPEKVA VKRALVNFVNOKLDRLGLSVQNLDTOFABGEBPKOVEDELFNAVUGVSVITI ESTKSGLKSEKLVEGLTEYSTDKDEPPKOVEDELFKLAPEKVA VKRALVNFVNOKLDRLGLSVQNLDTOFABGEBPKOVIDLLLLIGGLEGFF LHLKEFYLLPSNPSRMHINVTLALBLLJ/IGSGPADEV/LALK/ TIVNKDAKSTLRVLYGLFCKHTOKAHRDETHERAPN VKRALVNFVNOKLDRLGLSVQNLDTOFABAD VKRALVFLYDRYDSPADEVLDYLDFYDVEDTYNSVDKT TTVSVSQQPVSAPVPLAARASVAGHLSTSTTVSSGGRONDSTK KTLVTLIANNNAGSBELVQGGGGELLITONPAPGIGFMVTOPVIRG STAPVPRADTTOFTTVI PATLTTRSTVPOSGSOQTKSTPSTSTTP TAOPTSLGGLAVQSPQGSNGTTNFKLAPSFSPSPAVSTASFVT VKRFGVTTGENSNEVAKLVNTLNTIFSLGGBBGGVVVGNNANSAH\ GSGRTSGESSMKVTSI SVPFJLOGGGKKIGPKNAGFFNTFAL RGGMCYCCPEMVEYQKKGKSLDSEBSVSSAAMPSSEKTAPVAS /THESSTIPPLSISPY/TKVPENENVGDAVQTRLIMLDDDFYY GRDGGKVAQLINTFKVATSFCPHCTIKLKNNTFRNMKHHVE LDOGNGEVDGHTI CCHCYRQFSTPPOLOCHLENVHSPYESTTKC KKCCMAFESPLIFLQIMKUTHRPGMFYVCQVCQVKSSLYSEVD VIFFRHIBDTRHLLCPYCLKVFKNNANFQGNTWHIGKRNVYH\ CKKCRVQFLFAKKKI ERKLQHKKTFRFK KQLEGLKFGTVTTRA SRGQFTTYPVSSNDTTPSSALGEAPLTSSNDPLDVSLTYPFVQRS IQKRAVRMSMGRGCTCLESCFF IDPRHPTYVHCSLCRYST CCSRAYAHHMINNIVPRKSPKYLALFKNSVSGI KLACTSCTFVT SVGDAMAKHLVFNPSIRSSSI LPRGLITWIAHSHGGTTRDFWHDR RIKRWLRFGDASGGENLEGKYLSFEBELLTFLLAPLFSFA STATPPFTPTHPGALALPFLAFAGTADFVLFACCUTPCDAGERFRNPQ RRIKRWLRRFCDASGGENLEGKYLSFEBELLTFLLAFALFSFA VAHTLEPKOVAENBGLF IPFORQCIVMLAL	1	1		KNFNIHGTNKHWLIRQAKTPMTNSSIOFLDNAFRKRWOTLLSVD
### BFDIKVPLLVRGGEIKPNOTSKHLVANIDLGFTLIDIAGYDLMK TOMOGMSLLPILRGSANLTHRSDVLSGGERNVTDTCTGSLS PGV3QCPPDCVCEDAYNNTYACVRTMSALMRLQYCEPDDGDEVEV EVTALTADPOTITATAKTIDPELLGKMWYRLMMLQSCSGPTCRT PGVFDPGYRFDPRTMAKTIDPELLGKMWYRLMMLQSCSGPTCRT PGVFDPGYRFDPRTMSNRGSVRTRRFSKHLL AMELIPPGLUFEDDFRTMALLFFGIGGPFFALSFFLFSCVSSGW AMERMETELYDLLQLPKGVPPFAELSKGLKKKYLPPTSRKD PKRELQKPA\VIMBRINATILPETIGGPFFALSFFLFSCVSSGW AMERICAN VIMBRINATILPETIGGFPFALSFFLFSCVSSGW AMERICAN VIMBRINATILPETIGGFPFALSFFLFSCVSSGW AMERICAN VIMBRINATILPETIGGFPFALSFFLFSCVSSGW PKRELQKPA\VIMBRINATILLPETIGGFPYALSFFLFSCVSSGW FKRELQKPA\VIMBRINATILLPETIVGFBUGHFKLAPFKVNA VKBAIVNFVNQKLDRLGLSVQNLDTFJADGVILLLILGQLGGFF LHLKEFYLIFPNSPAEMLHNVTLALELL/IGGRAPQLPC/LALK/ TIVNKOAKSTIRVLVGLFCKHTCKAHRDRTHFHGAPN FVGGSMADTDLFMCCEBELEFPQKISDVIEDSVEDYNSVDKT TTGVSVGQPVSAPVFLAARSVGRHLSTSTVSSSGAQNSDSTK KTLVTLIANNAGMPLVQQGGPLLLTOMPAPGLGTMVTQPVLR PVQVMONANHVTSSPVASQPIPTITUPAPGLGTMVTQPVLRMVQVG VILNVQQGGTVPPTILVPAPGTIGFVEPVRVQPQVFSQNTSDTSTTFT TAQTPTSIGQLAVQSGQNCTTMFLAPSFSPPAVSTASFVT VKRPGVTGENSNEVAKLVNTLNTTISLQGSBGFVVSNNSSAH\ GSGRTSGPSSMKVTSSIPVPLQDGGRKTLOPRCNAG/FRVTSAL RGHMCYCCPENVEYQKGKSLDSEPSVSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGQUFKLIMLUDDFYY GRDGGKVAQLINTPKVATSFRCPHCTKKLKNNTRFNHKKHNVE LDQQNGEVDGHTICQHCXRGFSTPPGLCCHLENVHSPYSTTKC KLCEMAFSSEPLFLQMKKTHKPGLGGLARFUVTIRA SKGQPRTVPVSSNDTPSSALQEAAPLTSSMDPLDVFLYFPVQRS CKKCRVQFLFAKKKIERKLQHKKTFRKDLGELGKRGTVTTRA SKGQPRTVPVSSNDTPSSALQEAAPLTSSMDPLDVFLYFPVQRS CKKCRVQFLFAKKKIERKLQHKKTFRKDLGELGKFTVTTRA SKGQPRTVPVSSNDTPSSALQEAAPLTSSMDPLDVFLYFPVQRS CKKCRVQFLFAKKKIERKLQHKKTFRKDLGELGKTVTTRA SKGQPRTVPVSSNDTPSSALQEAAPLTSSMDPLDVFLYFPVQRS CKKCRVQFLFAKKKIERKLQHKKTFRKDLGELGKTVTTRA SKGQPRTVPVSSNDTPSSALGEAAPLTSSMDPLDVFLYFPVQRS CKKCRVGLFAKKNAMGRGOTLECSFFI PDPPNHFPTYVHCLCLCYSTT. SVGDAMAKHLVFNPSHRSSS LIPRGLTWITHALPTAPLSPSA STATPPPTPTHPQALALPPLAFACTCOTTPCAARFTRNPO RITRWLRRFNGASGGRVKISTFRAWFRHIHLTPHARRRA VAHTLPROVAENBGLFVKIRGSLEGKKISTWAVERFHIRHLTPHARRRA VAHTLPR	1			DLVEKLVKRLEFTGELMNTYIFYTSDNGYHTGOFSLPIDKROLY
TQMDGMSLLPILKGASNLTWRSDVILVEYQGGGRNVTDPTCPELS GVSQCPPDCVCEDDAYNNTYACTMSALMHLQYCFDDDGVFV EVYNLTADPOLITNIAKTIDPELLGKMMYRIMMLQSCSGPTCRT PGVFDPGYRPDPRIMFSNRGSVRTRRPSKRLL 6132 96 1241 ARGLLPPGLVPEDPRRTRRLLPFGTQGPFPALSRPLFSCVSSGW AWEAMEDFELLYDLLQLPKGVEFPAEELSKGGKKKYLPPTSRKD PKFEELQKPA\VIMBUINATLBFGTQGFPFALSRPLFSCVSSGW AWEAMEDELLYDLLQLPKGVEFPAEELSKGGKKKYLPPTSRKD PKFEELQKPA\VIMBUINATLBFUVGSLEEDHFOGLILHEL FQRLAALKLEABDIALTATSQKHKLTVVLEAVRKS\CSWRSGRP SGA\WSSINKNLDLSTLHLLVALAKRFQPDLSLPTRVQVGVITT ESTKSGLKSEKLVEQLTEYSTIDKEPPKDVFDELFKLAPEKVNA VKBALVNFVNQKLDRLGUSVQNLDTGPADQUILLLLIGGLEGFF LHLKEFYLIPNSPAEMHNNVTLALELL/IGGGPADPC/LALK/ TUNKDAKSTLRVLYGLFCHITQKAHRDRTPHGAPN 6133 2 4256 FUNGSMADTDLFFMECEEELEBGKFGKSISVEDSYSDEYDNYTOTT TTVSVSQQPVSAFVPIAHASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNAGNELVQGGGCPLILTGNAPGLGTMVTOPVLR PQVWQNANHVTSSVNASQPIFTTQGFPVRNVTPVQNAMNQVG IVLNVQQGGTVRPITLVPAFGTGFVRNVTPVQNAMNQVG IVLNVQQGGTVRPITLVPAFGTGFVRNVTPVQNAMNQVG STMPVXFTNTFTTJTFLTLITSTVDSGSQGVKSTSPSTSTP TATQPTSLGQLAVQSPGGSNQTTMPKLAPSFPSPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIFTSLGSPGFVVVSNNSAH\ GSQRTSGPESSKKVTSSIFVPUDQGGKKLCPCKNAQFFVTEAL RGHMCTCCPEMYEYQKKGKSLDSEPSVFSAKPFSFEKAPVAS //HPSSTPIPALSFPJY/TKVPEPNENVGDAVGTKLIMLDUDFYY GRDGCKVAQLTNFFKVATSFRCPHCTKRLKNILRFMNIMKHHVE LDQONGEVDGHTI-COHCNGFSTPOLQCHLENVHSPYESTTKC KICEMAFESEPLFLQHMKDTHKPGEPFYVQQVGVSSLYSEVD VHFRMHBDTRILLCPYCLKVFKNGKAFQQHMRRIGKR\NVYH\ CKCKTKQPLFAKDKIEHLQHHVTHSFKKYLGLEHLGHVFVITRA SRGQPRTVPVSSNDTPFSALQEAAPLITSSMDPLFVFLVFFQGS GCRAYAHMMINNIVPRKSSKYLALEKNSVSGIKLACTSCTFVT SVGDAMAKHLVVFNPSHRSSSILPRGLTMAHSRHCQTRGRVHDR NVKNYFPPSFFTNKAATVKSAGATPABEBELLTLAPALSPA STATPPFPTTHFQALALPPLATGRAGKAVVLFALCCTSCTGAAFHFRNPQ RKIRWLRFQASGGSGGGGGGGGTGGKGCRAAFHRRHLTFHARRA VAHTLPKDVAENAGLFIDFVQKGLILSKYVLFALCCTSCDAAFHFRNPQ RRIRWLRFQASGGGRILEGKYLSFRAEKLAEWUTCRGQOLP VKEETLPQKATKIGRSLEGGKISVFRAVHRIRHHLTPHARRA VAHTLPKDVAENAGLFIDFVCQVGRGINVQDQDEGSFVTQEPE LASGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		!		EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
FGVSQCFPDCVCSDAYMTYACVTIMSALIMILGYCSEDDDGEVEV EVINLTADPDOLIVINIAKTIDPELIGKMYNYRLMIGSCSGPTCRT PGVPDCYRTDPELMFSNGSVETRFPSKHLI AGGLIPPGLVPEDPRTRNLEDFGTQGPPFLSEREJFSCVSGW AWEAMEPELYDLLOLPKGVEPPAEEELSKGGKKKYLPPTSRKD PKFEELQKPA\VLMEBIINATLLPEHIVVRSLEEDMFDGLILHHL FGRLAALKLEABEDLATATSGKKLTVULEAVNRS\CSWRSGRP SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTRVQVEVITI ESTKSGLKSEKLVEGLTEYSTDKDEPPKODVDELFFKLAPEKVNA VKRALVNFVNQKLDRIGLSVGNLDTQFADGVILLLIGGLEGFF LHLKEFYLIPPNSPAEMLINVTLALELL/IGGGPAGLPC/LALK/ TIVNKDAKSTLRUVJSCFKCHDAKBDRTPHGAPN 6133 2 4256 FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQCPVSAPVPIAAHASVAGHLSTSTTVSSGAQNSDSTK KTLVTLIANNNAGNELVQGGGGVLITONPADGIGTMVTOPVLR PVQVMQNANHVTSSPVASQFIFTTTGGFPVRNVRPVGNMTAVRG STMFVRPTTNTFTTVIPATLTIRSTVPQSGSQCTKSTPSTSTTP TATQFTSLGQLAVGSPGGSNQTTMPHLAPSFPSPPAVSTASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGGFVVSNNSSAH\ GSGRTTGGPBSGNKVTSSIFVPDLQDGGRKLGRCNAQFRVTEAL RGHMCVCCPEMWFYCKKKSKLDSPSYSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPENNENVGDAVQTKLIMLVDDFYY GRDGKVAQLINFFKVATSFRCHCTKRLNNIRFMNIMKHVE LDQQNGVDGHTICHCHCYRGFSTPFOLQCHLENVISPTSTTKC KICEMAFESEPIFLQHMKDTRKPGEMFYVCQVGVRSSLYSEVD VHFRMHEDTRRILLCPYCLKYPTARPQCHLENNIPFEVARS SRQPRTTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLSCHCTYST CXRRAVRMSVMGRGTCLECSFIPPFNHFFTYVHCSLCRYST CCSRRYANHMINNIPPKKSRYLALFKNSVGIKLACTSCTFVT SVGDAMAHLLVPNSHRSSSILLGTWATAATRVAGCTFDVTDR SKRQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPQORS STATPPPTPTHPQALAIPPLATGGRELDWALAGTBLACTSCTFVT SVGDAMAHLLVPNSHRSSSILLGTWATAARROTDRVHDR RIKRWLRRFQASGGENLEGKYLSFRAEKLAEWULTGRGQLP VKETLEPQKAFKIGRGLGSLEGGFKISVFRARRHTHIPHARRA VAHTLPKOVAENAGLFIDFVQRQIHNQDLPLSMIVALDEISLFL DTEVLSSDDKRENALGTVGTGGFBWCDVULALLADGCTULPTLYFY SGQDMDRAMHDSTLLEGKKLSFFRAEKLAEWULTGRGQLP VKETLEPQKAFKIGRSLEGGFKISVERWARFRIKHTLTPHARRA VAHTLPKOVAENAGLFIDFVGRQILDFLUNTVALGEISLFL DTEVLSSDDKRENALGTVGTGGFBWCDVULALLADGCTULPTLTFT SGGODDOPANMPDSILLBLAKKSGYSDDELMELNSTVROKHTAQO GROUDPANNPOSILLBLAKKSGYSDDELMELNSTVROKHTAQO TEVLSSDDKRENALGTVGTGGFBWCDVULALLADGCTULPTLVFY	ļ		;	TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
6132 96 1241 AAGLPPGUTNIAKTIDELLGKMYKIMKLGSCSGPTCRT PGVPDGVARDPRIMFNINGSVARPSKEMEN FOR SUPPORTARDE PAIRSNINGSVARPSKEMEN AMEAMERPEFLYDLLGLPKGVEPPAEEELSKGKKKYLPPTSKRO PKFEELQKPA\UMBRINATIDEHIVVRSLEEDHFOGLIHHL FQRLAALKLEABEDIALTATSQKHKLTVVLEAVRRS\CSWRSGRP SGA\WESIPKNDLLSTLHLLVALAKRFQPDLSLPTHVQGVITT ESTKSGLKSEKLVEQLTEYSTUKBEPFKOVPBLFKLAEKKNA VKBALVNFVNQKLDRIGSVQNLDTQFADGVILLLLIGQLEGFF LHLKEFYLPPNSFABMINNVTLALELL/IGGRADPC/LALK\ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTFHGAPN 6133 2 4256 FVHGMADTDLFMECEEELEPMQKISDVLEDGVVEDYNSVDKT TTVSVSQCPVSAFVVIAHASVAHLSTSTVSSGAQNSDSTK KTLVTLIANNAGNELVQGGGPLILTONPAPGLGTMVJOPVLR PVOVMQNANHVTSSPVASOPLTTGGFPVRNVRPVQNAMNQVG IVLNVQQGVVRPTVILVPAPGTGFVKFVVSVPQNAMNQVG IVLNVQQGQTVRPITLVPAPGTGFVKFVVSVPQNSMYDV XGPGSGACKSTPSTSTTP TATQTPSLQGLAVQSPGSGANTSPKSTSTTP VKRPGVTGENSEVAKLVNTLNTTPSLGQSPGFVVVSNNSSAH\GSQRTSGPESSMKVTSSIFVFDLQDGGRKICPRCNAQFTVTFAL REMMYCCCPEMVETQKKKKSLDSEPSVPSAARPPSPEKTAFVVAS \/THPSSTPIPALSPPY/TKVPERNNGDAVQTKLIMLUDDFYY GRDGGKVAQLUTHFYRVATSRFCHCTKRLKNNIRTMNIMKHVE LDQGNGEVJGHTICQPYCLKYFNGNAFQQHTMRIMKHVZ LDQGNGEVJGHTICQPYCLKYFNGNAFQQHTMRIMKNIKHVZ LDQGNGEVJGHTICQPYCLKYFNGNAFQQHTMRIMKRKNVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLCPYCLKYFNGNAFQQHTMRIGKNVVTH\CKKCRVQFLFAKDKIEHLTSHADEPLAFAKAGATBABFEBLLTPLABLBSPA SGGGGSGGKGKEGLSVKKIKVVLPALCCCTEDAARHFRNPQ RIFKRWLRRFQASGGEBLEGKYLSFRAEKLAEWUTCTRGQOLP VESTLEFQKATKGRSLEGGFLYEKARVAPMLHHTLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDKENALCTCGTGFBWCDVULALLABGCTU-PTLVFY]	ł		PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDOEVFV
AGGLPPGLVPEDPRRTRNLLPFGIGPPFALSRPLFGCVSGW AWEAMEPEFLYDLLQLPKGVPPPABEELSKGGKKKKLPTTSKRO PREFECKPA/VLMEWINATLIPEHLVVSLEEDMFDGILIHL FQRLAALKLEAEDIALTATSQKHKLTVULEAVNRS CSWRSGRP SGA/WESIFNKULISTHLUALAKRFQPDLSLPTNVQWEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA VKRAIVNFVNQKLDRIGLSVQNLDTQFADGVILLLLIGGLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGGRGPAGLPC/LAKK/ TIVNKDAKSTLRVLYGIFCKHTQKARRDTPHGADN FVLIGSMADTDLFMEGEEELEPFWGKISDVIEDSVVEDYNSVDKT TTVSVSQQVSAPVPIAARASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNFLVQGGGGPLILTONPAFGLGTMVTOPVIR PVQVMONANHVTSSPVASQFITTIGFPVNVRPPQNAMPNOVG IVLNVQQGGVRPITLVPAFGTQFVVRVPVQVPSQMTPVRPG STMPVRPTINTFITVTYPATLTIRSTVPOSQSGQTKSTSTTSTTP TATQPTSLGGLAVQSFGGSNQTTNFKLAPSFSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGGSFGPVVVSNNSSAH\ GSQRTSGPESSKVTSSI PSVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKKSLDSEBVSBAKPPSPEXHAPVAS /THESSTPIPALSPPY/TKVPEPPNNVDAVQTKLIMLUNDFYY GRIGGEVAGLITHFPKVATSFRCPHCTKRLKNIFRMHMKHHVE LDQONSEVDGHTICHCTRQFSTPPOLOCHLENVHSPYESTTKC KICEMAFESEPLFLQHMKDTHKPGREMPYVCQVCQYRSLYSEVY VVFRMIHBSTTPIALSPPY/TKVPEPPNNVDAVGTKLINLNUDFYY GRIGGEVAGLTHFPKVATSFRCPHCTKRLKNIFRMHMKHHVE LDQONSEVDGHTICHCTRQFSTPPOLOCHLENVHSPYESTTKC KICEMAFESEPLFLQHMKDTHKPFRKPKQLEGLKPGTKVTIRA SRGQFTYPVSSNDTPFSALGAPLITSSMPLDPFFLYPPYORS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTVHCSLCRYST CCSRAYAHMINNHYPRKSPKYLALFKNSVGIKLACTSCTFVT SVGDAMAKHLUPNFSHRSSI LPRGLTWIARRGQTREVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLLAPALPSPA STATPPPTFTPHPALATPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFEBEKLAEEVLTQRSCOLP VNEETLFQKATKIGRSLEGGFKISFEBEKLAEEVLTQRSCOLP VNEETLFQKATKIGRSLEGGFKISFEBEKLAEEVLTQRSCOLP VNEETLFGKATKIGRSLEGGFKISFEBEKLAEEVLTQRSCOLP VNEETLFGKATKIGRSLEGGFKISFEBEKLAEEVLTQRRCOLP VNEETLFGKATKIGRSLEGGFKISFEBEKLAEEVLTQRRCOLP VNEETLFGKATKIGRSLEGGFKISFEBEKLAEEVLTGRRACDLFLFLARGRACHTACC	1	1		EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT
AWEAMSPETYDLIQDKGVPPASEELSKGGKKKYLPTSKRD PKFEELQKPA\ULMBWINATLIPHLIVRSLEEDMFDGLILHHL FORLAALKLEAEDIATATAOKKKLTVULEAVNRS\CSWRSGRP SGA\WESIFNKDLLSTHHLUVALAKRFQPDLSLPTNVQVEVTTI ESTKSGLKSKKLVEQUTEYSTDKDEPFDVPFDELFKLAPEKVNA VKRALVNFVNGKLDRIGJSVQNLDTDFADDYLLLLLIGGLEOFF LHLKEFYLTPNSPARMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTOKAHRDTPHGAPN 6133 2 4256 FVIGSMADTDLFWECEEELEPPOKTSDVIEDSVVEDTNSVDKT TTVSVSQQPVSAPVPTAAKASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNAGNPLVQQGGGFLILTQNPAPGIGTMVTQPVLR PVQVMQNAHNVTSSPVASQFIFTTTGGFPVRNVRPVQNAMMQVG IVLNVQQGGTVRFITLVPAPGTQFVRPVGVPSQVTSCPSTSTP STAPCYSLGQLAVQSPQSNQTTNPKLAPSFSPPAVSLASFVT VKRPGVTGENSHEVAKLINTLINTISSLQSPGPVVVSNNSSAH\ GSQRTSGPESSKKVTSSIVPLQDGGKKICPRCNAOFRVYEAL RGHMCYCCPEMVEYOKKGKSLDSEBSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGKVAQLITNFPKVATSFRCPHCTKRLKNNIRFMHIMKHVE LDQONGEVDGHTICHCKYGFSTPPQLCHLENVHSPYESTTKC KICEMAFSSEPILCHMKOTKHRGEMPYVCQVCYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAPQQHYMHQKR\NVYN\ CKKCRVQFLFAKDKIEHKLQHKTTRKPGLEGLKPGTKVTIRA SKGQRTVPVSSNDTPFSALGAPLITSSMPLPVFLYPPVORS IQKRAVKMSVMGROTCLECSFEIPDPPNHPPTVHCSLCRYST CCSRAYANHMINNIPPKKSPKYLALFKNSVGIKLAGTSCFFVT SVGDAMAKHLVENPSHRSSSILPRGLTWIAHSRRGQTRDRVHOR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLLAPALPSPA STATPPPTPTHPQALAPPLAFERGELNVDQDEGSFVTOEPPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFNNQ RRIRWLKRFQASGGENLEGKYLSFEBEKLAEWUTQRROCUP VNESTLEFQKATKIGRSLEGGFKISFEBEKLAEWUTQRROCUP RRIRWLKRFQASGGENLEGKYLSFEBEKLAEWUTQRROCUP VAFTLEFQKATKIGRSLEGGFKISFEBEKLAEWUTQRROCUP RRIRWLKRFQASGGENLEGKYLSFEBEKLAEWUTQRROCUP VAFTLEFQKATKIGRSLEGGFKISFEBEKLAEWUTQRROCUP RRIRWLKRFQASGGENLEGKYLSFEBEKLAEWUTQRROCUP VAFTLEFQKATKIGRSLEGGFKISFEBEKLAEWUTQRROCUP TURETLEFQKATKIGRSLEGGFKISFEBEKLAEWUTQRROCUP RRIRWLKRFQASGGENLEGKYLSFEBEKLAEWUTQRROCUP RRIRWLKRFQASGGENLEGKYLSFEBEKLAEWUTGRROCUP VAFTLEFGKATKIGRSLEGGFKISFEBEKLAEWUTGRROCUP VAFTLEFGKATKIGRSLEGGFKISFEBEKLAEWUTGRROCUP VAFTLEFGKATKIGRSLEGGFKISFEBEKLAEWUTGRROCUP VAFTLEFGKATKIGRSLEGGFKISFEBEKLAEWUTGRROCUP VAFTLEFGKATKIGRSLEGGFKISFEBEKLAEWUTGRROCUP VAFTLEFGKATKIGRSLEGGFTATTOROCUP				PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
PREECCKPA\ULBENINATLLEEHIVVRSLEEDMFDGLILHHL FQRLAAKLREEDTALTSCKKKLTVVLEAVNRS\CSWRSGRP SGA\WESIFNKDLLSTHLLVALAKREQPDLSLEPTNQVEVITI ESTKSGLKSEKLVSQLTEYSTDKDEPKDVDEDLFKLAPEKVNA VKRATVMFVNQKLDRLGSVQNLDTQFADGUILLLIGGLEGFF LHLKEFYLTDNSPABMLHNVTLALELL\IGRGPAQLPC\LALK\ TIVNKDAKSTLRVLYGEFCKHTQKAHRDRTHGAPN 6133 2 4256 FVEGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGPLILTONPAPGLGTMVTQPVLR PVQVMQNANNVTSSPVASQPIFTTQGFPVRNVRPVQNAMMQVG STMPVRPTTMTFTTVIPATITISSTVPQSQQOTKSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKREGVTGENSNEVAKLNVTLNTIPSLGQSBFGVVVSNNSSAH\ GSGRTSGPESSMKVTSSIPVDLQDGGKKICPRCNAQFRVTEAL RGHMCVCCPEMVESYQKKGKSLDSPSVPSAAKPPSPEKTAPVAS \THPSSTPIPALSPPY\TKVPEPNEVUGDAVQTKLIMLUDDFYY GRDGGKVAQLTNFPKVATSFRCHCKKIKNNIRFMMHKHIVE LDQQNGEVDGHTICQHCYRGFSTPFOLQCLHERVHSPYESTTKC KICEMAFESSPLDIGMKUTHSPGEMPYVOQCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDK IBHKLQHHKTFKPKQLBGLKGTKVTIRA SKGQPRTVPVSSNDTPFSALQEAAPLTSSNDPLDVFLIPPVQRS IQKRAVRKMSVMGRQTCLECSFFIPDPPNHFPTVVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKKLVPNPSHRSSSILPRGLTWIAHSSHGGTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATABEPELLTPLAPALPSPA GTATPPPTFTHQALALPJLATEGABCLNVDDQDGESFPTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCTSTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFAERKLAEWUTQRRQOLP VINEETLFQKAKTIGRSLEGGFKISVEMAMFMLRHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGFFMCDVVLAILADGTVLFTLVFY RGQMDQPANMPDSILLEAGGYSDDEIMELNSTRVQKKHTACO	6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLFSCVESGW
FORLAALKLEAEDIALTATSCKHKLITVULEAVINS\CSWRSGRP SGA/WESI FINKOLLSTHILUVALAKRFOPDLSLPTNVQVEVITI ESTKSGLKSEKLVEQLIEYSTDKDEPPKDVPDELFKLAPEKVNA VKRAIVWFVNQKLDRIGJSVQNLDTOFADGVILLLIGGLEGFF LHLKEFYLTPNS PAEMIHUTALELLI, IGEBPAQLPC\LALK\ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN 6133 2 4256 FVIGSMADTDLFMECEZEBLEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAANVAGHLESTSTVSSSGAONSDSTK KTLVTLIANNNAGNPLVQQGQFLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFTTTQGFPVENVRYPVQNAMMQVG IVLNVQQGQTVPITLVDMSTOPVPKPTVQPQVFSQMTDVRPQ STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPQGSNQTTNPKLAPSFPSPFAVSIASFVT VKRPGVTGENSNEVAKLVNTINTIPSLGQBSGPVVVSNNSSAH\ GSQRTSGPBSSMKVTSSIPVPDLQDGGRKLOPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTP1PALSPPY/TKVPENENVGDAVQTKIIMLVDDFYY GRDGGKVAQLTNSPKVATSFRCHCTKRLKNNIRFMHMMKHHVE LDQQNGEVDGHTICOHCYRQFSTPFQLQCHLENVHSPYESTTKC KLCEMAFSSEPLFLQBMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMHEDTRHLLCPYCLKVFRNGAFQQHYMRGKR\NVYH\ CKKCRVQFLFADKVSHEKLQHKTFRFKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLFVETLYFPVQRS IQKRAVKMSVMGRQTCLECSFFIPPPFNHFPTYVHCSLCRYST CCSRAYANIMINNHVPKRSVGIKLACTSCTFVT SVGDAMAKHLVPNPSHRSSILPRGLTWIAHSRHQGTRDRVHDR NYKNNYPPSFFTNKAATVKSAGATPABEPELLTFLAPALPSPA STATPPPTTPHQALALPSLATEGASCLMVDQDDGSSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFEABEKLAEWUTQRRQOCLP VNEETLFQKATKIGRSLEGGFKISVEMAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENARLQTVGTGEFWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEARGSGYSDDEIMELNSTRVWQKHTACO				AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
SGA/WESIFNRDLESTHHLUVALAKRPOPDLSLPTNVQVEVITI ESTKSGLKSEKLVEQLIETYSTDKDEPPKDVFDELFKLAPEKVNA VKRAIVNFVNKKLDRLGUSVQNLDTOFADCUILLLIGQLEGFF LHLKEFYLTPNSPARMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN 6133 2 4256 FVHGSNADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAARASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTONPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIPITTQGFPVRNVRPVQNAMMQVG IVLNVQQGQTVRPITLVPAPGTQFVRNVRPVQNAMMQVG IVLNVQQGQTVRPITLVPAPGTQFVRNVRPVQNSMAMPVSG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTTSTTP TATQPTSLGQLAVQSPQGSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLUNTLNTIPSLGQSPGBVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSESVPSAAKPPSPEKTAPVAS /HHPSSTPIPALSPPY/TKVPSPNENVGDAVQTKLIMLUDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHKHHYE LDQQNGEVDGHTICOHCYRGFSTPPQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAPQQHYMRHQKR\NVYH\ CNKCRVQFLFAKNKIEHLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPYSSNDTPPSALQEAAPLTSSMDPLPVELYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANIMINNHVPKSKFXYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHCGTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTTTHPQALALPPLATEGAECLNVDDQDEGSPTYQEPE LASGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRWLRRFQASQGENLEGGFKISYEMAVRFMLRHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL UNESTLEFQKATKIGRSLEGGFKISYEMAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVOTGSPCCOVLALLAGGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWGKHTAQO	1			PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
ESTKSGLKSEKLVEGLTEYSTDKDEPPKDVPDELFKLAPEKVNA VKRAIVMPVNOKLDRIGLSVQNLDTQFADGVILLLLIGQLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKARRDRTPHGAPN FVHGSMADTDLFMECEEELPPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNELVQQGGGPLILTQNPAPGIGTMVTQPVLR PVQVMQNANHYTSSPVSQIFITLTQNPAPGIGTMVTQPVLR PVQVMQNANHYTSSPVSDIFITLTQNPAPGIGTMVTQPVLR STMPVRPTTTTTTVIVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTTTTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGONQTTNPFLAPSPPPAPVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGFVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVPPLQDGGKRICPRCNAQFFVTEAL RGGMCYCGPENVEVQKKGKSLDSEPSVPSAAPPSPSPKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLUDDFYY GRIGGKVAQLTNTPKVATSFRCPHCTKRLKNNIRFNHNKHHVE LDQQNGEVVQCHTTCQCHCTRQFSTPPOLQCHLENVHSPYSTTKC KICEMAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKKONAFQQHMRHQKR\NVYH\ CKKCRVQFJFARKKIE INHLQHHKTFRKPGLEGLKEGTKVTIRA SGGQRTVPVSSBDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVKKMSVMGRQTCLECSFEIDPPNHFPTYHCSLCRYST CCSRAYANIMINNHVPKSPKYLALFKNSVSGIKLACTSSTFVT SVGDAMAKHLVFNFSHRSSSILPRGLTHIAHSRHGQTRDVHDR NVKNMYPPPSFPTNKAATVKSAGATPAFEFELLTFLAPALPSPA STATPPTTPHQALALPPLATEGAECINVPDQDBSSPVTOEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWRRFQASGGENLBGKYLSFEAEKLAEWULTQREQQLP VNESTLEFQKATKIGRSLEGGFKISYEMAVRFMLRHLTPHARRA VAHTLDFKOVAENAGLFIDPVQCIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALGVTGTEGECOVCOVLALLAGGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTAQO	ŀ			FORLAALKLEAEDIALTATSOKHKLTVVLEAVNRS\CSWRSGRP
VKRATVNFVNOKLDRIGLSVQNLDTQFADGVILLLIGQLEGFF LHLKEFYLTPNSPAEMHINVTLALELL/IGGPAGDPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTOKAHRDRTPHGAPN 6133 2 4256 FVHGSMADTDLFMECEBELEFWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSGAQNDSDTK KTLVTLIANNNAGNFLVQQGGQFLILTONPAPGLGFMVTOPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAPGTGFVKETVGVPQVYSQMTPVRPG STMPVRFTNTFTTVTATLTIRSTVPQSGQCD/TSSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSBGPVVVSNNSSAH\ GSGRTSGPESSMKVYSISPVPDLQGGGKICTPKCNAQFFVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /*HPSSTPIPALSPPY/TKVPEDNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNTP FKATSFRCPHCTGRAVGTKTEAL KICEWAFESSPLFLQHMKOTHKPGEMPYVCQVCQYRSSLYSEVD VMFRMIHEDTRHLLGPYCLKVPFKNGANPQQHYMRIQKR (NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQERTVPVSSNDTPSSALQEAPLTSSMDPLEVFLYSPVQRS IQKRAVKMSWMGRQTCLECSFFI IPDPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNESHRSSS ILPRGLTWIAHSRKGQTRDRVHDR NVKNMYPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGRECLNVDDQDEGSFVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGSGVKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGSTUSKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGSTUSKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGSTUSKSTSWAWNFMKRHHTLTPHARRA VAHTLPKDVAENAGLFTDFVQRQINNQDLPLSMLVATDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPAMMPDSILLEAKESGYSDDEIMELWSTRVWGKHTACO	1	į į		SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
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TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSBGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRGFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLQHMKDTHKPGEMFYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFFFAKDKIEHKLQHHKTFRPPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTTRDVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRHLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	1 1			SAWDAN DELAMARAMENT EN AN ELD CAMPO CO COMMONDO CONTRACTOR DE CAMP
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GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHIVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSILPRGLTWIAHSRHGGTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISVEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO		1		VKRPGVTGENSNEVAKT.VNTI.NTTDGL.GOODGDURTIGUNGGATA
RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLUDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRGFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQPLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKNSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISVEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO		•		GSORTSGPESSMKVTSSTPVFDLODGGPKTCDPCNAOFDWPAT
/THPSSTPIPALSPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTMFPKVATSFRCPHCTKRLKNNIRFMRHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWULTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	1 1	j		RGHMCYCCPEMVEYOKKGKSLDSEPSVPSAAKDDSPEKTADUAC
GRDGGKVAQLINFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRRPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTTRDVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	1 1			/THPSSTPIPALSPPY/TKVPEPNENVGDAVOTKI,TMI,VDDEVY
LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYYCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRRSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPFPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISVEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	i i	ł		GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQPLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISVEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	[[ł	i	LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABFBELLTFLAPALPSPA STATPPPPTPTHPQALALPPLATEGAECLNVDDQDEGSFVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISVEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO				
CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO				VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
SRGOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWULTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO] [CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRRSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTTGDVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRHLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO				SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPBAEPELLTPLAPALPSPA STATPPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISVEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO]			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKUVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO				CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO				SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	i i		1	NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
RRIRRWLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISVEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTBVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	1		ľ	STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO		ì]	LASGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO			[RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	f	1		VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO			ŀ	VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL	1	j	·	
RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL	j	1	1	RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
	L			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL

ſ	SEQ	Predicted	Predicted end	,
- 1	ID	beginning	nucleotide	Amino acid segment containing signal peptide
- 1	NO:	nucleotide	-	[[M=Alanine, C=CVSteine, D=Aspartic Acid p
- 1		location	location	Glucamic Acid, F=Phenvlalanine G=Glucino
- 1			corresponding	H=Histidine, I=Isoleucine, K=Lysine
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
-		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
- 1		sequence	1 -	\=possible nucleotide insertion)
				DVCIVDTVVVIDIUVVVVCORDIV
- 1				DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
- 1	•	l	i .	LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
- 1		1	ļ	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
- -	6134	† 2 –	4256	FYGFEEADLDLMEI
		1	4456	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
- 1		1	j	TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAONSDSTK
- 1		ŀ		KTLVTLIANNNAGNPLVOOGGOPLILTONPAPGI.GTMVTOPVI.D
		}	ŀ	PVQVMQNANHVTSSPVASQPIFITTOGFPVRNVRPVONAMNOVG
- 1		1	i	IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
				STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
		ĺ	į.	TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			{	VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
- 1				GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
- (RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
ı				/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
1				GPDGCVIAOLTNEDVIA TOTTO DEL CONTROLLO DE LA CO
1				GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1				LDOONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
-				KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1				VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1				CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1		i		SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
- [IQKKAVRKMSVMGRQTCLECSFEIPDFPNHFPTVVHCSLCPVcm
1				CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1				SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGOTPDDVUDD
1				NVKNMYPPPSFPTNKAATVKSAGATPAEPERI,I,TDI,ADAT,DCDA
1	- 1			STATPPPTPTHPQALALPPLATEGAECLNVDDODEGSDVTORDE
1	ł	Į.	i	LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEOAAEHEDNBO
1	l	}		RRIRRWLRRFQASQGENLEGKYLSFBAEEKLAEWVI.TOREOOT.D
ſ	- f	i	ł	VNEETLFQKATKIGRSLEGGFKISYEWAVRFMIRHHITDHADDA
1		1	1	VAHTLPKDVAENAGLFIDFVOROIHNODLPLSMTVATDETSLET
1		,		DTEVLSSDDRKENALQTVGTGEPWCDVVIATLADGTVI.DTLUEV
1	1	1	j	RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1	1	j]	RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
	i		-	DVCIKRTVKNFLHKKWKEOAREMADTACDSDVIJOIJITJWIJGEV
	İ			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1	1	i i		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
_				FYGFEEADLDLMEI
1	6135	2		FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
1	1	}		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1			Ī	KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
	1	1	1	PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
İ	ļ		i	IVINVOOCOTVPPTTIADA BOTTO DITENTIANTO CONTRACTOR CONTRA
1		j	j	IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1		į	. [STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
		i	1.	TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
1	- 1	Į.	1.	VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
ŀ		Í	1	GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
l			} :	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
		j	1.	/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
	1		10	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHLUG
	-			LDQQNGEVDGHTICQHCYROFSTPFOLOCHLENVHSPVESTTVC
	-	Į.	1 1	KICEWAFESEPLFLQHMKDTHKPGEMPYVCOVCOVRSSIVERUD
	- 1	1	1	VHFRMIHEDTRHLLCPYCLKVFKNGNAFOOHYMRHOKR\NVYH\
	ſ	•	10	CNKCRVQFLFAKDKIEHKLOHHKTFRKPKOLEGIKPGTKVTTPA
	1	}	! \$	RGQPRTVPVSSNDTPPSALOEAAPLTSSMDPI.PVFI.VPDVORC
	1		1 3	QKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
			l c	CSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT

SEQ	Predicted	Predicted end	Aming again
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- [location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible rucleotide insertion)
		 	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
Ì			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
	İ		LASGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
)	}		RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
		l .	VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
1			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
1	}	ļ	DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVI.PTI.VFV
-			RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWOKHTACO
1			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKTOPI.
1			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLOLVLVWLCRV
ı			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMOEELTAS
İ			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHOLFEGESETES
6136	1704		FYGFEEADLDLMEI
) 0230	1,04	539	FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGQVAS
			SLFRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
ŀ			DLEEEIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIQ
1			INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEYGQIESVRFR
1			SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
	l i		RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVBESAIEK HFLDCGSIMAVRIVRDKMTGIGKGFGYVLPENTDSVHLALKLNN
	!		SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
			AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
			MWNMLIVAMCLA\LLGLPGKAOELOGHVS\IILAGEOLGDLAKK
			YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKOGOELMAKALES
1			LSCPKDMAPSHCAEHKDQFLQLSOYROLKTAEDYOALNKDTEAG
1			LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLDVV
1 1			LEKPFGHDHFSAQQLATELGTFFOEEEMYRVDHYLGKOAVAOTI.
i I			PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV
1			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL
			QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
			RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS
1			QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
[]			LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLBSLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
1 1			QQQPEQLVPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
1 1			ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW
]			AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM
1	1		PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH
ļ l		}	TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV
ľ			AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
6130			DAFLG
6138	4587	934	EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
i i		1	TDTSHLLSAVKGQERFSLYOTRSLIHELKNKEIHFORRRTTCAL
		!	TLEAGEKLLLTTDLKTKESVGRRISOLODSWKDMEPOLAEMIKO
! [İ	FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
ļ		ł	ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVT,KEQTE
1	ľ		HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM
į	j	ļ	ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL
			IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI
i i		1	QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD
ļ			LORDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
			LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB
1		į	RTAACPNSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRRLRHFT
			ZAROKUKATANEGIAKANANDKKATAAKKUKHET

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		1	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			NOREEFEGTRESILVWLTEMDLQLTNVEHFSESDADDKMRQLNG
			FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEELHR
			YCQEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
	i		DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE
		J	WDHTGRRGGPSSSH\EEDEEAQYY\SALSGKSISDGHSWHVPDS
		1	PSCPEHHYKOMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG
			KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
			LKIKONLOOLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE
	ľ	ł	LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
	1	1	LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
	1		SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
		1	
			LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM
,			ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
			GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLLACLL
	1	i _	PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
613 <i>9</i>	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
	1		TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
			YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
			TORFLSOHROGEPEASPPRTLSDLLLASMVAGVVSVGLGGPVDL
	1	i	IKIRLQMQTPPVSGRQPRFEVQGSGSCG\EPAYQGPVHCITTIV
	1		RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG
	ĺ		PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
			LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA
	Į.	1	IRGDHAVTSP
6140	594	136	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP
6140	594	136	RCORP/OPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
			SVAPOAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
		1	
		1	FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
			ARRIRRATOVRITG
6141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
	ł	1	ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
		ł	PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY
	Į.		KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
	1		NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK
	ł	1	AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
	ł	<u>}</u>	VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
)	DEFVFDVWGVIGDAKRRGL
6142	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN
		1	LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
			FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL
		1	REKOLSHSLRAVSTDPPHHDHHDEFC\LMP
6143	2802	270	FRMRIFLHCPWNOOMWKIWNLLETSLESCKAHLSIQKLLKER\Q
0147	2002	2/0	\OLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
			LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN
	1	1	SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
		1	FIVDEV\HER\SVQSDFLLIILKBILQKRSDLHLILMSATVDSE
			KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
			QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
		1	YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI
			FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
	1		TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
	1		QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
l		1	YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN
	1		AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
	ľ	1	SERVET SECTION OF THE PROPERTY OF THE PROPERTY OF THE CONTRACT OF THE PROPERTY
	1	1	COLDBYATE A SIMTEY CRETTP TO COLDEND A KRATAMANCOUT.
			GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	Seconine W. Mhusenine, K=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
Ì	1	•	LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
1	i	ĺ	YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLQTH
1		•	GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS
	1	ŀ	IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
		j	LQIITELIKTENN
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
1	1		VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
	1		VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
İ			FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
i			QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE
			DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
]		GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
1]		DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
			QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
1			\VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPQD
			/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
1	i l		EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
			L
6146	428	781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
1			R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
	1		EIVTKERHREINKQATRGDCLAFQMRAGLLP
6147	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE
	_		GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
1	i		ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
			DEMDRLATNMAVITDFSARISATLQDRHERITKLAGVHALLRKL
			QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
1 1	ľ		IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA
1	1		EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
	i i		SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
}	.]		ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
			EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
1			GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
1		i	CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
1 1	1		RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
1 1			RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
, ,			VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG
1			GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
1	į		CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
	j		CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
			KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
			SYXAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
1	ļ	ł	PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT
			SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES
] [ŀ		VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
1			
1 1	Į		LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
			LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW
]		}	DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
			LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS
]	ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
ļ l		1	ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
} I			THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
			KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK
[į	IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD
<u>l</u>			QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

SEQ	Predicted	Predicted end	I had a second and
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	sequence	Codon, /=possible nucleotide deletion
ļ	seducite		\=possible nucleotide insertion \
			PVAEVLDTEGSIONFFRKYAPSENGPNGISAEUMDTVIKSCACV
- 1			CVITYILGVGDRHLDNLLLTKTGKLPHIDFGYILGPDPKDLDDD
J	1	ĺ	MKLNKEMVEGMGGTQSEOYOEFRKOCYTAFI,HI,RDYSNI,TI,NI,D
1	ł		SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID
		1	ESVHALFAAVVEQIHKFAQYWRK
6149	1.	1413	RVDPRVRENGTANPIKNGKTSPASKDQRTGKKTSVQGQVQKGND
ĺ	1		ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL
		ĺ	GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
]	j		GPTODINTILLTEROY CORNELIER DISTRIBUTE TO THE STATE OF THE
1	ĺ	}	GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ
1		İ	PQQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA
		1	VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
			FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT
ł	ł		STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS
	i		VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\LSWHPP\HQGL
	1		S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F
6150	372		LIELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKO
0230	3/2	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR
	1		LNXHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEEDWNDGNC
6151			QEGWPPMDGSEGIRITDIDTSGIF
DT2'	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
ı	l i		TPPIVQSYAQPSLQYIQGOOIFTAHPOGVVVOPADAVTTYVADO
	i I		QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVI.PPNMKTAPDDPC
1]		KIYYYHVITROTOWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
}	1		PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSOFTVOCLNDVD
İ	1 1		KPDCKVG\RITTEDFKHLARKLTHGVMNKBLKYCKNPE\DLEC
			NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
			GKTDSRERKSCGPFCSTPVSTVLLMIHHPGEFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
1	1		PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
ĺ	l		GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC
	1		KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW
1 :	1 1		LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
			NGEPLAAEKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLITCFNVGSGLHLQVLSTRNENKLLPKH
			PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
1			TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG
	1		YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
			AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
			GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR
			ILDIANDAL BIOLEGISTI DI VERRIGINGEVIDRIVE NEGLISTI DI LICINI DI LI
			ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN
ŀ			WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD
			FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
1			SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
	1	i	ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
!	1		TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
			SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ
1	1	1	FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP
- 1	1		AALALMILAFLLLLLVPLLLLMCHCGKGAKGFTPTDGTTPMTUD
j	1	i	WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGGG
i	ŀ	1	SASIVKGQHEMSEMDGRWEEHRSLLSGRATOFTGATGAT\MTTTP
ļ	ł	1	TTITARATGASRDVAGAOAAAVALNEEFLKNYFTDKAASVTEED
ı	1		ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDR FLDDT.CI
Į	Í	[KFKTLAEVCLGQKIDINKEIEOROKPATETSMNTASHSLCEOTM
ĺ			VNSENTYSSGSSFPVPKSLOEANAEKVTOEIVTERSVSSDONOV
		11	VATPLPDPMASRNVIATETSYVTGSTMPPTTVIIGPGODOSLIV
			TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH
			The state of the s

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Ī	location		Glutamic Acid, F=Phenvlalanine Grainsine
ļ	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K-Tareine
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, P-Arginine
	residue of	residue of	S=Serine, T=Threonine, V=Valine
i	amino acid	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown +-ch
ł	sequence	sequence	Codon, /=possible nucleotide deletion
<u> </u>	aedueuce		\=possible nucleotide insertion)
	İ		LQDVPYVMVRERESFLAPSSGVOPTI,AMPNIAVGONUTUTEDUL
ĺ			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLDDEGLERGGU
6154			SNSTITTSSTRVTKHSTVOHSYS
8134	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLOMUSKIDI TDAVN
	1		SDTAHIKSIBITSILNGLOASESSAEDSEORDERGAODMONDOR
1			EESKIDHLINNRNDLISKEEONSSSLLEENKUHADIALISKEVEVE
1			SPERLEREDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKBOIK
1	ľ	ł	RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNGSSDED
ŀ	1		EESTKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSFYARVATVTT
i			NNSDERLQNSRAKDRKDVWSSIOGONPKKTLKELESDSDTBAAA
ł			SPPHPAPEEGVAEESLOTVAEERSCSDSVELEKDDDVARDOVDT
1	į i		EEKTVEVNDRKAEFPSSGSNFSA+IPI.PVI.HI.NPI.LOGI +OVGE
	<u> </u>		RQUSSVIVSEPLAPNOEEVRSIKSETDSTIEVDSVAGRIODI OG
	1		ERE*LASRF*CQCELEO**SARTRTS*KSLYRSEKSPDCGCPDV
6155			FIKKAEKKP*SNSGKOOKEGK
0133	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVOKEDBADVTV
			YLKSHFNPCVGVLIKPSWVLAPAHCYLPNT.KVMLGNPVGDVDCC
1 3	l		TEQT_NPIQIVRYWNYSHSAPODDIMITKI AVDAMINDUNOS IN I
			POPTINVRPGTVCLLSGLDWSOENSGRHPDIRONI.PADIMEDDR
1 1			CORTEQUESHRNSLCVKFVKVFSRIFGEVAVATVICKDVLOGID
6156			VGHFMGGDVGIYTNVYKYVSWIENTAKDK
9120	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNODTRKLLMTWATKAN
1 1	1		VMKKSETYAPLFCLPSFHKFCKGLLADTIVEDVNICT.OACCCLU
1	. 1		ALSSSLPDDLLQRCVDVCRVOLVHRGTCIROAFGKLLVCIDLCV
1 1	ĺ		FLSNNNHTEIQEISLALRSHMSKAPSNTFHPODESD/MICETIV
1 1			GNSHRIGKONWLERLFYSCORLDKRDOSTIPRNII.KTDAM WOW
1 . 1	ı		AIWEAAQFTVLSKLRTPLGRAODTFOTTEGTTESTACUTT NDDO
1	ŀ		DVSQWTTADNDEGHGNNQLRLVLLLOYLENTEKIMVNAVEGGAN
}			ALTSPPKVIRTFLYTNROTCODWLTRIRLSTMPVGLARGODART
1 1			VRHGFDLLTEMKTTSLSOGNELEVSIMMVVEALCELUCDER TOO
1	1		TAVWSSSIVGKHLLWINSVAOOAEGRFEKASVRYOFHT CAMTCU
	1		DCCISSFDKSVLTLASAGCKSASLKHCLNGESPKSVILGVDTDGG
	1		PEVINYLGNKACECYISTADWAAVOEWONATHDI.KKGTGGTGIN
1 1	1	}	LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
			IDMKKLERNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
1 1	ł	Į.	PPPGRAHFQKWLMDGTVLCKLINSLYPPGOEDIPKICECVMN By
1 1			QMEQISQFLKAAETYGVRTTDIFOTVDIWEGKDMAAUODTI MAI
]]			GSVAVTKDDGCYRGEPSWFHRKAOONRRGFSEEOLROGONUTGI
6158	<u></u>		QMGSNKGASQAGMTGYGMPROIM*DAASCP
0238	441	1482	LGSLIVLSLHCKVIFSSOSLERAMKEKAVDIJURTLACNDGLACN
			PILEGEDHNONTGVDPIIDHVODRETD/SRSESPHEEPS
]	ŀ	ì	KKSRSRSHSRDKRKDTREKIKEKERVKEKDPEKEDEDEVEDDE
	1	l I	KERGKNKORDKEREKDREKDKEKDREREREKEHEKDROKEVEVE
	1	1	VDKEKEREKDRSKEIDEKRKKDKKSRTPPRSVNASPPSPSSSSS
!]		RRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKDEKEDD
		[-	HISERRERERSTSMRKSSNDRDGKEKLEKNSTSLKEKEHNERD
6159			SSVSKEVDDKDAPRTEENKIOHNGNCOLNEENLSTKTEAU
0133	53	84 .	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNOSEDDVMSLTU
1	ļ	1.3	RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSt.PVGSCV
1		į.	111GTPILTFVKDPQLEVNFYTGMDBDSDIAFOFRI.HFCHDa.tm
1		. [1]	NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGOR
1		1 -	IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVOFF
6160			DVSVSCDCTTAYQPG
6160	1626	1790	AGAKFFP*F*KVADAOPTESEKEIYNOVNVVLKDAEGILEDLOG
			YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ŀ			LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
1			ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
i			SLFYAEATPMLKTLSDATTKFVSENKNLPIENTIDCLSTMASVC
1			RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
1	1		TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI
6161	455	1569	KSMLQ*QLLTLVNKG
0202	1 222	1305	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH* KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISSDS
			TGQLHLLMVNETRPRLQKVASWQAHQFEANIAAFNYWHPEIVYS
			GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
1	1		GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
1			CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
1			RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
Į.			ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
-			LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFGHWTYE
			CTGKRKYLHRPSRTAELKKALKEKENRLLLQQSIGETNVERKAK
			KKRSKSVTSSSSSSSSSSASDSSSESEETSTSSSSEDSDTDESS
1			SSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
		·	EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL
			TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD
			MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
1			MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIBLIRQR ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
1	1		GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAON
			ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
1			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
1			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
i i			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
<u> </u>			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
1			LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMERMTTDIN
	i		ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
	1	•	PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
	ł		VQAKLGALELNORDAAAETELRVHPPCORHCPEPPSAPEENKAT
	İ	,	SKAPOGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPOEYORN
	1		GGERFG
6165	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
	ţ		NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
}	ŀ	ļ	WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
•			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
i			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
l	i		RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
	ļ		LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE

SEQ	Predicted	Predicted end	Amino coid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Į	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
1	ł		ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
ļ			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
1			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1	1		VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
L			GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
1			LDLPREAFEAASREDFELQGYAFEAAEEQLRRPRIVHVGLVONR
1	i		IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFOEAWTMP
1			FAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE
			RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
1 .	[EGNLGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP
			SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
1			NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS
6167	1220	1044	VPALG
1 0207	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
1 1			LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
·			VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
1 1			HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF
]			LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK*APLYLTPEGWS
1			LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG
	i		DRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDGKWV
]	}		VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST QPFSLKNLDK
6168	84	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK
1 1			GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ
1 1	}		ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
1 1			DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG
l			EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
		1	PPGFVLKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF
			LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP
			ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRDVD
1 1	I	ļ	ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
1-51-5-L			EREGTENGAIDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
		1	AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFORFVT
		į	PLKEALEAYRREQKGKKEASEQKKKDKDKKTDSEEODKSRDEDN
			DEDEERLEEEEQNEEEEVDN*KGRETVAPWKVPLEMRRATCFCE
6170	62		AFPCWAE
/-	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
	1		AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA
	į.		VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
			TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWPKQHCGRW*VV
6171	382	941	G*GDGLCLICFELNLCMSDVITICT
	J.42	341	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
		ļ	MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN
		ĺ	SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD
í			RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT NATLRYTKSK
6172	651		
-		rc	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
1		1;	SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV
			TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA

SEO	Predicted	Predicted end	Dmino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C-Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
}			QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
}	ļ	i	FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
ł		•	SDILRYLFPVPKDDSHRVITFANODDYISFRHHVYKKTDHRMVE
			LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
			LSTE*AAPRPLGQLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
1			LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
i			ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIOHO
			RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
1			TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
			GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
İ			HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
6174	1000		MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
01/4	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
			MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
6175	2204	334	LDHIRERSQGPSLGP*H*WFSKKA
		23.1	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
ł			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
1			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
			GBDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM
1 1			MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
1 3			PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
1 1			CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
1			SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
]			DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILVP
1			KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
1			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
1 1			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
1 1			PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
6176	3040		FHLNTKL
02,0	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
		•	GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
			SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
1 1			AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
6177	1400	992	RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
'		7,2	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
1 [İ	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
	1		PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP VCPI
6178	1027	254	STQRGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
1			HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
	j	1	LHLAI PAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
}		1	NIFREQUALIQUALIESRIDCQHRCGIFQYETISCNNCTDSHVA
1		l	CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
		l	THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
j l	ļ	<u> </u>	PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
		1	WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
			FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECON*
			SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
			SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
			MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE
			TTT TO TO TO TO TO TAKE THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		}	GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
1			TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
1			VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
1			HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
1			LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
			KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
			PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
			MCEQALLIKRRRLLSPEDMNKLMFLKSNML
5181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
1			YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
			VSLLELLHIYVGIESNHLLPRFLQLTERIIILFVVITSQEEVQE
			KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
1			IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
			YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
			KDRLWIQCSK*NTGSILVEKFLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
1			VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQ
			VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR
			FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
		•	CWARAHSLTSSIPGAWITNFSLTMMVIFFLORRSPPILPTLDSL
1 1			KTLADAEDKCVIEGNNCTFVRDLSRIKFSQNTETLELLLKEFFE
1 1			YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
1 1			SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
			STOT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC
			GSGCGGCGSSCGGCGSGCGCGSGCGCSSCGGCGS
1			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
1 1			GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC
1 1			CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
			VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
1 1	i		EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
1 1			FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
	1		ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR
1			LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
]	1		HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
1	İ		QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
1	1		PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
1	İ		NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
1 1			TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
1	,	į	DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI
			NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR
			GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
] [MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
1			FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ
			QLRKNQQLQRFIQWLKEAEEESSEDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
			IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR
1			HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
	}		GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
]			REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
6186	569		GCQEAEMQTPRRLGWGWYHTLTLYLWEEK
0100	303	238	VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA

SEQ Predicted beginning nucleotide location corresponding to first amino acid segment containing significant corresponding to first amino acid residue of amino acid sequence	c Acid, E= =Glycine,
No: nucleotide location corresponding to first amino acid residue of amino acid sequence Record	c Acid, E= =Glycine,
corresponding to first amino acid residue of amino acid residue of amino acid sequence Corresponding to first amino acid residue of amino acid sequence Codon, /=possible nucleotide insertion Codon, /=possible nucleotide dele	ne
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequen	ne,
to first amino acid residue of amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginin S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele \=possible nucleotide insertion) KERKVKNKVKNKADTEEVFNNSPTNOEKMPTSA NIRNQMETLHSQPHQEENLCFENSFSLINLTP PNRETSEANKERRKMTSKSSESNIYSPLTSFIT LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVC EFENCHKERTQEKWGFPMCHYLKEERWCCGNNA AAGQCIPTESLFYRAVLQDIIKDCYGITKCDRH LDYVRRSLKKIGLDESKLPEKIIMNYYEKYKPR VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLI VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVC PSGSRVGSRYD DAWGPETRLARILNPDSFIEPRGRLPELEATRI AAPJMERKFMVLVGYTGSVAALKLPLLVSKLLDD ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSS AMWSHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSSK GKIGGYPHLINGGPALSLPRGQACSRLNWTEGPE GKIGGYPHLINGGPALSLPRGQACSRLNWTEGPE A 6188 238 1534 KGFVNAGFLMAELQVSPQWKAPEMSQICLSCGHP NIGYFICTRCAGTHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVYEKVM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNLT PSPSSSCSRKVVVGSMPTAGSAGSVPENINLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAQMAYPT PNSIMGSMMPPPVGMVAQFGASGMVAPMAMPARGY VVRIGMMTTQQAGGMAGMAQMPOTVYGVQDADOLO	
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele \(\)=possible nucleotide insertion) KERKVKNKVKNKADTEEVFNNSPTNOEKMPTSA NIRNQMETLHSQPHQEENLCFENSFSLINLLFI PNRETSEANKERRKMTSKSSESNIYSPLTSFIT LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVC EFENCHKERTQEKWGFPMCHYLKEERWCCGRNA AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRH LDYVRRSLKKIGLDESKLPEKIINMYYEKYKPR VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLI VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVC PSGSRVGSRYD AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDI ERAKHFYSPQDIPVTLYSDADEWEMWSRSSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLIVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLLNGCPALSLPRGQACSRLNWTEGFG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHF NIGVFICIRCAGHRNLGWHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSSEVPEKKLEPVYPEKVLM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLINLFPEP QLSKDSILSLYGSOTPQMFTQAMFMAPAQMAYPT PNSIMGSMMPPPVGWAQFGASGMVAPMAMPAQT	gine,
residue of amino acid sequence	e,
amino acid sequence Codon, /=possible nucleotide dele	
sequence Sequence	wn, *=Stop
KERKVKNKVANKADTEEVFNNSPTNOEKMPTSA NIRNQMETLHSQPHQEENLCFENSFSLINLIPI PNRETSEANKERRKMTSKSSESNIYSPLTSFIT LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKÖVC EFFENQHKERTQEKWGFPMCHYLKEERWCCGRNA AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRH LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPR VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLI VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSV PSGSRVSSRYD 6187 1701 771 DAWGPETRLARILNPDSFIEPRPGRLPELEATRI AAPLMERKPHVLVGVTGSVAALKLPLLVSKLLDI ERAKHFYSPQDIPVTLYSDADEWEMKKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRS AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLLNGGPALSLPRGQACSRINWTEGPG A A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHE NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVYFKKVKM RKSSFKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGMAYPT PNSIMGSMMPPPYGMVAQPGASGMVAPMAPAGMAYPT PNSIMGSMMPPPYGMVAQPGASGMVAPMAPAGMAYPT VPNGMMTTQQAGYMAGMAAMPCTVYGVOPAOOLO	tion,
NITANQMETLHSPHQEENLCFENSFSLINLLPT PNRETSEANKERRKMTSKSESNIYSPLTSFIT LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVC EFENQHKERTQEKWGFPMCHYLKEERWCCGRNAI AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRH LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRI VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLI VIALKKQV*FPLKQIIRCISL*DSAGCAEEVSV PSGSRVGSRYD DAWGPETRLARILNPDSFTEPRPGRLPBLEATRI AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDD ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCWNAWDRSK AMWEHPITAQQVDLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGFG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDVTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDVTQ INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSTLSLYGSQTPQMPTQAMFMAPACMAYPAT VPNSIMGSMMPPPVCGWVAQPGASGMVAPMAMPAGY VPNSIMGTTQQAGYMAGMAAMPOTYYGVOPAOOLO	
PRRETSEANKERREMTSKSSESNIYSPLTSFIT LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVC. EFENQHKERTQEKWGFPMCHYLKEERWCCGRNAI AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRH LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRI VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLII VIALKKQQ*FFLKQIIRCISL*DSAGCAEEVSVC PSGSRVGSRYV PSGSRVGSRYV AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDJ ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGE GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHF NIGVFICITRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDVTQ INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAGY VPNSIMGSMMPPPVCGWVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVCGWVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVCGWVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVCGWVAQPGASGMVAPMAMPAGY	ILPDFSGSVIS
LEDCLMYGLATCGDLAPNTLRIFTSNSEIKGVC EFENQHKERTQEKWGFPMCHYLKEERWCCGRNA AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRH LDYVRRSLKKLGLDESKLERKIIMNYYEKYKPR VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLI VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVC PSGSRVGSRYD DAWGPETRLARILNPDSFIEPRPGRLPELEATRI AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDJ ERAKHFYSPQDIPVTLYSDADEWEMMKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSH AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGL TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHE NIGVFICTRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETPRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGGTPQMPTQAMFMAPAGY VPNSIMGSMMPPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPPVGMVAQPGASGMVAPMAMPAGY	NAVEPTSSQQI
6187 1701 771 DAWGPETRLERVEGENALVELOSER PROCESSALVELOS PROCESSAL	ADSELHDIIKD
AAGGEPTESLFYRAVLQDIIKDCYGITKCDRH LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPR VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLI VIALKKQQ+FPLKQIIRCISL*DSAGCAEEVSVC PSGSRVGSRYD AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDD ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEM GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHF NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKENDDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAGMYPGT VPNSIMGSMPPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMPTQQAGYMAGMAAMPOTVYGVOPAOOLO	SVGCCYHLLSE
6187 1701 771 DAWGPETRLARILINPDSFIEPRPGRLPELEATRI AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDI ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVT LLVAPLDANTLIGKVASGICDNLLTCVMRAWDRSS AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEM GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVLM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGY VPNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY	RMSACLALERV
VVLAPCIETLILIDRLCYLKEQEDIAWSALVKLI VIALKKQV*FPIKQIIRCISI*DSAGCAEEVSVI PSGSRVGSRYD ANDEREKPHVLVGVTGSVAALKLPLLVSKLLDI ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCWMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGU TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGFG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHE NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYG INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGY PNSIMGSMMPPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGTMTQQAGTMAGMAAMPDTVYGVOPAOOLO	/GKIYSKCSSF
6187 1701 771 DAWGPETRLARILINPDSFIEPRPGRLPELEATRI AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDJ ERAKHFYSPQDIPVTLYSDADEWEMMKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*FGISVMGVPLYSEG GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHF NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRBVEY INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAGY VPNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY	INELEAFNMLK
6187 1701 771 DAWGPETRLARILINPDSFIEPRPGRLPELEATRI AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDJ ERAKHFYSPQDIPVTLYSDADEWEMMKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*FGISVMGVPLYSEG GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHF NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRRVE INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAGY VPNSIMGSMMPPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPPVGMVAQPGASGMVAPMAMPAGY	TOPUKSDBAVA
6187 1701 771 DÄWGPETRLARILNPDSFIEPRPGRLPELEATRI AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDJ ERAKHFYSPQDIPVTLYSDADEWEMMKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHF NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETPRRPQIDPAVEGFIRDKYE INAFRKENDDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSTLSLYGGOTPQMPTQAMFMAPAGMYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY	DGGPALRDAP
AAPLMERKPHVLVGVTGSVAALKLPLLVSKLLDJ ERAKHFYSPQDIPVTLYSDADEWEMMKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSH AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGL TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEM GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKENDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAGY VPNSIMGSMPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMPPPVGMVAQPGASGMVAPMAMPAGY VPNSIMGSMPTQQAGYMAGMAAMPOTTYGVOPAOOLO	
AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDJ ERAKHFYSPQDIPVTLYSDADEWEMMKSRSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSH AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGMYPT PNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTYYGVOPAOOLO	HMEPKASCPA
ERAKHYSPQDIPVTLYSDADEWEMKRSSDPVI LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSK AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGL TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEM GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGT VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	PGLEVAUUTT
AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGL TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEW GKIGGYPHLINGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGMAYPGT VPNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY VPNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGTMAGMAAMPOTVYGVOPAOOLO	HTDI.PPWant.
AMMEHPITAQQVDQLKAFGYVEIPCVAKKLVCGI TIVDKVKEVLFQHSGFQQS+GISVMGVPLYSEM GKIGGYPHLINGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETPRRPQIDPAVEGFIRDKYE INAFREKENDKWKRGSEPVPEKKLEPVVFBKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAGMYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGTMAGMAAMPOTVYGVOPAOOLO	PLIFCDAMNT
GKIGGYPHLINGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKENDKWKRGSEPVPEKKLEPVVPEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGC VPNGMMTTQQAGTMAGMAAMPOTVYGVOPAOOLO	EGT.CAMAEVO
GKIGGYPHILNGGPALSLPRGQACSRLNWTEGPG A 6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGMAYPT PNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	VOAKSUKMDU
6188 238 1534 KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFBRVVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPAGMAYPT PNSIMGSMMPPPVCMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTYYGVOPAOOLO	LSFFOPGEAA
RGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHP NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFBKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSTLSLYGSQTPQMPTQAMFMAPAGMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	
NIGVFICTRCAGTHRNLGVHISRVKSVNLDQWTQ NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFBKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGGOTPQMPTQAMFMAPAGMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGTMAGMAAMPOTVYGVOPAOOLO	SA*GPRWASW
NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYE INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKM RKSSPKSTAPVMDLLGLDAPVACS IANSKTSNTL PSPSSCSRKVVGSMPTAGSAGSVPENLNLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPACMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	ECTOCMORMS
INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKM RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSGSRKVVGSMPTAGSAGSVPENLNIFFEP QLSKDSILSLYGSQTPQMPTQAMFMAPACMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	KKKVMDDet.D
RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTL PSPSSGSRKVVGSMPTAGSAGSVPENINLFPEP QLSKDSILSLYGSQTPQMPTQAMFMAPACMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	POKKEDPOLP
QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	EKDIDIJI. A SV
QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPT PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGY VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	GSKSEEIGKK
VPNGMMTTQQAGYMAGMAAMPOTVYGVOPAOOLO	AYDS#DGW7D
VPMGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLO	MGGNQASMMG
	WNLTQMTQQM
6189 1297 793 IGEPLICAL PRINCIPLE OF THE	NK .
I DEPLODICELIPGUVQQLOMGEVHPGTGAOGSA	AQSVAGEVQL
TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQ	IVQPVARQVQ
RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGG	CVFAANACDL
VVQDHEGAHAARQATGHALQRVIVQVRRVQDLEA	*RVPSGLPR
RVRAFMILHNQITGIGREDFATTYFLEELNLSYN	RITSPQVHRD
AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVI	CRNELAALAR
GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHI	QLLDIAGNQ
LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTP	LKGIFLRFN
KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKI	RGRLGKEKE
6190 66 1309 TIJGNUSELLSEBEVICEGERINGS MADERICA	
1509 ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNOTTG	QCECRPGYQ
GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPC	NSSCKCOCK
VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASC	DALTGACIN
CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAV	TSTGSCSTK
SSELEPECDQCKDGYIGPNCNKCENGYVNFDSICP	KCOCHCHO
PVKTPKICKPESGECINCLHNTTGFWCENCL*GYV	HDLEGNOTE
	TIOTIFEUE
TSENSTSALADVSWTQFNIIILTVIIIVVVI.LMGF	VCAVVMVDE
IQNRKLNAPFWTIELKEDNISFSSYHDSIPNADVS	GLLEDDGNE
VAPNGQLTLTTPIHNYKA	
VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHI	1
MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEM	POOPKCPS .
QDYMFSLISGS	PPOOPECPS EAIILSKLM
TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGT	EAIILSKLM
KGGLVSDAYGEDDFSRLGGDEDGYEREEDENSROSI	EAVISABER
PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDE:	EAIILSKLM EAVGSAAEE
RCSNHLQDKIQKLYERKIKEGMDMNYIIORKKEFRI	EAVGSAAEE EDDDSETEK
QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQI	EATILSKLM EAVGSAAEE EDDDSETEK IKIPPEPPG

SEQ	Predicted	Predicted end	I American and I
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	J	\=possible nucleotide insertion)
Ì			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
ļ			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
Ì			KGGLVSDAYGEDDFSRLGGDEDGYEEEEDBNSROSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
ı	1		RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI
1			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
			DSAI?VTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKO
6194	3	950	
	1	230	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGTEAVGSAAEE KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
ł			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
			QPCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
ļ			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
l	l i		DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
			YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
			PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
6196		•	PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
6136	1512	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLIOREDSH
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEOMVLDYISKLLDIJC
			HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSI.
1			FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL
			MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
1 1			NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS
6197	3	819	NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL
	- 1	0.25	ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
			PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
1 1			RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
1 1			SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
1 . 1			RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS
L			YRHKNSW
6198	111	1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
1		}	RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLODSO
			REMPPPPPPPPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASOFT.
			LACGVLWFSGYGHIWSQNATNLVSSLLTLLKOLEPTAWLDSGTW
			GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRROSV
1 1	İ		SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP
, 1			TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
1 1			AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKFV
1 1			DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG
1 1	1	1	YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
	J	j	EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER
	İ	ļ	GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII
ļ		l	VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE
6199	144	1211	WYDENCESCERNING TO THE THE THE THE THE THE THE THE THE THE
			MARENGESSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
J			TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV
	ļ	1	YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGD
	1		VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	We'Trantonhan W There's a state of the
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	Dequence	Codon, /=possible nucleotide deletion,
<u> </u>			\=possible nucleotide insertion)
- 1			FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
1		İ	NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ
1	1	1	AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF
6200	702	- 25	HAL*
1 3233	102	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
	1	1	WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
	1	į	PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
1	1	!	QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
6201		<u> </u>	QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
1	1		RKRILGSASPEEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
			DGSQGFKQRR
6202	2	426	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE
ł	1		DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
J			KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISQ
			DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAPASQHPA
1	1 1		TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYOERMNKGER
	()		LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSODIOKTIKKTA
}			RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKOGLNGV
-	i		PILSEEELSLLDEFYKLVDPERDMSLRLNBQYEHASIHLWDLLE
ļ	i		GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA
]		SAPAVEDQVPEAEPEPAEEYTEQSEVESTEYVNROFMAETOFTS
1	ļ <u></u>		GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAOAD
1	1		PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAOPM
1	1		NPTQNMDMPQLVCPPVHSESRLAQPNQVPVOPEATOVPLVSSTS
1	l		EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDOTTASSS
	[LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFKMNAPVP
1 1	ł	ł	PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELOOEOLOTVVG
1	i I		TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNOPYYNSRGVSRGGS
1 1	ľ		RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTOSOFSAP
		1	RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
6004			NTQQVN
6204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
	ļ	}	PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
1			RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP
1		1	CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC
1 1	1	1	ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVT
1 1		Į.	YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
1			NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
[]	İ	İ	HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
l i	İ]	AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
] [1	i i	EAPRRSFAGGTWDWEYLGFASPEEYAEFOYRRHRORRRGDVHS
)		LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
1 1	ł	1	SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIOLSLOESGLA
; I		1	LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
; !	}		LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
1			AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
1 1	1		CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
<u> </u>			PGGGKQHPQAW
6205	1		RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
	j		SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
	İ	l	KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
		-	QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
		f.	LDKELDEYMHGGKKMGSKBEENGQGHLKRKRPVKDRLGNRPEMN
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	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid R-
- 1	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine G=Glucine
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
ı		corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1		residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- (sequence	sequence	Codon, /=possible nucleotide deletion,
⊢		Bedgettee		\=pcssible nucleotide insertion)
1				YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRIIGNKKA
				IELLMETAEVEQNGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
				QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
			•	DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD LDIF
H	6206	10	1442	
			4442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
				APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLM
	ĺ			IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAPFIPEGTFTTVW
				FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA
				ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
				VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
	[TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
	i			FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
				RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
_				KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
	6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
				GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
	ł	į		SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
1				SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEPVP
ı				GQPYCGRTAPSCTEAPLQGSVTKEESEKEOTAVETKKOLCPYAA
	'	İ		VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1	1	1		HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
			· -	HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVBE
				KEEKQKLILKYKRAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1	Ì	ĺ		GRRESPOROKVGTSSRYRAORRNHFWELIEERENSNPFDNDEEE
\vdash	6208	2924	1471	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
	1			TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
	1			GGGGGSDGSGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY SVVCKYFQRGYCIYGDRCRYEHSKPLKQBEATATELTTKSSLAA
	1		•	SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
				GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
1			ì	VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1				HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1	,	1		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
	1	ļ		KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
	1	İ		GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEER
<u>-</u>	6209	1750		VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDI.
Ι΄	0209	1758	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLOEENSVTHHEVKCOGK
1			Į.	PLAGIYRKREEKRNAGNAVRSAMKSEEOKIKDARKGPLVPFPNO
1		į	1	KSEAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKOAPRKKAOGK
l				TQQNRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM
	1			KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
l	}		i	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
				TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL
-	210	3761	387	IFGMSKLRMVLLBDSGSADFRRHFVNLSPFTITVVLLLSACFVT
	1			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMBAV
٠.	. }		.	SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
		1	. 1	CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
			ľ	IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
		İ	1	SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
	- 1		1.	ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
		·		QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
		j		WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVETORI.
				LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL

	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
		amino acid	sequence	Codon, /=possible nucleotide deletion
		sequence	L	\=possible nucleotide insertion)
				FLSSCNGNETSLWDCKNWOWGGLTCDHYREAKTTCSAUDEDDTU
				GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCPRIOCGTVAL
				SILGGAHFGEGNGQIWAEEFOCEGHESHLSLCDWADDDCCTCCW
				SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTIGAWGSLCNSHWD
- 1				IEDAHVLCQQLKCGVALSTPGGARFGKGNGOIWRHMFHCTGTFO
-				HMGDCPVTALGASLCPSEQVASVICSGNOSOTLSSCNSSSIGPT
- 1				RPTIPEESAVACIESGOLRLVNGGGRCAGRVEIYHEGSWGTICD
	i			DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGDTWLDEMVCN
- 1	1			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSI.RI.TSFASRE
	ļ			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCROLGCADYGKIND
-1	İ			ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
ı				WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
- 1	1			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
- 1	1			ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
-1		•		VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
ı	6211	3761	387	EMNSCLNADDLDLMNSSGGHSEPH
			307	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
1]		SSLGGTDKELRLVDGENKCSGRVEVKVQBEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
1		1		CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
ı	1			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
f	1	i		SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
ı	1			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
ı	1			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCOGHEDAVWOCKHUR
1	ł			WGKHYCNHNEDAGVTCSDGSDLELRLRGGGGRCAGTUFUFTOD:
1		!		LGKVCDRGWGLKEADVVCROLGCGSALKTSVOVVSKIOA TRATTENT
1				FLSSCNGNETSLWDCKNWOWGGLTCDHYEEAKTTCGAHDEDDIA
ı	1			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELOCGTVA
				SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
1	1			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
ı	1			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
		1		HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
				RPTIPEESAVACIESGOLRLVNGGGRCAGRVBIYHEGSWGTICD DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
ı	į.	}		GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
	1	j		ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
-	-			ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
				WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAOV
1			Í	VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSIWDCD
ı	- 1		1	ARRWGHSECGHKEDAAVNCTDISVOKTPOKATTGRSSPOSSETA
1				VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHOIOYR
 - -	6212			EMNSCLNADDLDLMNSSGGHSEPH
	0212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
		1	İ	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSDGI
	1	1		GCSKPHDEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
	1	İ		QKNNCVMPEDVKNFYLMINGFHMIWSVKLDEHIIPLGSMAINSI
				SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDOPEKPHFDSPS
	İ	i	,	VIFELDS CNGSGKVCLVYKSGKPALAEDTEIWFLDRALVWHFLT
	1			DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
	ĺ	j		NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVOPAGGOK
-	6213	1		GPSGPSGPSTSSTSKSSSGSGNPTRK
		-	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
		4	1	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
]	GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
	1			QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
	1	<u></u>		SKLTOLTOSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS

SEQ	Predicted	Predicted end	Amino acid cognonia
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- 1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	sequence	Codon, /=possible nucleotide deletion,
 			\=possible nucleotide insertion)
			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
ł	Į.	İ	DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
İ]		NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
6214	2	460	GPSGPSGPSTSSTSKSSSGSGNPTRK
	1	1 400	HELAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRTGWSFVGWV
İ		1	VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKRFSAYN
1	İ		YRTYAVRRIRDAFRENKNVKDPVBIQTLVNKAKRDLGVIRRQVH
6215	2	1849	IGQLYSTDKLIIENRDMPRT
]	1 -	1043	FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV
i	1		MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISHFHLDH
1	i .		CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAVDKKGE
İ			ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAGHVLGA
			AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST
1			YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAQELC
J]		ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNQKIRKT
1			FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF
			RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKMEFLKQ
· •			KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQGL
			LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHQLRFTC
			RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL
			LQANAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGLPQAPS
6216	11	393	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS
1 1			GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE
			FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDPKEPEQ
			LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG
1 1			FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA
1 1	J		HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK
1 1			KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS
1 1			AGSQRGRGGGGGNFMGRGGNFGGGGGGGGGGGGGGGGGGGGGGG
	ļ		GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYG
1 1	i		NQGGGYGGGGYDGYNEGGNFGGGNYGGGGNYNDFGNYSGOOGS
			NYGPMKGGSFGGRSSGSPYGGGYGSGGGGGGGGGGGRRF
6218	1305	906	SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPV7KVA
		1	NDNAPEHALRPGFLSTFALATDOGSKLGLSKNKSIICYYNTYOV
-			VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELROVVEVS
6219	2	890	AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADR PHORDEL
1		1	IGVSGGTASGKSTVCEKIMELLGONEVEORORKVVILSODREVK
1	, 1		VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP
]	1	!	TYDFVTHSRLPETTVVYPADVVLFEGILVFYSORIRDMFHT.PT.F
1 1	1	!	VDTDSDVRLSRRVLRDVRRGRDLEQILTOYTTFVKPAFEEPCLD
1 1		ł	TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG
6220	222		RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
0220	227	764	EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN
	1		KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIOCENROIRFI.OO
]]			enkelrtsleehosalelimskyreomfrlimaskkodpgiimk
ļ .	1		LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ
6221	98		NVH
	20	916	RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP
] [1	NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG
	İ	1.	AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK
, ,	J		YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNOHINRLDE
	1		AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
			DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL
i_			LDLREKRK

055			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid E-ph
ļ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
j	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
- 1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, Y=Unknown + Da
		sequence	Comon, /=possible nucleotide deletion
	sequence	.] .	\=possible nucleotide insertion)
6222	2	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
	1	Į.	PRENDAMETORCHI ECTOTTA EDITATATATATATATATATATATATATATATATATATATA
į.	i	i	PRRNPAWSLQAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH
		[EFQAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLV
1	1	l .	SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNLGTIA
1		1	RSGSKAFLDALQNQAEASSKIIGOFGVGFVSAFMIADDIVERNOD
	1	1	SAAPGSLGYQWLSDGSGVPEIAEASGVPTCTKTTTULVCDGVPD
1			SSEARVRDVVTKYSNFVSPPLYLNGRRMNTLOATUMMDDVDVD
ĺ	1	Į.	WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
İ		1	FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
	ļ	; }	PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF
	i	ĺ	FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
1	į.		EVASEMBACTERITYELGADIANTESSALPSGQLTSLS
Í	ĺ		EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
J	1		EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
	1		CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG
!	l		AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRAS
6223	3		EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRINELLVVA EDU
1	, -	715	DAWARTMAGMVDFQDEEQVKSFLENMEVECNVHCVHRKDDDCCV
İ			KLVDILEGIRKNFDEAAKVLKFNCEFNOHSDSCVVI.CA VVXIMOV
1			GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAUDGOVNED
1	1 1		GQPDLGKARDYYTRACDGGYTSSCFNT,SAMFLOGADGEDVDWDT
	1		ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA
6224			QQVHKEQQKGVQPLTFG
	1	133	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHEK
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARQAFLAFGDVTVDFT
1	1 1		QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPELIRRLEQ
Ī	[GEVPWGEEDDDDCDCACTVARIUS DVOT OF STREET
1	1 1		GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
ł	1 1		QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
1	1	i	SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH
1	1 1		KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG
	1		RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH
1 :	1 1		TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
1 1	1		NASIFVVHKRIHSGEKPYRCOECGRGFSNKSHLTTHOPTHCGEV
	[]		PFACKUCKQSFSVKGSLLRHORTHSGEKPFVCKDCFDCFCAVcm
	1		LVINGRIHSGEXPFVCRECGOGFIOKSTIVKHOITHGERVORUS (
j i	[KDCGRGF1QKSTFTLHQRTHSEEKPYGCRECGPPFPDKggynty
1		1	LRAHLGEKRFFCRDCGRGFTLKPNLTIHORTHSGEKPEMCKOCE
1)	, ,	!	KSFSLKANLLRHQWTHSGERPFNCKDCGRGFTI.KSTT.I.FHOVTH
1			SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
1 1		1	WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
!!		1	KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
		į.	YYSKHLKRHLREKRFCTGSVGEASS
6226	29	266	TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
	43		- WASHING OF STRUMENT OF THE S
	23	1	TMPGGGGGT DVGmgr GWT GT TWO GT
6227			IMEGGGQSLRVSTGLSWLLSLPWRAORIRAGESVA (
6227	2581	890	MEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVONGSVHOKDGLNDDDFFPVLSBOARR
6227		890	IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
6227		890	IMBEGGGSLRVSTGLSWLLSLPWRAGRIRAGRSYA MSASSLLEGRPKGGGNKVQNGSVHQRDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGDHGFNTWPSGIDES
6227		890	IMEGGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQRDGLNDDDFEFYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGAMIDGOSAFANDER
6227		890	IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEFYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITENT
6227		890	IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP MNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFN7FPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKOOPKLKTKNGIAGSG
6227		890	IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP MNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFN7FPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKOOPKLKTKNGIAGSG
6227		890	IMEGGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP MNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSOALVONIGOPTOGSPORVG
6227		890	IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQRDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFN7*PSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQDYVG
6227		890	IMEGGGSLRVSTGLSWLLSLPWRAGRIRAGRSYA MSASSLLEQRPKGGGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFPPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGGSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPJKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPQPAQLSVQQQAAQFTRWV APRNRGSGFGHNGVDGNGVGOSDAGSGSTPSEPHDVLEKLBGIN
6227		890	IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEWANV
6227		890	IMEGGGSLRYSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP MNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGQQSAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAFMKSAVDVNTGAG
6227		890	IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEWANV

SEQ	Predicted	Predicted end	I have
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Trunt orban Variance, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion,
6228	47	1978	\=possible nucleotide insertion)
1			GRRCRRGAVMELAQEARELGCWAVEEMGVPVAARAPESTLRRL
ŀ			CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
1			ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
1			QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
	i		DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
]		}	SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
j	1		EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
	1	ĺ	RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
j	1		ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
l	ł		LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
ŀ			PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
1			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1	1		RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQBKQ QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
L			ELCQGLSLPQWRLRWVQAQGALQKLCS
6229	1571	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEEFG
	1		NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG
1	1	•	NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL
	}		LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI
	1		HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
	1		VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
	1		ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
			AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
			VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
			NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP
	1 1		PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
	İ		SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
	1		TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
	1 1		SOSSGLAAKFVIHCHIPOWGSDKCEEOLEETIKNCLSAAEDKKL
	1		KSVAFPPFPSGRNCFPKOTAAOVTLKATSAHFDDSSAGGIVNDV
6231			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLOSLOSSLVSFRG
	1		LGVTALSTLYGGMLLSSMFLPPLLIERIGCKGTI II.SMCGVVAR
	1		SVGNFFASWYTLIPTSILLGLGAAPLWSACCTYLTTTCNTHARY
	1	ļ	AGKRGKDMVNQYFGIFFLIFOSSGVWGNI,TSSI,VFGOTDGOEDT
	1		PEBULTSCHASDCLMATTTTNSTORPSOOLVYTLIGTYTGSGV7.
6232	3679	7.475	AVLMIAAFLQPIRDVQRESE
	55,5	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
		j	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGETACBUTDTC
]	KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSVINMDA
			IMEALKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFTGDDTUA
į		1	IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY
	J	1	PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL
	,	ſ	LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSTORPNOKURER
			APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY
	ļ		FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
}	1		INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
			1QPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVITEGY
i	[THN1ALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMT.TKSFV
	[1	NOLLALASSLEVAFQLRAOHFOENSRMPVIKPDIANWELSVKLU
- 1	1	,	DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPIJ.SVSVDGT
		i i	QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKEMI.EKV
.			TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGOETCVTEAMWMONG
6233			MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
0433 I	1	2654	HSTRENLNAGNPNFPSEGHLVRSTGPGGSFAKHMVAQCVSPKGP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	N-Termine, Ternreonine, Vevaline,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	Doduciice		\=possible nucleotide insertion)
1	1		LACSRTYFFGATHVPYLGGDSKLPKKTEQIRLLSQIYAAVIEAV
1		ł	LAGIACYAKTSSLTKAKEVAEQTLGSGLDSFELIPFKAALRSKM
1			TFHIHAVNNOGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
	'	,	LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
	1		VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLOSWP
			EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
1			ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYOAFYSEVF
1	}		SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAOKLFSALSOPAG
1	J		EKRSSLKLLSAKLPELDWFLQHFAISSISOEPVMRTHLPVLLOO
1			AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
1			MVYRQIMDSSECFHAAHFQRYLSSALEAOONRSAROSAYIRKKT
.			RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS
ł			CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEORHPLLVOLOSI.
1)		IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYI.
	ļ		MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIOS
	1		SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL
			EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLROSA
1	1		KQKPQRKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTOFV
ĺ	1		NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQELEQQEYHDLF
			ELKP
6234	1731	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL
İ			DKQSDIQNLNEERILALOLCGWIKKGTDVDVGPFLNSLVOEGRW
ł	! !		ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
1			DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVI.YEN
1	1		KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
			LTKDGVDLMESYVDRTGDVQTASYCMIQGSPLDVLKDERVQYWI
Ì			ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG
	i		KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
ļ	!		ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
1	i I		CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV
6235	1		QP
1 0233	1 - 1	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPQ
1	ľ		DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATQ
			IVMGGVTGWCAGFLFQKVGKLAATAVGGGFLLLQIASHSGYVQI
1			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEFIKQNIVI
6236	1	703	SSGFVGGFLLGLAS
	*	103	WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
] }		·	NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE
]			NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
.			SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT
!!!		ŀ	LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ
6237	312	720	DELSQRLARLRDQV
, J.,	314	720	PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA
J	}	ļ	LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL
	İ	j	GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK
6238	2	4666	CKK
	* ∤	*000	EBVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI
.		ĺ	CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF
ļ		į	YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE
l	ł	ļ	TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
i i			KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL
l		1	INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
ľ	ļ	ŀ	MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG
ļ		ļ	LVMLNNLVKAFTEAATGSSADFVKDLAPFMILNSLGLTISVSPS
l	į	}	DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK
		l	LFFILLTFVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ŀ			DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN
			IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS
			KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL
		•	LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
1	1		YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
İ	ł		FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK
			MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
		•	KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC
]		ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFLLINHTK
ł			NELVQYNQSSLSEIEDSLPPGKAVFYTWADPVGSRRLKWRCRKS
1			HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVFK
			VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD
}			VVWETKPKKKARWKPMSVKHTEKLEREFKBYTESSPSEDKVIQL
			DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
1			SFRIQIYRIQIQNQIHGAVFPPVFYPVKPPKSVTMDSAPKPFTD VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE
			AEVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
]			IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLLKSIGATLTD
			VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
1			GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
			LKALVGGAVGCLACAASKITGAMAKGVAAMTMDEDYOOKRREAM
			NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAOKGGAAG
i i			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
1			PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD
6239	2108	634	DDDDDDDDESDLNH
0233	2100	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA
1			THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM
	İ		FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
]]			WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG
1 1	Ì		ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
1 1			WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL
1 1			PHKELRFIIYAF?MLNITAARGCSYLLNNYKKSWLYKAGSLLVI
1		i	GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
			DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
			PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS
6240	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
[]			DPLSSGSRSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ
			TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL
ļ i			AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLOEREKL
	.		LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP
	Ī	1	LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS
		İ	SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS
- 6207			ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNABEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT
.		l	RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
		!	EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ
			KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
			FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
j			TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
- 1		}	WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC
		ł	LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE
1			GTKAIEKNEÖKWKKAWKITZÖEKLITÖKINDMIKTKIDWAEGTЬ

SEQ Predicted Predicted end nucleotide NO: nucleotide location corresponding to first Predicted end nucleotide Hallocation corresponding to first Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Amino acid segment containin	11 R-
NO: nucleotide location corresponding H=Histidine, I=Isoleucine, K=Iysine	id, E=
location corresponding H=Histidine, I=Isoleucine, K=Iysine	
corresponding hardstraine, largoleucine, Kalysine,	cine,
I COLLEGICATED I CO TITAT : Lelenciae Memorbiani.	
corresponding to first L=Leucine, M=Methionine, N=Asparagine to first amino acid P=Proline, Q=Glutamine, R=Arginine,	≥,
amino acid residue of S=Serine, T=Threonine, V=Valine,	•
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown,	
amino acid sequence Codon, /=possible nucleotide deletion	*=Stop
sequence \=possible nucleotide deletion	ł.,
FFSKL Insertion)	
6242 198 1310 QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPF SSEDIDQMFSTLLGENDLLTQSLGVDTLPPPDPNPPR	RAVEMGE
GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQ	AEFNYSV
NQHHSASLQASIFSGAASLGYGTNVAATGISQYEDDL	AQKESLQ
VLDLPLPPPPPPEPLSQEEEEAQAKADKIKLALEKLKE	PPPPADP
VKVHMNDNSTKSLMVDERQLARDVLDNLFBKTHCDCN	AKVKKLV
IYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEK	ADMCLAE
KNPQNFYLDNRGKKESKETNEKMNAKNKESLLEVRLI	EEKYAVF
KDVCSIFKSFASENNGKI	LQSGRKE
6243 1509 614 RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWP	
TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTR	PSSAPAT
AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAAWASTI	RATCRSA
MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRV	TTGCCPA
SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRT	RIGPPAH
RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQ	KAVDPLK
GPPILAPILSTPILSRWSCYFPRSRTAOGWHIS	DITABLE
6244 2119 1745 FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVN	AD TASA
FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSK	VI-DEAVE
EMVNIIEYNKELQAKVNILRROLAELETEDGMOESP	
1148 LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITN	VT7.ST.T
ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPV	TVSNCT.
KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFT.S	SKLTKW
KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTELALLYY	CIENGER '
EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPY	JUSKSSP :
RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFT	TOLIEV
NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMOVTY	T.DESTG. I
MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLP	AAWGFW
PRG	1
SLWFWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSS	CGQHPV
QATHRGAVSNSLMLCILKLASOMPLENTTVOOMVFMLT	SNIALS
HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWIK	T.I.LNTS
SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIE	HNVCFS
PANKPKILANEKVITVLAACLESENQNAQRIGAAALWA	LIYNYQ
KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYY	LKCLEN
6247 3 1678 NSPUMCPMTERGACCI PRUADVOVENA	.
NOKYNGFWIEFSAGSERFMAKKUNKNSKELGLVPLTDD	TSHAGP
PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGA	FGSSFL
YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTL	LWSVTV
SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAA	LLMACS
LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKE	IRGSLG
QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVV	PAVVQL
LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQ	EABEAL
AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQ	LCGLNA
IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSG	LVIEHL
GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSI	/GILAI
IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWL	NPAVG
LLFPPIQKSLDTYCFLVFATICITGAIYLYFVLPETKNI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP	RTYAEI
6248 56 1773 VPPPRMMAAVPRGLEDGAVTDGKINGRP	
[VFFFRINDAVPPGLEPWNRVRIPKAGNRSAVTVONPGA]	TDLCI
AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMG	HKPHL
ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTI	CACAAB
SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGI	QEFII
LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVAF YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKI	TOPMP
LINEQSPRASEETLLGISKKAKQMKINVQMNVDLGQPVF	LNKLF
1 WODELINGTON WATER VENT OF THE PROPERTY OF THE PROPERT	MKRVP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
		i	VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
1			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
ł			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVONPGAALDI.CI
1	į.		AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
			ALKOVEQCLKRLKNMNLEGSIQDLFELFSSNENOPLTTKVCVVP
1	l		SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLOEFII
1			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLOEVARIOPMP
1			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
			LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
			KEESSEFDVRAFCNOLKHKATQETSFDFKCSQSRLKTTKYSSQK
}	j		VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
l .			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
1			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
6250	232	1306	HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
1		1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKQLETVLDD
			LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
1 1			REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELBEALTSA
1 1			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
1			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
			SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
			VEGDHO
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
1 1			PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
1			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
1	j		KMEKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCOADIRHILNK
1 1]		NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
1 1			AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
6252			EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE
1 0252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
į į	j	į	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
	1		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
1			KLPHSKAKTRSRLEVARABEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL
		j	AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
	J		TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
1		ŀ	TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
1 • 1	1	1	KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
]]	GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
{		Ì	SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPARLIC
	1	į	LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
	į	ĺ	SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
]	ALDREVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
		ĺ	PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVABABEBETSIKAARSBLLLAEEPGFLEGE
		†	DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

Designing nucleotide coation corresponding to first amino acid acid amino acid amino acid acid amino acid	SEQ	Predicted	Drodicted	
MO: nuclectide corresponding to first amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid			Predicted end	
Cocation Corresponding Coffice	1			Glutamic Acid F-Phone-1-1-1
corresponding to first samin acid samino acid residue of amino acid sequence acid sequence a				H-Wishiding Targeleusing W. S.
to first amino acid residue of samino acid amino acid amino acid amino acid amino acid amino acid amino acid anino acid anino acid anino acid anino acid acquence Percian P	1	corresponding		Installed M-Methioning N-Assessing
residue of amino acid sequence		to first	il .	P=Proline. O=Glutamine R-Arginine
##Tryptophan, Y=Tyrosine, X=Unkeletion amino acid sequence ##Tryptophan, Y=Tyrosine, X=Unkeletion Apaposible nucleotide deletion Apaposible nucleotide insert	1		residue of	S=Serine, T=Threonine, V=Valine
sequence AVAQNRMLHIUNGGIBLECIRCORVIRLEFLIPHFLIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE TOPLITUDISVIGUIGATION INTERPLIPH LIATASE GQGASEPS LEQUIVARIAN GORGANIAN INTERPLIPH LIATASE SHAQSHARVER SERVICA CONTINUAL SERVICION INTERPLIPH LIATASE SATASIAVERRE VIVORE PERPURSA GORDALAR PICARA PROL GAPREPPERSA ALDREVA HALGERIS SERVICA CONTINUAL PROPERTION INTERPLIPH LIATASE SHAQSHAR CONTINUAL SERVICIA CONTINUAL PROPERTION INTERPLIPH LIATASE SHAQSHARVER CONTINUAL PROPERTION INTERPLIPH LIATASE SHAQSHARVER CONTINUAL PROPERTION INTERPLIPH LIATASE SHAPPING CONTINUAL PROPERTION INTERPLIPH LIATASE SHAPPING CONTINUAL PROPERTION INTERPLIPH LIATASE SHAPPING CONTINUAL PROPERTION INTERPLIPH LIATASE SHAPPING CONTINUAL PROPERTION INTERPLIPH LIATASE SHAPPING LIATASE PRADATITI AND LIATASE SHAPPING CONTINUAL PROPERTION INTERPLIPH LIATASE SHAPPING LIATASE PRADATITI AND LIATASE SHAPPING LIATASE PRADATITI AND LIATASE SHAPPING LIATASE PRADATITI AND LIATASE SHAPPING LIATASE PRADATITI AND LIATASE SHAPPING LIATASE PRADATITI AND LIATASE SHAPPING LIATASE PRADATITI AND LIATASE SHAPPING LIATASE PRADATITI AND	l	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
AVADAMBMIN I PÜRÖGG EHLÖRI ERCORVITLISTE PHIPLIATAS TÖFLTYLDVS UGK I VALAINARAGRILDVINGAN FYNANIHLIGISNO TVÄNANIKARI I PÜRÖG EHLÖRI ERCORVITLISTE PHIPLIATAS TÖFLTYLDVS UGK I VALAINARAGRILDVINGAN PYNANIHLIGISNO TVÄNAS PÄNKER PLÄKTLÄHER GÖRGRI VÄNGEN TYNATS ELDHÖL KIFDLAGTY QELSTRITL HÖRGRILAFS ÖRGLLVAGMÖD VANIVA GÖGGAS PISLAG PÜRÜLAGÜKTA PÜRÜRÜN ÜNE GÖGKAS PISLAG PÜRÜLAGÜK BERÜRÜN PÜRÜRÜN ÜNE GÖGKAS PISLAG PÜRÜLAGÜK BERÜRÜN ÜN ÜLE VALA GÖGKAS PISLAG PÜRÜLAGÜK BERÜRÜN ÜN ÜLE VALA GÖGKAS PISLAG BERÜRÜN ÜN ÜLE VALA GÖGKAS PISLAG BERÜRÜN ÜN ÜLE VALA KARPTGAR PÄÄLA GÖGKAS PISLAG KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR PÄÄLA KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR PÄÄLA GÖRÄR KARPTGAR PÄÄLA GÖRÄR ÄÄLÄ GÄÄR ÄÄLÄ GÄÄRÄ KÄÄLÄ GÄÄRÄ ÄÄÄNÄÄ KÄÄLÄ KÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄÄ	}		sequence	Codon, /=possible nucleotide deletion.
AVAQAMBAHI YDNOGIEHACIRRCORVIRLEFLEFHFILATASS TOFITILDUS VOSKUI VALAINARGARDUMSON YHIHAGISING TVSLMSSPAMKEPILAKILCHROGURAVADISTOTMATSCIJHOU. KIFDLEGTYJG LESTETLHEAGRILAFSORGILHAGAMODUVAINA GQOKAS PSILEGYYLTHILAGOPHOLJOPC PFDVLJOVCHTGOTY SMLVPGACEDYNFGGLESNYERSKORGREWALKEVYBALI OL LEPRALAEVDU ISLROGKKOCIERLGYDGAAAFOPKOKOR SSTASIVKRIKKVINDEHRIKKVOSCOCHHKERAKARTGARPS ALDREVR 6254 155 1139 HAGGREGSGELSAACCCEPALELBASSGRIPALAFORARPS ALDREVR GQAPRE PPERSAAGSTMLLKEVRICHBUTVDEVKIGQLYMISKH SHROGSHGGBUEVVONDEPEDDHIMMOOPPEKEVYLINKSLEPSA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEJSKA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEJSKA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEJSKA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEJSKA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEJSKA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEDSKA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEDSKA RAVVPKIPYVERANNYPPYTTEYKTGYPEKEVYLINKSLEDSKA RAVVPKIPYVERANNYPPYTTEYKTGYLINKSLEDSKAPH KOSCIJALGEBENYSSALSCTABELEFYHKGIASITASTFINE SEXTGRGOLBENYSSALSCTABELEFYHKGIASITASTFINE LSPOCEPYKLRILLIANDASTRONNONNENERPERSAAGSTOLLIAGASTOLABSATIK NYSLLOODSCILLISHARAKICICKUSKITSTFINE LSPOCEPYKLRILLISHAVANNONNENERPERSAAGSTOLAKARDSETE RREMSYNHULEVESLINLISHASSPRARABELINGASTOTARARDSETE RREMSYNHULEVESLINLISHASSPRARABELINGASTOTARARDSETE RREMSYNHULEVESLINLISHASSPRARABELINGANGOLAKVEVB VOURISSKOLTERKICOSVUSSPRARABELINGANGOLAKVEVB VOURISSKOLTERKICOSVUSSPRARABELINGANGOLAKVEVB VOURISSKOLTERKICOSVUSSPRARABELINGANGOLAKVEVB VOURISSKOLTERKICOSVUSSPRARABELINGASSOGOVKID INTENNEM BGRUPPHNOYPSTOPLARAGICHTENITATATATATATATATATATATATATATATATATATATA		sequence		\=possible nucleotide insertion)
TOTATILDVSYGKIVAALNARAGRILDVMSQNPYMAVIHLIGISING TVSLMSPAMKEPLAKILCHROGRVRAVUNSTOTYMATSCLOHOL KIFDLAGTYQPLSTRILDHGAGHLAFSORGLUVAGMGUYNIRA GQGKASPPSLEGPVIJTHALSGVRIGUTGGTTY SMLVPGAGENFFDGLESNPYRSRKORGMEVKALLEKVPAALIC LDPRALAEVUVISLEGGKKEVPHOLOPPOPKEKOKG STASLVKRKKWMDEERDKVRQSLQQOHKEAKAKPTGARPS ALDRFVR HALGSRGSGDLSAAACGCPALELARAGGRALAAPGAAAPAGL GAPPFPPGAGAAGATMLLKEVYLCHPUTVDEVKIQGLYWISH SHOOSINGGRGWEVVALUEWINDPEDDHIIGMQCPTEKKYVINSK STASLVKRKKWMDEERDKVRQSLQQOHKEAKAKPTGARPS ALDRFVR RAVVPKIPYTYEKAMIYPYTITEYTCSFLEKFSHIBITKYEN KGSNDTIFDMBAGDVERVCFIDIAGCEPTSVKTYKISDFCHKK SERTORGQLREGWRDSNGFIMCSYLLCHPUTVDEVKIQGLYWISH RAVVPKIPYTYEKAMIYPYTITEYTCSFLEKFSHIBITKYEN KGSNDTIFDMBAGDVERVCFIDIAGCEPTSVKTYKESDPKHK SERTORGQLREGWRDSNGFIMCSYKLLTVVKFEVWGLGTRVGGVV HKVVROILLIGHGAAFAWDENTYDMTMDDVEVKFWGVY HKVVROILLIGHGAAFAWDENTYDMTMDDVEVKFWGVY HKVVROILLIGHGAAFAWDENTYDMTMDDVEVKFWGVY HKVVROILLIGHGAAFAWDENTYDMTMDDVEVKFWGVY HKVVROILLIGHGAAFAWDENTYDMTMDDVEVKFWGVY HKVROILLIGHGAAFAWDENTSMTTENTHAMIC GRONDERVSSHALGTANTYTKSGCALSVKRVIKQQLEEVSNGWT VYALAGASKMGNMENERSLAGRVCHLVASSHEPTFHANSILKEPS RABQCLTGULGENYSSALSCTASLASRYCHLVASSHEPTFHANSILKEPS RABQCLTGULGENYSSALSCTASLASRYCHLVASSHEPTFHANSILKEPS RABQCLTGULGENYSSALSCTASLASRYCHLVASSFORMOGNATURF SPROFFFCKLQSTSTIKLASPSPRNPARFIAVONNOQLALKVEG VVCHOSKRCHFRACTGVCLUNVSSTLOSKGGNYCHTASSTTCHAMIC GNOVENNOYFSTOFLUNFALIGHHITVESSVKDANSITWKTG PRTT;FYKKLGSTSTIKLASPSPRNPARFIAVONNOQLALKVEG VVCHOSKRCHFRACTGSVCLUNVSSTLOSKGGNYATHFE RRMSVTANHLUSPSTLOKKGNYCHSTANSTLOSKGGNYATHFE GRAGASLINKLIRSNIVNNTNOVEVLORDNSTRIKKYTDEN GRYFFICKLGSTSTKAMINGFNSTLOSKGGNYATHSARKTOBERK EDRAAGSLINKLIRSNIVNNTNOVEVLORDNSTRIKKYTDEN GRYFFICKLGASTATURAKTOBERK EDRAAGSLINKLIRSNIVNNTNOVEVLORDNSTRIKKYTDEN GRYFFICKLGASTATURAKTOBERK EDRAAGSLINKLIRSNIVNTNARARKTOBERK EDRAAGSLINKLIRSNIVNTNARARKTOBERK EDRAAGSLINKLIRSNIVNTNARARKTOBERK EDRAAGSLINKLIRSNIVNTNARARKTOBERK EDRAAGSLINKLIRSNIVNTNARARKTOBERK EDRAAGSLINKLIRSNIVNTNARARKTOBERK EDRAAGSLINKLIRSNIVNTNARARKTOBERK EDRAAGSLINKLIRSNIVNTNARAGROPALLORGSCORTURA GKYPENDAARGROPATARAGROPATAGROPATAGROPATAGROPATAGROPATAGROPATAGR	1			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
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GGAPRP PRESSAGGRYLLKEYRICMELTVERYKIGGLYMISCH SHSOSDRGEGVEVVQMEPEDPHIGMOCPTERTYLNSKLPSWA RAVVPRITYVTERAMYTYPTITETTCS-IPKFSIHIETKYENN KGSNDTIFNDRAKOVEREVCFIDIACDEIPKFYKESEDPKHFK SEKTGRGOLREGMEDBERGPIMCSYKLTYFEVMIGLTRYEDGDV HKVVRDILLICHRQAPAWDERVPMTMDDVREYEKMHEQTNIK VCNGHSSPVDDIESHAQATGT 6255 1 1444 PTEPGOELLVSLATVIFVASQKALSVESKAVIKQULEVSNOGHT VYRIAROAGRMGNIDDARKALVOSLLTVJASKHFYFWLINSLKEPS HAROCLTGLQEENYSSALSCIAESLKFYHKGIASLTASTPINP LSPOCEFVKLRIDLLQAFSQLICTCHSLKTSP PRAINTITANTL GONDLORCGRISNOMKOSMEERSLASKYGULVQASFDADSATLR NVELOQOSCLLISHALEALILDPESSASTCGVSSTGTAHADSSEY RRMMSVYNHVLEEVESLANKYTDVSWHTTACLCHAITALLKVPL SFORVFFQKLQSTSIKLALSSPSNPAPAEPIANTOMATHAM EGRVEPHNDYFSTOPLLKFATLGTHNITVESSVGANGATLWKTG VVOHGSKOSLFFRIGVSCLNVSSTLOSKSGQDYKIPDINMTMEM EGRVEPHNDYFSTOPLLKFATLGTHNITVESSVGANGATLWKTG VVOHGSKASELSKHLHKKERKLFYDTNOADVIKTANDAEKTDEEK EDRAAQSLLNKLIRSNLVDNTNQVEULGRDDNSDLISVKSFEEL RLKPQLLQGVYAMGFKRPSKIQENALPENALTOMEDRAL VEDGCAAAGELSMHLHKERKIKPTDNOADVIKTNAMAEKTDEEK EDRAAQSLLNKLIRSNLVDNTNQVEULGRDDNSDLISVKSFEEL RLKPQLLQGVYAMGFKRPSKIQENALPENALADELSKEGHOVA GKFYBELKLAYANGCNKLERGQWISSQUVISTOTTUDNCSKLK FIDPKKIKVVULDEADVMALTQGHQDGJRIORMIPRNCOMILF SATTEDSVMKFAGKVVPDPMVIKIRBEETLDTIKQYYULCSSR DEKKGALCNLYGATITAGAMIFCHTERKALAALBLEKSKEGHOVA LLSGEMWEGRAAVIERRFEGKSKULVTTNVCARGIDVEGVUSVV INFDLIPVBGGPMBVETLHRIGRTGTGANIAADELSKEGHOVA LLSGEMWEGRAAVIERRFEGKSKULVTTNVCARGIDVEGVUSVV INFDLIPVBGGPMBVETLHRIGRTGTGANIAADELSKEGHOVA LLSGEMWEGRAAVIERRFEGKSKULVTTNVCARGIDVEGVUSVV INFDLIPVBGGPMBVETLHRIGRTGTGALAANMVDSKHSM NILNRIGGHFNIKKIERLDTDDLDEIBKIN 6257 210 615 AFIPAMAELIQKKLGGEVEKYQOLGKDLSKSMSGROKLEAQLTE NNIVKEELALLDGSNVVYKLLGGVUKKGELGEARATVCKRLDYI TAELKRYESGLERDLERGSEQORETLAQLQGEFGRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLGGEVEKYQOLGKDLSKSMSGROKLEAQLTE NNIVKEELALLDGSNVVYKLLGGFURKGRINGISGLIT SKNCCSRKEPDEFBVCKKLLIGULVKKGELGEARATVCKRLDYI TAELKRYESGLERDLERGSEQORETLAQLQGEFGRAQAAKAGAPG KA 6259 2 1540 LLEKGFPSOCHEERKRKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRSKTFINLEGGLOKSFCMIKRISGLII KKNCSRKEPDEFBVCKKLLIDIRIEKTITCHSKSWINISGKIIN NHOLDERJTEESIKLNINGBPHLBERFITIK	6254	155	1120	
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KGSNDTIFDNEAKDVEREVCFIDIACDEIPRYKESEDPKHFK SENTGRGGQLREGWRSHQPMCSTKLVTVKEVWGLCTRVEGOV HKVVROILLIGHRQAFAWVDEWYDMTMDDVREYEKMHEQTNIK VCXOHSSPVDIESHAQTST 1 1444 PTERQOELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT VYRIARQASRMONIDMAKELYOSLLTQVASKHFYFMINSLKEFS HABQCLTGLGGENVSSALSCIAESKFYHKGIASLTAASTPINP LSFQCSFVKLRIDLLQAFSQLICTCNSKKTSPPPALATTIANTL GNDLQKCGRISNONKOMEEFRSLEKYHKKIBSLTAASTPINP LSFQCSFVKLRIDLLQAFSQLICTCNSKKTSPPPALATTIANTL GNDLQKCGRISNONKOMEEFRSLEKYHKKIBSLTAASTPINP RYSLQQQSCLLISHAIEALLDPESASPGVSGTGYAHADSSYE RRMMSVYNHVILEEUSLINKKYTPPSTADLATTIANTL SFQRYFPKOKLOGSTSIKLALSPSPRPAPAPHADSYET RYSLGOOSTIKLALSPSPRPAPAPHATACLCRAITALLKVPL SFQRYFPKOKLOGSTSIKLALSPSPRPAPAPHADSIVALA VOHGSKPGLFRKIQSVCLUNVSSTLQSKSGQDYKIPIDDMYTHEM SGRYEPHRDYSSTGPLINFALIGTTUVSSVKONDSTLWKTG PRATTIFVKSLEDPYSQQTELQQQQAQQPLQQQQQRNAYTRF CRGAGAFAASSISNIHIKERKIRPDTNGSVVKTHANARKTDBEEK EDRAAQSLLINKILRSKINJDNTNQVCLOPDPNSPLYSVKSPEEL RIKKPQLLQGVYAMGFNRPSKLVPSLESTSYPPAFGTMATDSWALA VUDGRAAASSISNIHIKERKIRPDTNGAVVKTHANARKTDBEEK EDRAAQSLLINKILRSKINJDNTNQVCLOPDPNSPLYSVKSPEEL RIKKPQLLQGVYAMGFNRPSKLQENGALPHMLAGPPONLIAGSOSG TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYEBLAQTGKVTEQM GKFYEELKLAYAVGKKEBGCKISEGIVISTGFTULDCKKIE SATFEBDSWKFAGKVUPDPNVIKKIRESTLDTIKGYVUCSSK DEKKQALCNILYGAITTAQAMIFCHTRKTASWLAABLSKEGHQVA LISGEMWWBCRAAVIERPEGKESTUTTVVACARGIDVEQVSVV INFOLPVUKCGNPDNDETYLHRIGRTGFKKGLAVMWDSKHSM NILNRIQSHFNKIBELLOGNUVEKLIGPVUKQSLGSBARATVGKRLDYI TABLKKYESQLRDLERQSEQQRETLAQLQQGFQRAQAAKGAPG KA AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVEKLIGPVUKQSLGSBARATVGKRLDYI TABLKRYESQLRDLERQSEQQRETLAQLQQGFQRAQAAKGAPG KA AFIPAMAELIQKKLQGEVEKYQQLGKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVEKLIGPVUKQSLGSBARATVGKRLDYI TABLKRYESQLRDLERQSEQQRETLAQLQQGFQRAQAAKAGAPG KA SVEMGORGSKTFNLGTDEVSLAWPYXICDSCEMBLKNITSGLII SKRXCSRKKPDEFRVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI MYHQDLSQDSFGQSFETSKNGGFHDEAAFFTNKRSGIGSTVCK YNECGRFFIESSLKLIN SGRPHLEMEFSCICGSFFORMLRFGH GRADH				RAVVPKI FYVTEKAWNYVDYTITEUTCOOT DETOTITED
SEXTGRGQLREGMRDSHOPIGMSYKLUTVKPEVWGLQTEVEQFV HXVVRIDILLIGHRQAPAWDEWTYMTHOUNGEVEKMHEQTNIK VCNGHSSPUDDIESHAQTST 1 1444 PTEPQQELIVSIATUTFVASQKALSVESKAVIKQQLESVSNGWT VYRIARQASRMGNHOMAREHZQSLLTQVASKHFYFMLNSLKEFS HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPINP LSPQCEFVUKIRIDILQAFSQLICTGLAKTSPPPAFATTIANTL GNDLQRCGRISNOMKOSMEEFRSLASRYGDLVQASFDADSATLR NVELQOSCLLISHAIEAILIDGASSAFQCEYSTGTAHADSEYE RRMMSYVHHVLEEVESLNGKYTPVSYMHTACLCNAITALLKVPL SFQRYFFQKLQSTSIKLALSBSPRNPAREPIAQCHNQQLALKVEG VVQHGSKBGLFFKLQSVCLNVSSTLQSKSGQDYKLPIDNMTNEM EQRVEPHNDYFSTOPLLNFAILGTHNITUSSVKDANSIVWKTG ERRAAGSLINKLISHSVFLORSTOPLONGORAATRF PRTTIFVKSLEDPYSQOIRLQCQOACOPLQQQORAATRF ERRAAGSLINKLISHNIVDNTNOVEVLQRDMSSPLYSVKSFEEL RLKPQLLQGVVAMGFNRPSKIQENALPIMLABPPQNLIAQSOSG TOKTAAFVIAMLSQVEANVKTNANAREKTDEEK ERRAAGSLLNKLISHSVPSLESTSTSVPFARGTMATDSWALA VUEQBAAABSLISNLHKEEKIKEDTNGAUVKTNANAREKTDEEK ERRAAGSLLNKLISHNIVDNTNOVEVLQRDMSSPLYSVKSFEEL RLKPQLLQGVVAMGFNRPSKIQENALPIMLABPPQNLIAQSOSG TOKTAAFVIAMLSQVEANVKYOPDNVIKLKREBETLDTIKQYVVLCSSR DEKRQALCULGSPTKALAUTVRNAVARGNLERGORISBOUVIGTPGTVLDWCSKLK FIDPKKINFVLDEADVMIATGLOFSVENGULFFRNCQMLLF SATPEDSVWKPAQKVVPDPNVIKLKREBETLDTIKQTVVLCSSR DEKRQALCULIGATITAGAMIFCHTIKKTASMIAAELSKECHQVA LLSGEMMVEGRAAVIERFPERGKKULVTVTNVCARGIDVSVVV INFDLPVDKNCONPDNETYLHRIGRTGRFGKRGLAVNNVDSKHSM NILNKIGBHNNKKERRLDTDTDLOFALQOSFGRAAAAKGAPG KA 6257 210 615 AFIPAMABLIQKKLQGEVEKYQOLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDVI TAEIKRYESQLRDLERQSSQQCRETAGQLQOSFGRAAAAKGAPG KA 6258 210 615 AFIPAMABLIQKKLQGEVEKYQOLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDVI TAEIKRYESQLRDLERQSSQCRETAGQLQOSFGRAAAKAGAPG KA 6259 2 1540 LLEEGFFSQCHPERKWVDVLESSQENEDDHFWELLFHNNKTV SVENGGDRSKTFFILGTDPVLLKWYPYKICDSCRNNLKNISGLII SKKNCSRKKPDFPNVCEKLLDIRREKTPIGEKSYKYDQKRNAI MYHQDLSQPSFGGSFFTFILGTDPVLEKMYPYKICDSCRNNLKNISGLII SKKNCSRKKPDFPNVCEKLLDIRREKTPIGRSGVENLKRICH VYNECGRTFIESLKLNISGRPHLEMEPYGCSICOKSFCMILRRGH VYNECGRTFIESLKLNISGRPHLEMEPYGCSICOKSFCMILRRGH KYNEKSBALKHQIVHGGRSVYVENGGNSTKKHHTOLRRAHT	j]		KGSNDTIFDNEAKDVEREVCFIDTACDFTDEDVVVECEDOVIN
#KWVRDILLIGHRQAFAWUDEWYDMTHDDUREYEKMMHEQTNIK VCNQHSSPYDDIESHAQTST 1 1444 PTEPQQELLVSIATVIFYASQKALSVESKAVIKQQLESVSNGWT VYRIARQASRMGNHDMAKELYQSLITQVASKHFYEMIASIKEFS HABQCLTGLQEENYSSALSCIASSKFYHKGIASLTAASTPINP LSFQCSFV&LRIDLLQAFSQLICTCNSLKTSPPPAIATTIANTL GNDLQRCGRISNOMRQSMEEPSKASKTGLVQASSFDADSATLR NVELQQOSCLLISHAIRALILDESSASPQEYGSTGTAHADSEYE RRMMSVNHVLEEVESLNGKYTPVSVHTACLCNAIIALLKYPL SFQRYFFCKLQSTSIKLALSSPSPNPAEPIAVONQCLALKVEG VVQHGSKBCLFFKXQSVCLNVSSTLQSKSGQYKKTPINNMTNEM GRVEPHDNYFSTDFLIMFAILGHNITVESSVKDANGSIVKKTG PRTTIFVKSLEPPYSQQIRLQQQQAQQPLQQQQCRNAYTRF 6256 1 1542 CRGAGAEPAANFREFRSLVPSLESTSTSVPFAFGTMATDSWALA VDEQBAAAESLSNLHLKEBKIKPTINGAVVKTNAMAEKTDEERK EDRAAQSLLNKLIRSNLVDHTNQVEVLQBDNSPLYSVKSFEEL ARKPQLLQGVYAMGFNRPSKIGRALDFINLABSPONLIAQSOG TGKTAAFVLAMLSQUEPANKYPQCLCLSPTYELALQTGKVIEQM GKFYPELKLAYAVRGNKLERGQKISEUTGFTGTVLDWGSKK FIDPKKIKVFVLDEADVMIATQGHQDQSIRTQRMLPRNCOMLLF SATFEDSWKRAQKVVPDPNVIKLKREESTLDTIKQYYVLCSSR DEKFQALCINLYGAITAQAMIFCHTATSMIAABLSKEGHQVA LLSGEMMVRQRAAVIERPRSGKKSVLVTTNVCARGIDVEQVSVV INFDLPVVDKDGNPDNETYLHRIGRTGRFGKGLAVNNVDSKHEM NILKRIGEHNKKLERLDTDLDLETEKIAN 6257 210 615 AFIFAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKGELGEARATYGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIFAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATYGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 ILEKGFFSQCHPERKNKVDDVLESSGENBEDHFWELLFHNNKTV SVENGORGSKTFRIGTDPVSLRNYPYKICDSCENNLKNISGLII SKKNCSRKKPDFNVCEKLLDIRREKTPTGBEGSYKYDQKRNAI WYHODLSQPSFGGSFFYSKNGGGPHDEAAFFTKNERQIGIETVCK YNECGRFFIESLKLNISGRPHLEMEPYCCSICGKSFCMNLRRGH WYHODLSQPSFGGSFFYSKNGGGPHDEAAFFTKNERQIGIETVCK YNECGRFFIESLKLNISGRPHEMEPYCCSICGKSFCMNLRRGH GRAALTKONLYRMGSKYDYFNGGSTFONNENSKKSHITOURRAHT	i			SEKTGRGQLREGWRDSHOPIMCSYKLVTVKFEVWGLOTPVFORV
6255 1 1444 PTEPGOELLVSIATVIFVASCKALSVESKAVIKCQLEEVSNORT VYRIAROASRMONHOMAKELVQSLLTQVASKHFYFWLNSLKEFS HAEQCLTGLQEENYSSALSCTABSLKFYHKIASLTAASTFIND LSFQCSFVKLRIDLQAFSQLICTCNSLKTSPPFAIATTIANTL GNDLQRCGRISNOMKQSMEERSLASRYGDLVQASFDADSATLR NVELQOQSCLLISHAIEALILDSASPQLEVGSTGTAHADSEYE RRMMSVYNHVLEEVESLNKYTPVSYMHTACLCNAIIALLKYPL SFQRYFFKKLQSTGIKLALSBSPRNPAREIPLAQNNQQLAKVGG VVCHGSKPCLFRKTG,SVCLNVSSTLQSKSGQDYKLPILOMINEM BQRVEPHNDYFSTOPLLNFAILGTHNITVESSVKDANSIVWKTG PPTITYVSLEBPYSQQIRLQQQQQQOQDQCQQRNAYTRF 6256 1 1542 CRGAGAEPAANPRSPRSLVPSLESTSTSVPFAFGTMATDSWALA VDEQEAAAESLSNLHLKERXIKPDTMGAVVKTNAMAEKTDEEK EDRAAQSLLNKLI KSNLVDMTNQULQDDNSPLYSVKSFBEL RIKPQLLGGVYAMGFNRPSKIQENALPLMLAEPPQNLIAQSQG TGKTAAFVLAMLSQVEPANKYPGCLCLSPTVSLAUCTGLWCGVG GKFYPELKLAYAVRGNKLBERGGYSISQIVIGTPGTVLDWCSKLK FIDPKKIKVFVLDEADVHIATCGHQDOSITYGLAUCTGLWCSK AKPLENGAVAVRGNKLBERGGYLSQIVIGTPGTVLDWCSKLK FIDPKKIKVFVLDEADVHIATCGHQDOSITYGRHLPRNCOMLLF SATFEDSWKKRAQKAVDPDRYLKRREBSTLDTIKQNLPRNCOMLLF SATFEDSWKRAQKAVDPDRYLKRREBSTLDTIKQNLPRNCOMLLF SATFEDSWKRAQKAVDPDRYLKREBSTLTGRHLPRNCOMLLF LLSGEMMVBCRAAVIERFREKKVLVTTNVCARGIDVEQVSVV LINFDLPVDKCOMPINNTYLHLRGREFYGKKGLAVMVDSKHSM NILNRIGSHRNKKTERLDTDDLDEIKINN AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEBLALLDGSNVVFKLLGPVLVKQGLGEARATTGKRELDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEBLALLDGSNVVFKLLGPVLVKQELGEARATTGKRELDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA AFIPAMAELIQKKLQGEVEKYQOLQKDLSKSMSGRQKLEAQLTE NNIVKEBLALLDGSNVVFKLLGPVLVKQELGEARATTGKRELDYI TAEIKRYESQLRDLERQSEQGRETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 615 AFIPAMSELIQKKLQGEVEKYQOLQKDLSKSMSGRQKLEAQLTE NNIVKEBLALLDGSNVFKLLDIRRENTFICHESYXKYDQKRNAI SHYDDLSOPSFGGSFTSKNNCQGFDDRAAFTFKNRSQLISTVCK VMCGGRFFIESLKLNISQRPHLEMEPYGCSIGGKSFCMNLRRGH VXPGCGRFFIESLKLNISQRPHLEMEPYGCSIGGKSFCMNLRRGH WCCGRFFIESLKLNISQRPHLEMEPYGCSIGGRFCMALRRGH WCCGRFFIESLKLNISQRPHLEMEPYGCSIGGKSFCMNLRRGH KXPKCSRALKHQIVYRNGGSKYDVENGGNSTRKKHTOOLRRAHT				HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEOTNIK
VYRIARQASEMGNHDMAKRIVGSLLTQUSKIKFFWIMINSLEFS HARQCITGLQEENYSSALSCIAESLKFHKGIASLTAASTPIND LSPOCEFVKLRIDLLQAFSQLICTCRISKFHKGIASLTAASTPIND LSPOCEFVKLRIDLLQAFSQLICTCRISKFHKGIASLTAASTPIND LSPOCEFVKLRIDLLQAFSQLICTCRISKFHKGIASLTAASTPIND ROMLORGRISNQMKQSMEEFRSLASRGGULYQASFDADSATLR NVELQQQSCLLISHALEALILDFESASRGEYGSTGTHADGEYE RRMMSYYNNVLEEVESLNCKYVSYSTHMACLCRAITALLKVPL SFQRYFFQKLQSTSIKLALSPSPRNPARPIAVQNNQQLALKVEG VVQHGSKPGLIFRKIQSVCLINYSYNJMAKACICARITALKVPL SFQRYFPGKLQSTSIKLALSPSPRNPARPIAVQNNQQLALKVEG VVQHGSKPGLIFRKIQSVCLINYSTLQXSKQQDYKIPIDMMTNEM EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANSIVWKTG PRITIFVKSLEPPYSQCIRLQQQAQQOPLQQQQRNAYTRF EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANSIVWKTG PRITIFVKSLEPPYSQCIRLQQQAQQOPLQQQQQRNAYTRF EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL RLKPQLLQGVYAMGFNRPSKTQENAVVKTNANAEKTDEERK EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL RLKPQLLQGVYAMGFNRPSKTQENAVVKTNANAEKTDEERK EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYLSVKSFEEL RLKPQLLQGVYAMGFNRPSKTQENAVVKTNANAEKTDEERK EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLLALQTGKVILOM GKFYFELKLAVAVGNKLERGCKISGUTVITTOVLANGSUG TCKTAAFVLANLSQVEPANKVPQCLCLSPTYELALQTGKVILOM GKFYFELKLAVAVGNKLERGCKISGUTVITTOVLANGSUG GKFYFELKLAVAVGNKLERGCKISGUTVITTOVLARGIDVEQKVL SATFEDSWKKFAQKVVPDPNVIKKREBETLDTIKQYVVLCSSK DEKKQALCNLVGATTIAQAMTETRIKTASMLABELSKEHQVA LLSGEMMWQRAAVIERPRECKEKVLVTTAVCARGIDVEQVSVV INFDLPVDKCORDNDETYLLRIFTRTRASMLABELSKEHQVA LLSGEMMWQRAAVIERPRECKEKVLVTTAVCARGIDVEQVSVV INFDLPVDKCORDNDETYLLRIFTRTRASMLABLISKEHQVA NILNRIQBHFNKKIERLDTDDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVYKLIGFTREKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVYKLIGPVLVKQEIGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQORETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVYKLIGPVLVKQEIGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQORETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 ILEKGFFSQCHPERKWKVDDVLESSQENDEDHFWELLFHNNKTV SVEMGDRGSKIFFRIGTDPVSLRNYPYKICDSCEMMLKNISGLII SKKNCSKKRPERNVCEKLLDITRHEKTHQATTRILERGYKYND WYNDLSQPSFGSSFTSNGQGFFDSAFFTNKRSQLGETVCK YNECGRIFIGSLUHMGKSVY				VCNQHSSPVDDIESHAQTST
VYXIAROAGRMGNHDMAKELYQSLLTOVASKHFYEMINSLKEFS HAROCLTIGLOGENYSSALSCIABSLKFYHKGIASLTARSTPLNP LSFOCEFVKLRIDLLQAFSQLICTCNSLKTSPPRAIATTIAMTL GNDLOKOGKISNOMKOSMEEFRSLASRYGDLYQASFDADSATLR NVELOQOSCLISHAIEAILDERSASFOEYGSTGTHAHADESYE RRMMSYYNHVLEEVESLNGKYTPUSYMHTACLCNAITALLKUPL SFORTSFOKUQSTSIKLASPAPRNPAEPIAVONNQQLALKVUG VVQHGSKPGLFPKTQSVCLNVSSTLQSKSGQDYKIPIDNMYNEM EQRVEPHNDYFSTQFLLMFAILGTHNITVESSVKDANSIVWKTG VVQHGSKPGLFPKTQSVCLNVSSTLQSKSGQDYKIPIDNMYNEM EQRVEPHNDYFSTQFLLMFAILGTHNITVESSVKDANSIVWKTG PRTTIFVKSLEDPYSOQIRLOQAQOPLOQAQORNAYTRF PRTTIFVKSLEDPYSOQIRLOQAQOPLOQAQORNAYTRF PRTTIFVKSLEDPYSOQIRLOQAVKTANARKTDEERK SERRAAGSLINKLIKESNLUPNTNQVEVLQRDDMSPLYSVKSFEEL RIKPQLLQGVYAMGFNRPSKTQENALPHMLABPPONLIAQSOSG TOKTAAFVLANLSQVEPAMKYPQCLCLSPTYELALQTGKVIEGOM GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWGSKLK FIDPKKIKVFVLDEADVMIATQGIQDQSIRIQRNIPRNCOMLLF SATTFBDSWKKRAQKVVPPDNYLKRREETLDTIKOYYVLCSSR DEKFQALCNLYGATTIAQAMIFCHTRKTASWLAAELSKEGHQVA LLSGEMMVBORAAVIERFREKKEKVLVTAVCARGIDVEQVSVV INFPDLPVDKGGNPDNETYLHRIGRTGRFGRGKLAVMNVDSKHSM NILNRIQEHFMKKTERLDTDDLDEIEKIAN AFIPAMABLIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGEVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAFG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGEVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAFG KA 6259 2 1540 LLEKGFFSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKIFFILGTDPVSLRNYPYXICDSCEMMLKNISGLII SKKNCSRKKPDEPNVCEKLLDTRHEKFIGEKSYKYDQKRNAI MYHQDLSOPSFGGSFEYSKNGQFHDEAAFFINKSGQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRRGH QRALTKDNPYEYNEYGEIFCDMSAFIILHGGATTRKILERYKVSD KTMEKSALLKGU VHMGSKSYDVDNENGSNFSKKSHLTOLRRRHT	6255	1	1444	PTRPQQELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT
LSPQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMITL GNDLQRGGRISNOMKQSMEERSLLSARYIDLYQASPDADSATLR NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTHABDEYE RRMMSVYNHVLEEVESILGKYTDVYSMHTACLCNAITALLKVPL SFQRYFFGKLQSTSIKLASPSPRNPPAEPTAVQNNQQLAKVEG VVQHGSKPGLFRKIQSVCLNVSSTLQSKGQDYKIPIDNMTNEM EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVKNTG PRITIFVKSLEPPYSQQIRLQQQQAQQPLQQQQQRNYTRF 6256 1 1542 CRGAGAEPANPRSPRSLVFSLESTSTSVPPAEGTMATDSWALA VDEQEAARSLSNIHLKERK KPDTNGAVVKTNANAEKTDEEK EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSFLYSVKSFEEL RLKPQLLGGVYAMGFRRPSKIQENAPLMAEPPQNLIAQSQSG TGKKTAAFVLAMLSQVEPAMKYPQCLCLSPTYELALDTGKYIEQM GKFYPELKLAYAVRGKLERGQKISEQIVIGTPGTVLDWCSKLK FIDPKKIKVFVLDEADVNIKKREESTIPTIKGRYUPVLSSR DEKFQALCNLYGAITTAQAMIFCHTRKTASWLAABLSKECHQVA LLSGGMMVBGRAAVIERPREGKKVLVTTNVCARGIDVEQVSVV INFDLPVDKDGNPDNETTLHRIGRTGRFGKRGLAVMWDSKHSM NILNRIGSHFRKKIERLDTDDLDEIEKINN AFIPAMABLIGKKLGGEVEKVQUQAQDGDJSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMABLIGKKLGGEVEKYQOLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 ILEKGFPSQCHPERKWKUDDVLESSGENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKLCDSCENNLKNISCLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYNDOKNNAI NYHQDLSQDSFGQSFEYSKNGPHDRAAFTNIKRSQLETYCK NECGRTFIESLKLNISQRPHLEMEPYGCSICGKSPCMNLRFGH QRALITKDNPYEYNEYGEIFCDNSAFITHQGAYTEKLIREPKYND KYMEKSALLKHQI VHMGSKSYDYNENGSNPYKKSHLTOLRRAM				VYRIARQASRMGNHDMAKELYQSLLTOVASKHFYFWLNSLKEFS
GNDLQRGRISNOMKQSMEEFRSLARRIGDLYQASFDADSATLR NVELQQSCSLISHAIEALILDPSASFQEYGSTGTAHADSEYE RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL SFQRYFFQKLQSTSIKLALSPSPRIPAPEPTAVQNNQQLALKVEG VVQHGSKPGIFRKIQSVCLNVSSTLQSKSGQDYKIPIDIMTNEM EQRVEPHNDYFSTQPLLNFAILGTHNITVESSVKDANGIVWKTG PRTTIFVKSLEDPYSQQIRLQQQQAOPIQQQQQRNAYTRF 6256 1 1542 CRGAGAEPAANPRSPRSLVYSLESTSTSVPPAPGTMATDSWALA VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK EDRAAQSLLNKLIRSNLVDNTNQVEVUQEDPDNSPLYSVKSFEEL RLKPQLLQGVYAMGFMRPSKSIQENALPHMASEPQNLIAGQSGG TGKTAAFVLAMLSQVBPANKYPQCLCLSPTYELALQTGKVIEQM GKYYPEKKLAYAVRGNKLERGQKISEQIVIGTPGTVLDNCSKLK FIDRKIKVFVLDEADVNLATQGHQDQSIRIQRMPSRNCQMLLF SATFBDSWKKFAQKVVPDPNVIKLREESTLDTIKQYYVLCSSR DEKFQALCNLYGAITIAQAMIFTHTRTASWLAAELSKEGHQVA LLSGEMMVGRAAVIERFREGKEKVLVTTNVCARGIDVEGVSVV INFDLPVDKOGNPDNETYLHRIGTRFGKRGLAVMWVDSKHSM NILNRIGEHFINKKIERLDPDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQUTE NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEPGRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQUTE NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFGRAQAKAGAPG KA 6259 2 1540 ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSKKKPDEFNVCEKLLLDIRKYPICEKSGYKYDQKRNAI NYHQDLSQDSFGQSFFEYSKUNGGRHDEAAFTNIKKSGLGETVCK NDEGGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH WYNGGLSKPIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH CRAHKTORN WYNGGLSTARKSHCHILDFRINKSTULTERVSVD KTWEKSALLKIQI YHMGKSKSYDYNENGSNYKKSHITCDFRKND]			HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPINP
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6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGGGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT	6257	210	615	AFTDAMARI TOVVI OCEURYVOOY CYCL
TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT			422	NNIVKEELALLDGSMAPKILGDW WYOELGDSSTEEL
6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTB NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLFFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT	l l	j	İ	TAEI KRYESOL DDI EPOSEOODETT ACLOOD DOLLA ON A TOTAL
6258 210 615 AFIPAMAELIQKKLQGEVEKYQOLQKDLSKSMSGROKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAETKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 1 LEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESTLKLNISQRPHLEMEPYGCSICGKSFCNNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNPSKKSHLTOLRRAHT				KA KA
NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 1LEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESTKLNISQRPHLEMEPYGCSICGKSFCNNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT	6258	210	615	
TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6259 2 1540 ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYQAKRNAI NYHQDLSQDSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT				NNIVKEELALLDGSNVVFKLIGPUI.VKOELGRADATUGKDI DUT
6259 2 1540 ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYQDKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT				TAEIKRYESOLRDLEROSEOORETLAOLOOEFORAOAAKAGARG
SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMDLKNIKGTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMDLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT				KA
SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT	6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSOENEDDHFWELLFHNNKTV
SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFEQSFEYSKNGGGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT	- 1		}	SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLTY
NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT			l	SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDOKRNAI
YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT		. 1	[NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK
KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT			1	YNECGRIFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH
TWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ	- 1		1	QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ		l		KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT
	<u> </u>	<u> </u>		GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ

SEQ	Predicted	Predicted end	Amino agid gogmont gontalidad
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHQRTHTGEKP
		i	YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL
			IVHQRTHTGEKPYKCNECGKTFCEKSALTKHQRTHTGEKPYECN
			ACGKTFSQRSVLTKHQRIHTRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
			RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF
			RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELROHGPPNI
1 1			VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI
			NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
-			SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGOPGPWPG
			MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
			NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCBIA
			QEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
1 1			EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
			EIARKLQEEELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKA
1			KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPA
6262	2		RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
5252	-	1759	PECHSOGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
1			GSTRLVSQGLEALRSBHQAVLQSISQTIECLQQGGHEEGLVHEK
1 1			ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR
] [LCQENQWLRDELAGTQQRLQRSEQAVAQLEEEKKHLEFLGQLRQ
1 1			YDEDGHTSBEKEGDATKDSLDDLFPNEEEEDPSNGLSRGQGATA
1			AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
1 1	1		TSGRGHPDVATMLNILALVYRDONKYKEAAHLLNDALSIRESTL GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
1 1	1		NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
1 1			PNVARTKNNLASCYLKQGKYAEAETLYKEILTRAHVQEFGSVDD
			DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV
		[NTTLRNLGALYRROGKLEAAETLEECALRSRRQGTDPISQTKVA
1 1	1		ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLQR
			SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
1 1			IEVRRCSMPSVICEHTKQFQTISEESNQGSLLTVPGDTSPSPKP
1 . 1		,	EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT
1 1			APVNTVMDSPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
		i	PNSNIPDQESSLQSFCNSENKVLKENADFLSLROTELPGNSCAO
f . l			DPASFMPPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ
į į			KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
1			IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
1 1			SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
1 1	1		AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ
1	l l	i	QSTQPEMHKYGQLVKVELEENABDDKTENQIPQRMTRNKANTMA
1	!		NQSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
]	İ		VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER
] [ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
	1	1	DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLQHSIE
			REKLIVSNEQEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
			PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
	!		QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD VNDDFELTPI
6264	143		
		1900	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
	l l	1	TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	l l		
l			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
		ı	WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

SEQ Predicted Predicted end nucleotide location Corresponding to first amino acid residue of amino acid sequence Sequence Predicted end nucleotide location Corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide Amino acid segment containing signal per (A=Alanine, C=Cysteine, D=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Summon acid segment containing signal per (A=Alanine, C=Cysteine, D=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, C=Cysteine, D=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, C=Cysteine, D=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, D=Methionine, N=Asparagine, S=Serine, T=Threonine, V=Valine, M=Tryptophan, Y=Tyrosine, L=Leucine, M=Methionine, N=Asparagine, S=Serine, T=Threonine, V=Valine, M=Tryptophan, Y=Tyrosine, L=Leucine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, V=Serine, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtophan, M=Typtopha	E= LQDE VLTY VQKVQ AAQL KPGG
No: nucleotide location corresponding to first amino acid residue of amino acid amino acid sequence corresponding to first amino acid residue of amino acid amino acid complete to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, N=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, N=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, N=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Arginine, S=Serine, T=Threonine, V=Valine, C=Codon, /=possible nucleotide deletion.	LQDE LQDE VLTY QKVQ AAQL KPGG
location corresponding to first amino acid residue of amino acid amino acid camino acid amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid camino acid camino acid sequence corresponding to first amino acid corresponding to first L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion.	LQDE VLTY QKVQ AAQL KPGG
corresponding to first amino acid residue of amino acid amino acid residue of amino acid sequence codon, /=possible nucleotide deletion.	LQDE VLTY QKVQ AAQL KPGG
to first amino acid residue of amino acid residue of amino acid amino acid residue of amino acid sequence Codon, /=possible nucleotide deletion.	LQDE VLTY QKVQ AAQL KPGG
amino acid residue of residue of amino acid sequence Codon, /=possible nucleotide deletion.	LQDE VLTY QKVQ AAQL KPGG
residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, *=S amino acid sequence Codon, /=possible nucleotide deletion.	LQDE VLTY QKVQ AAQL KPGG
amino acid sequence Codon, /=possible nucleotide deletion.	LQDE VLTY QKVQ AAQL KPGG
i i i i i i i i i i i i i i i i i i i	VLTY QKVQ AAQL KPGG
	VLTY QKVQ AAQL KPGG
SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEK	VLTY QKVQ AAQL KPGG
ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESI	QKVQ AAQL KPGG
INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMG	AAQL KPGG
LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKI	KPGG
DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYS	DATI.
YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVI	
QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQM	MEER
EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARV	TEEK
CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKT	DREK
6265 143 1960 KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKI	TONT
TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSH	TONI
WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTL	AVT.I.
SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENE	NEDG
ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKL	TOGT
SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEK	LODE
ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESL	VLTY
INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDOOMG	okvo
LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFOKKL	AAOL
DKKRDDFCKQNQEASSDRCSALLOVIFSPLEEEVKAGIYS	KPGG
YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVT	DAIL
QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYOOM	MEEK
EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARV	SKER
COGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI	
SHONONIA PCELISLONK RPSLYGSLTCQGIGLDGIPEV	PASE
GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSI	CTD
ISSRGCLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNC	RFF
PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTA	VDR
GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVG SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSR(ADN
LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPV	LVF
RSGAPVLSLLSVRDGFTASQGDGSCFTVQQDLDYVTELTG	MATH
PVYKVATWEKQIYTCCRDGLVRRYQLSDL	ו מטש
6267 3 622 LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFRE	TINE
NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELR	TMY
RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINAI	NZV.
ITRAKNRILDEVIVEEDSYLAHPTRORAKIQHSRRPPTRG	TWN
VASTSTSDGMLTLDLIQEEDPSPEEPTSLC	*11.11.2
6268 160 1368 HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQD	VAV
DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENK	ELA
PNSDIPEERPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQ	DTV
LKQMESAQEKDLPQKKHFDNRESQANSGALDTNOVSLOKID	NPE
SQANSGALDTNQVLLHKIPPRKRLRKRDSOVKSMKHNSRVK	THO
KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSE	CGK
IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTOHOR	VHS
GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCODCGKA	FRO
SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNR	TKR
KKKQPTS	- 1
6269 2886 1449 HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFD	ATL
TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVI.	IGT
GSSVKLDKELDLAVKTMVEISRTQPLTRREOLHVSAVETFA	NGN
FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYOEOMRDS	VAR
IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALS	INP
TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLAC	INY
WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSC	ML
YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMAS	.GA
HDPQTTQELLTTLRDASESPGENCQHLLARDVGLPLCQALV	BAE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	I I I I I I I I I I I I I I I I I I I
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
]	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
		 	DGNPDRVLELL PIPURTUON COORS
L	ļ	}	DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQ
6270	23	2086	SVTVTI GERGOGERDOVUK FINESESSESSESSESSESSESSESSESSESSESSESSESSE
1			SYTYTLGSEGDGRPPTYHLBEMEQEPQNGEPAEIKIIREAYKKA FLFVNKGLNTDELGQKBEAKNYYKQGIGHLLRGISISSKESEHT
1			GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP
ı			KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
			PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
1			EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS
1	1		YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDWLYPLVPDRSPVLK
			CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLLRQMS
l			DLRLQANWNRAEEENEFQIPGRTRPSSDQLKEASGTDVKQLDQG
			NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPEEKPKELPEW
1]		SEKVAHNILSGASWVSWGLVKGAEITGKAIQKGASKLRERIQPE
			EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK
			ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST
			VWQGLECAAKCIVNNVSAETVOTVRYKYGVNAGRATUUAUDONU
1	1		I NYGYTAYNINNIGIKAMVKKTATOTGHTLLEDYOTVDNEODENO
6271			EGAANVNVRGEKDEQTKEVKRAKKDK
02/1	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVEEEVNIPNPPMLATCA
Í			TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFROVMIII DCMAINTE
	ľ		1 IHDP QPHVIVHCAAERRPDVVENOPDAASOLNVDASCNIAKEA
			AAVGAPLIYISSDYVFDGTNPPYREEDTPAPINI.VCVTVI DCEIK
}			AVDENNEGAAVERIPILYGEVEKLEESAVTVMFDKVOFCNEGAN
Ĭ			MUHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTEHWSGNEON
1			I ALEMACALADAFNLPSSHLRPITDSPVIGAORPRNAOLDCCVI
6272	1136		ETLGIGQRTPFRIGIKESLWPFLIDKRWROTVFH
	1130	528	GAVMEDAAAPGRTEGVLERQGAPPAAGQGGALVELTPTPGGLAL
1 1			VSPYHTHRAGDPLDLVALAEOVOKADEFTRANATNKT.TVIAEOT
}			QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIVVIVKPECCO
1 1			QIFSIISPKEWGTSCPHDFLGAYKLOHDISWTPVFDTFVODAVI
6273	256	843	SMMDTLLSQSVALPPCTEPNFQGLTH
		047	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIA
			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV
1			HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS
_ 1			ITCFVRKWKBKVAWPRLTKEDIKFVWLSVDFDNWRDWEGDEEME LAHVEHYABVRDNTYCVLPT
6274	56	1142	APAMANACCACACARROY COLOR
	l		AAAAMAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLT3VLRHVQSLEFDPGTPGSERTEALYYTDDTAMARALVQSL
			LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR
ł			DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
Į.	1		AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED
- 1		1	LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS
Ī	1	1	ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI
			SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA
			QSLHRVFQKS
6275	20	565	SRRGRARCLARGSRR PVPRPAKTMAFMVKTMVGGQLKNLTGSLG
			GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR
		ĺ	KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI
			EEDTEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE
			KCHVM
6276	797		TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE
ſ	l l	1	SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP
	•	[-	VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV
1	1	1	LGSGYREOLI.TDMLEI.COCI.MODUCEOMORUT Z CYCOME CO-
	į	1	LGSGYREQLLTDMLELCQGLWQPVSFQMQAMLLCHSTAGAIGRL LASSPRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYYRLPQ

SEQ	Predicted	Predicted end	I mino poi
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
6277	4600	2744	MAFRIEMGLYYSYFKTIVEAPSFLNGVWMIMNDKLTEYPLVINT
			LKRFNLYPEVILASWYRIYTKIMDLIGIQTKICWTVTIGEGLSP
		1	TESCEGLEDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGL
1			VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQMLLVTHILRA
1			TKLYRGSLIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVGY
		1	IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG
	1		ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA
1	1		NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT
1	i		LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY
1	i		HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC
	Į.		KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW
			IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART
		•	KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM
1			PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV
-			KE
6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
1			IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCOLVLGAG
1			ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKO
			YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA
			PVPSACFRNICKOMTKMHEAIFDLLPEEQTOMLFLRINASYKLH
ļ			LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN
6279	127	1687	MAEIWEQKR
		7601	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL
Ì	j		LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA
	1		AESLINSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQKPRPEAE
			PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLORSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR
i			LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYFAFI
i .	[EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFER:
	[LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEAEEVDTVDVS
			GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE
			ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR
			LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFL
			QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK
6280	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE
j l			DVDLAQVLAYLLRRGQVRLVQGGGAANLOFIOALLDSEEENDRA
	ľ		WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGOLGLRRAA
	ĺ		QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
			YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
			RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
		ł	LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREONRRTLO
j l		;	IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
			PVGALAGHQDGITFIDSKGDARYLISNSKDOTIKLWDIRRESSP
			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
	. }		GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
	ł	,	LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
6281	857	0515	PESEECASAPAPVPQSSTPFSSPQ
0201	037	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE
ļ		}	DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA
- 1	<u> </u>	}	WDGRLGDRYNPPVDATPDTRELEFNEIKTQVBLATGQLGLRRAA
İ	ļ		QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
	!		YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
	ĺ	ĺ	RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
		•	LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
j	1	1	IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR

SEQ Predicted Predicted end Amino acid segment containing s (A=Alanine, C=Cysteine, D=Aspar Indication Corresponding Corresponding Indication I	tic Acid, E=
NO: nucleotide location corresponding location corresponding H=Histidine, I=Isoleucine, K=Lw	tic Acid, E=
delicoponding (nemiscidine, leisoleucine, Kelar	G=Glycine,
I THE PROPERTY OF THE PROPERTY	sine,
	ragine,
S=Serine, T=Threonine, V=Valine	
amino acid W=Tryptophan, Y=Tyrosine Y=Tibb	
codon, /=possible nucleotide de	letion
\=possible nucleotide insertion	1
EGMEASRQAATQQNWDYRWOOVPKKAWRKI,Y)	L.DCDCCT MURDOW
GVLHTLIRCRFSPIHSTGOOFIYSGCSTGRIN	WALL COULTING
LINAKACVRDVSWHPFEEKIVSSSWDCNT.DI.	WQYRQAEYFQDDM
6282 125 906 RMAACPALKAYLUDI.SCRILLINGS	
	ALKRLRGASVIIR
FVTNTTKESKQDLLERLRKLEFDISEDEIFTS VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAE	SLTAARSLLERKQ
RLLLDGAPLIAIHKARYYKRKDGLALGPGPFV	PEHFHYQILNQAF
VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCR	TALEXATUTKAT
GILVKIGKYRASDEEKINPPPYLTCESFPHAV	MHTI.OUT T
LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLT	COUVERDED
KKQLPSIPKNALPITKPTSPAPAAOSTNGTUA	SYCOPYTEVETT
ABFTLVVKQKLPGVYVQPSYRSALMWFGVTFT	PHGI.VODGUEVE
TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSG	ET DUKD A DA VIJO
RNHNHIWQVLMYARRVFYKIDTASPLNPRAAV	T.VEVETATAL EVOV
VVDSVKVCTARLFDQPKIEDPYAISFSPWNPS	WHITEADERMI TO
6284 1 2879 RSVIDGETTS SPINGS OF STREET	KTVAT
1 TOTA TO THE STANFOLSKY RYMANKWOW ROD	EELIGQISDIRV
QNLQVERENVQKRTFTRWINLHLEKCNPPLEV	KDLFVDIQDGKI
LMALLEVLSGRNLLHEYKSSSHRIFRLINNIAK. VSIDAAEIADGNPSLVLGLIWNIILFFQIKEL	ALKFLEDSNVKL
LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRI	TGNLSRNSPSSS
KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSI	KAIKALLAWVQR
RENLEKAPSIAQDALHIPRLIEDEDIMUDTDD	EOCTMOVED OFF
LRFPEGEAEDIFDSDKEVPIESTFVRIKETDGT	POPERTURE MINE
GERTYTVNHETSHPPPSKVFVCDKPEGMKPPP7	LDGUGGUAT and
STEFMHQIIDOVLOGGPGKTSDISRDSDESSTI	CCCDVGVGDGDG
DFIRTYHFEADTYKDPFCSKNLSLCFEGSDD1	VAKEEL DODGER
LAVEVALEKEQKQESSKIPESSSDKVAGDTEL.	JEGENDINGO GGG
CNGALESTARHDEESHSLSPPGFNTVMADGEOT	FESTATE MODELTERS TO THE
EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVE	SPHETKPDEDA
EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDK EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEE	CHEPHODSGEEA
EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPL	EGEDDDLQGVG
YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEP	DECAMBBY DODE
EEADGSQSSSSSVPGESLPSASDOVT,VI,SPCG	VCTTOACEDAD
I HAPHEDROQUETKENDPMDSHOSOESPNI,ENTA	MDI.FEMBREDO
ISSAKERKHVDHVESSLFVAPGSVOSSDDT.F	EDCCDVCTDCD
1SHSDSSIYLRRHTHRSSESDHFSLCSVEEPSP	50
SCATENILLEMWWFQQGLSFLPSALVIWTSAAFT	PSYITAVTLHII
IDPALPIISDIGTVAPEKCLFGAMLNIAAVI.CT:	ATTVIDVVAIRE (
ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFO	QKTTLFAAHVS
GAVLTFGMGSLYMFVQTILSYQMQPKHGKQVFI	WIRLLLVIWCG
VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDK EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLT	GYVLHMITTAA
I NERTRIAGENT	LLYDTAPCPIN
6286 1619 276 KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFY	MDAY/
PFSIPAASEIADLSNI INKLLKDKNEFHKHVEFI	THICKYAVDDV
POURIMEMENISSBEVVEIEYVEKYTAPOPEOCN	ARHIDDMICCIN
GAEEWILTGSYDKTSRIWSLEGKSIMTIVGHTDU	WKDNV PRINKKU
SESCEDESASMOQTILLWEWNVERNKVKALHCCR	CHACCUMETA
VDGSGTKFCSGSWDKMLKIWSTVPTDEEDEMEES	יישראאסספואיי
EQUGLIRIPIVTLSGHMEAVSSVLWSDARFICSA	SWDUTTOUND
VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTD	T TO GO THE THE THE THE THE
ADGSUVSLTSHTGWVTSVKWSPTHEOOLISGS	T.DNTUVI.wow
RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGAD	nklysyrysp

SEQ	Predicted	Predicted end	l having and
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
•	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleofide deletion
	sequence	<u>L</u> .	\=possible nucleotide insertion)
<u> </u>			TTSHVGA
6287	278	1482	MQFFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
- }			APAKLQVQKILCDLLLPENLKEGLKESSWSSI.DCTKNDDDDDDDD
I	1		VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAOSAOSINSTR
ļ		}	MPAREDCLKRVSSEPVLSVOEKGVLLKRKLSTIRODVTVNJEDCD
1			NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMPLFFF
1			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
			QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVDTEVCTMA
1	,		YPTVPCPLHVFEPRYRLMIRRSIOTGTKOFGMCVSDTONGFADY
1			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
6288	1		I APEDA
1	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1	1	1	MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
1			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM .
1	1		KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNVCSEAAQKRSLDR
6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1	1		MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
1	i		HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
j			KVGLAIKPGTSVEYLAPWANOIDMALVMTVEPGFGGOKFMEDMM
1]		PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMTVSGSATM
6290			RSEDPRSVINLLRNVCSEAAOKRSLDR
0230	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRMISRYTRKA
]]		VPQSLELKGITKHALNHHPPPEKLEETSPTSDSHEKDTSSOSVE
	ĺ		DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGVGFLD
1	,		QNATEKVQTMFTAIDELLYEOKLSVHTKSLOEECOOWTASEDUI.
i			RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
1			GKKLHFSSYAHKASSIAKSSFCSMERDEEDSIIVSEGIIEEY
			LAFDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY
	1	İ	VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV
1 1	}		LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
			TSSLSYTVQSTRRRNPPFRTLHPISTSHSCAETPRSVEEILRGA
	1		RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK
		1	PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT
, !		ļ	QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG
6291			P
0291	1732	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES
]]]		PFAKYNRLGQLSCALCNTPVKSELLWOTHVIGKOHPEKVAET.KG
i I		ļ	AKEASQGSSASSAPOSVKRKAPDADDODVKRAKATIJIDOVODET
į j	[İ	SAWIINFDKIGKEFIRATPSKPSGLSLLPDVEDEFFFFFFFFFF
i i			GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNDDK
1 [1	AFILERSGSIEKAETHEKVVERRENTAEALPEGFFDDPRVDADV
j 1			RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ
[1	1	IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN
6292	1835	1142	ADSDDEGELQDLLSQDWRVKGALL TCDGAMKMVADWTDBVQNGQQQQQQQQ
		3	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
[LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLIMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
	i]]	SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
	į	[]	LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
			AKEPPPPYVSA
6293	2382		FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
			VGSRTLPVDFHIKMVESMKYPFROGMRLEVVDKSOVSRTPMAVV
			DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

S	EQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	D	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
N	0:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-		to first	amino acid	P=Proine, Q=Glutamine, R=Arginine
İ		amino acid	residue of	S=Serine, T=Threonine, V=Valine
1		residue of	amino acid	W=Tryptophan, Y=Tyrosine X=Imknowm +-C+on
		amino acid	sequence	Codon, /=possible nucleotide deletion
		sequence		\=possible nucleotide insertion)
				MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVVTRCCWEFFCMV
				LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWECV
1		`		HASSHAIFPATFCQKNDIELTPPKGYEAOTFNWENYLEKTKSKA
- [APSRLFNMDCPNHGFKVGMKLEAVDLMEPRI.TCVATVKPVATURI.
j				LSIHFDGWDSEYDQWVDCESPDIYPVGWCEI,TGYOLOBBUAARB
1	J			ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLROGSKKPLLEDD
				POGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE
629	94	354		NIKQETDD
"	_	224	1814	AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
	ı			KNVIATASDYDMAEITNIRPSFDVSPVVAGI.TGASVI.tr/CVCVcv
				VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
ł	- 1			VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
1	1			LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
i				DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
1	ı	•		VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
1	- 1			RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
				SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
1	- 1	ì		RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD
				RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
629	5	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
				TRRLSSSESPQRDPPPPPPPPPLLRLPLPPPPQQRPRLQEETEAA
				QVLADMRGVGLGPALPPPPPPYVILEEGGIRAYFTLGAECPGWDS
1	- 1	Í	1	TIESGYGEAPPPTESLEALPTPRASGGSLEIDFQVVQSSSFGGE
				GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMRSSR
1				RRRRRRRKQRKVKRESRERNAERMESILQALEDIQLDLEAVNI
				KAGKAFLRLKRKFIQMRRPFLERRDLIIGHTPGFWVKAFT.NUDB
	ļ			ISILINRRDEDIFRYLTNLOVODLRHISMGYKMKI.VFOTNDVET
1				NMVIVKEFQRNRSGRLVSHSTPIRWHRGOEPOAPPHGNODAGUG
-			1	FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYIRERGSDTVDVV
1	ŀ			QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETTHDIV
1	ł		1	ISDFMETTDYFETTDNEITDINENICDSENDDHMWWDMMETTDN
i		}		NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNNENTY
ł			į	GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
1	- 1		į.	SDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
L				SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS DLEDVLQVPNGWANPGKRGKTG
6296	5	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
1	- 1	ł	-	EAVRPARERLARKELROKRMQQFSRDSAYSSNKDSTCLLTERDT
l		1		LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
				KWALIHKRVRLSVFGARWGRIYFGK
6297	' [1	922	QRAAAASPSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGFLS
		ł		VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGEVELOGIAZZ
i	l			VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVN
1		Į	1.	NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLpwapi.si.papi.
		ļ	11	MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTPPDEGV
	- 1		[]	FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEO
6298				GARGSMPAYSGNNMDKSDSELNNEVAARKRNLALDEAGORSTM
0238	İ	3	985 5	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
	- 1	1	1	PFGPHRGLSVLLARI PQRAPRWLPACROKTSLSFLNR PDLDNT.h
	- 1	1	1.2	YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACTPED
	- 1	İ	1.3	YSGVGSSDGNSEESTLGKWRKDVLS1IDDLADGPOILVGSSIGG
	Ì	İ	1 0	*LMLHAAIARPEKVVALIGVATAADTLVTKFNOLPVRLKKEVEM
	- 1		F	GVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPTRI.
	-]	ļI	HGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
				LLVYTIDDLIDKLSTIVN

SEQ	Predicted	Predicted end	1 Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
l	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	sequence	sequence	Codon, /=possible nucleotide deletion,
6299	512	814	\=possible nucleotide insertion)
	1	014	ECDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
	ŀ		SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
6300	121		MKEEEVQLRNNH
1 0300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWRQGARA
1	ſ	f	AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGGPR
İ			LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
1			ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE
6301	516		WFEVNRSCPEHPSD
0301	270	284	GKFVPVNWEPPQPLFFPKYLRCYRCLLETKELGCLLGSDICLTP
1 .	j		AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW
6302	400		IFSQYCFLDFCNDPQNRGLYTP
0302	490	745	IFGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS
6303			PVLLNCLPGDLRPLDELYAOKLKYKAISEELDHALNDMTSI.
0303	2	1951	YWNEYGGGLLWQSWQEKHPGQALSSEPWNFPDTKEEWEOHYSOL
			YWYYLEQFQYWEAQGWTFDASOSCDTDTYTSKTEADDKNDEKCM
	1		KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKTNSEEUT
1			QSQLDSCTSHDGHQQLSEVSSKRECPASGOSEPRNGGTNERSNS
	i i		SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
	l		PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
	[HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK
			SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
.]	ľ		DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV
1			PDEQDCVTQEVPDSRQAETEAEVKKKKNKKKNKKVNGLPPEIAA
			VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR
1 1	ı		VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA
]	i		RNNAEVYGIADKIEFICGDFLLLASFLKADVVPLSPPWGGPDYA
	İ		TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
6304	1	1420	LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
""	- 1	1438	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE
1 1	l		DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
i l			WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ
1	1		WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL
1		1	AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL
	Ĭ		CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
1 1			TDGGARPVIWWAPDVOHLSDPDEDONSLALGWLOYOALLAHSCN
[[ł	WPGQAPCPGIHHTEWARLALFDFLLOVHDRLDRYCCGFEPERSD
			PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP
]			EDKLNFRLLEGIDGF?ESAVKVLASGCLQNMLLKSLQMDPVFWE
6305	99		SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
0303	22	420	NMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES
]	1		RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD
6306			VQGKILTKSEQFKMPEGR
0.30%	1	1874	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
	İ	1	KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD
	1	1	ESEDSGVIPGSHSENALHASEEEEGEGGKAOSSLGVIPLMRVVO
1			SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFO
		į.	NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
		i	TYFVGEMPGGTPGGPSGQGAKAARGWETAIROALMPVILODAPS
ı			APGHAPHRQASLSISVSNSQIQENVDIATVYOIFPDEVLGSGOF
- 1		1	GVVYGGKHRKTGRDVAVKVIDKLRFPTKOESOLRNEVAILOSLR
1		f	HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
İ	İ	1	TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPOVKLC
		1	DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNOGYNRSLDMWSVG
	1	1	VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID
- 1		i	LINNLLQVKMRKRYSVDKSLSHPWLOEYOTWLDLRELEGKMGER
			YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S-Carino T. Thursday, K=Arginine,
į	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	seducince	Codon, /=possible nucleotide deletion,
<u> </u>	Dequence		\=possible nucleotide insertion)
6307	2136	589	LAERISVL
****		303	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKFRHVFG
1	i	l .	QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGGAFL
	ŀ	!	VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
ı	1	İ	TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
			SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
1			ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
			GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
1			VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
ı			GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
			PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
1			DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
6308			QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	. 2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
	[LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
1		,	PKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGIK
	1		WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLOSYVDAGTPMYT.
1	i		VIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
			VAFDCMKNYLDAIYDVTVVYEGKDDGGORRESPTMTEFLCKECP
			KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD
			PERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
			YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
:	ļ		VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLOL
6310			KLGPALKIYEYHVKPLQTKHLKNNSS
6210	36	979	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
1 1	1		AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV
1 1			DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
]	J		IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR
1 1			KADMMESLALGFDDGKTKTSGI LEALHRYYQNAATDVRRVWLSS
1 1		İ	VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP
1		j	CIPKIQSMIEDANKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
6311	1	- COE	LTSLRV
"""	*	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
1 1	- 1		ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL
1	ł	i	PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN
		1	MVPRVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL
1 1	· · · · · · · · · · · · · · · · · · ·		KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI
6312	213	1400	KRYAR
		7400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
1 1	i		GKTEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
1 1	ı	1	RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
1 1	1	1	VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
1 1		ļ	DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA
			IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
1	1	1	GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD
1 1		1.	VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
6313	2	2072	YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
	-	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
	1	13	FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
] [1	RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
[]		1:	TOEPLVEIEGVSKMAFRHLIEFTYTAKLMIOGEEEANDVWKAAE
1	ļ	11	FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
!!	1	1	TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKOSVK
		1.3	YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCPSDPTSK
			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE

SEQ	Predicted	Predicted end	Amino acid segment cort
īaī	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- {	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
1			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
i			LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
	1		PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
			TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
1			QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
ł			MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
L			AEDLETKPTVDSEAEKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
1			FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
1	1		RLNEQREODRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
1	}		TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
1]		FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
Į.	i !		TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK
			YIQSTGSSDDSALALLADITSKYRQGDRKGOIKEDGCPSDPTSK
			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
1			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKORTGKKIHVC
			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTI.KCH
1 :			LTACQTGVGAKKGRKKLYECQVCNSVFNSWDOFKDHLVTHTGDK
			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVO
	1		TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEOVHPDLLQDS
			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNO
			MPVEVQTELLEADLDHVTPEIMNOBERESSOADAAEAAREDHED
6315	1	7015	AEDLETKPTVDSEAEKAENEDRTALPVLE
1 3313	·	1015	LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA
			IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY
			PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI
i 1			VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF
			HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
1 !]		VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP
1			GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
6316	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR
l i			MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEELALEQAKKES
1	j		EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL
1			ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA
			EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY
	}		MHCVNHAKQSMLEKGG
6317	102	839	PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN
	1		FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
1	1		TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN
		į	EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
	1		QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD
			PAITAAKQNTRLKETPPPPQPNCAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
1 1	į.	1	LGPLLSPFPLPAGSWHROMLRSSLRFPITNSAGAPCKAAGRMNT
1	ł		LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACOEHRTGT
[1		VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
[,	ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAOAIIIVFNIN
[DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
	ļ		EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVT.A
<u> </u>			ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319	88	717	AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELORLT
		ļ	ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES
			CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML
			SYGVTTLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATSSVFQEV

SEQ	Predicted	Predicted end	13-1
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding		H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
ł	ł	i	RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
1			IGKAYABELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
]		VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
	ŀ		EDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
	ŀ		PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
1	1		MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
}			FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
			RNS FSSSWFHLNTNVMSGSNGSKENSHNKARTS PYPGSKVERSQ
1		1	VENERACHTARMODAR DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIO DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COM
1		•	VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
J			FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
1			NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
1			IPGGMVDPGEKISATLKREFGEBALNSLOKTSAEKREIEEKLHK
İ		•	LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGBIMDNLM
	ł l		LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
6322	3,15		EADCHAL
6322	2047	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
1			WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKOPSLTLEL
			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
- 1			RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF
1			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVROT
1			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
		_	SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
1	i		PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
	1		EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
	1		LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
L	1		MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
1 1	i		RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
1 1	ì		PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
1 1	İ		SELGTTCLWTETGTDGLWTDPHRSDLQFQPEBASPWTQPGVHGP
1 1	ł		WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
1 1	j		PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
l f			QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
ŀ	Į.		EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS
]		İ	RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
			KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC
			EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
1			SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
1	1		EEHAOGAVTKPRYMOWPRTMCCTCTT CERTROTENT CONTRACTOR
	i	j	EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNINF
] [1		KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
			KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
6325	165	D44	WAEGNREDGYLWGLDNMICLLQGLAQS
		944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
1	1		SRLSSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRSRRRHQ
	1		RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
	į		RSRSRSRGRSYCGRAYAIARGORYYGFGRTVYPBEHSRWRDRSR
		ļ	TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
			VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
		i	VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTOTL
L			GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Trimbones V mane;
l l	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	204	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QAWGGVGQEASSGVP
6327	1	1337	
1		1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
ł			DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
	1		GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
			LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS
	j		RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
l	ł I		ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
			AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI
			SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS
1			RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
			GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEBEMHTDAKIRAENGTGSSPRGPGCSL
			RHFACEQNLLSRPDGSASFLQGDTSVLAGVYGPAEVKVSKEIFN
			KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI
			TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
1			SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT
			ELQQCLAAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT
			SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNT.
			RGDIERKSLAINEEFVSIFKEVKEELESISEDVOAMSNCCODMT
ì			SRLQAAKEQTQDLIVKTTKLQSESOKLEIRAOVADAPLSKFOLT
1 1			SDEMSLLRGTREGPITEDFFKALGRVKOIHNDVKVLLRTNOOTA
1 1			GLEIMEQMALLQETAYERLYRWAQSECRTLTOESCDVSPVLTOA
1 1			MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR
1 1			PIEMHSHDPLRYVGDMLAWLHOATASEKEHLEALLKHVTTOGVE
1 1	i i		ENIQEVVGHITEGVCRPLKVRIEOVIVAEPGAVILLYKISNLIKF
1 1	1	i	YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKIMD
1			KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDAROADEV
1 1			QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
1 [EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ
1 1	1		HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
1 1	l		LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR
6330	1151		SPQQVQTLLS
""	7777	333	FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL
1	1	i	PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
1 1		J	KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC
			EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
1 1			RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
	1		NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN
6331	3	495	
1 - F	-	7,7,7	QQQQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
į I	1	. 1	LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
	i	1	RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1 1	878	VTFONKEDINGET DITTE DE TYCANONIA
j 1		0,0	VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI
	i		NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
		İ	SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
]			SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
	ſ	l	ELRPGORQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
j [1	VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TETTETATACCECTOCOUCANICA
	-	7401	TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
			QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG
	İ	j	GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP
			MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS

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Despinning	SEQ	Predicted	Predicted end	
Not nucleotide corresponding to first corresponding to first amino acid residue of amino acid residue of amino acid sequence corresponding to first correspon		l.		Amino acid segment containing signal peptide
Corresponding to first anino acid anino acid residue of section. Helistidine, Y-Isoleucine, N-Asparagine, anino acid anino acid sequence (Section to the control of section to the control of section to the control of section to the control of section to the control of sequence (Section to the control of sequence) (Section to the control of sequence) (Section to the control of sequence) (Section to the control of sequence) (Section to the control of sequence) (Section to the control of sequence) (Sequen	NO:		I .	Glutamic Acid, Farhenylalasia, Carlos
to first amino acid residue of anino acid sequence anino acid sequ	1	location		H=Histidire T=Tsolevoire V=Lucire
amino acid residue of amino acid	1	corresponding	to first	L=Leucine, M=Methionine N-Asparagine
residue of amino acid sequence source of amino acid sequence seque	ł		amino acid	P=Proline, Q=Glutamine, R=Arginine
### ### ### ### ### ### ### ### ### ##			residue of	S=Serine, T=Threonine, V=Valine.
sequence Codon, /-possible nucleotide insertion				W=Tryptophan, Y=Tyrosine, X=Unknown *=Chan
Apossable nucleotide insertion		3	sequence	Codon, /=possible nucleotide deletion
COMMENSION OF THE STANDARD PROPERTY OF THE PROPERTY OF SELECTION OF THE STANDARD SELECTION OF THE STANDARD SELECTION OF THE STANDARD SELECTION OF THE SELECTION	ļ	sequence		\=possible nucleotide insertion)
COMMENSION OF THE STANDARD PROPERTY OF THE PROPERTY OF SELECTION OF THE STANDARD SELECTION OF THE STANDARD SELECTION OF THE STANDARD SELECTION OF THE SELECTION	i		·	GAKSMWTEHKSPDGRTYYYNTETKOSTWEKPDDLKTPAEQLLSK
ARABANAVARARARARARARANNYSTSSENTVESTYPVYUPEP EVTSIVATVUNENTYTISTEREQQQISTERIQDGSVEVSSNYG ERTSKQETVADPTPKEEEESQPAKETTYNYTEERKQAPKELL KEKAVPENNSVEQAMMI INDEPSSALAKISEKKQAPNAYKVOT EKK GONPSGRAAGFARAAMPSSPLRVAVVCSSNQMESMEARINILSKE GSVRSFGIGTHVKLJGPAPDKNYAVVCSSNQMESMEARINILSKE GSVRSFGIGTHVKLJGPAPDKNYAVVCSSNQMESMEARINILSKE ELYTONSILMHDENRIKIK KEPERFONKCHJULTGERVAV QVUDLINSEGGETCQDVHVAVAUDIODINEERATIGAFLICELCQC IOHTEMMERE IDELLQEFEEKSGRTFLHITVGLITGERVAV QVVDLINSEGGETCQDVHVAVAUDIODINEERATIGAFLICELCQC IOHTEMMERE IDELLQEFEEKSGRTFLHITVGLITGERVAV QVVDLINSEGGETCQDVHVAVAUDIODINEERATIGAFLICELCQC IOHTEMMERE IDELLQEFEEKSGRTFLHITVGLITGERVAV QVVDLINSEGGETCQDVHVAVAUDIODINEERATIGAFLICELCQC IOHTEMMERE IDELLQEFEEKSGRTFLHITVGLITGERVAV QVVDLINSEGGETCQDVHVAVAUDIODINEERATIGAFLICELCQC IOHTEMARE IDELLQEFEEKSGRTFLHITVGLITGERVAV GERALIALILIGIDKI MAY GENERALIGHT GOPVITAVVQRVETH LUTGOLVAROVGHL ARAGOMILITGH SIGNAGAMAN THE GOPVITAVVQRVETH LUTGOLVAROVGHL ARAGOMILITGH SIGNAGAMAN THE GOPVITAVVQRVETH LUTGOLVAROVGHL ARAGOMILITGH SIGNAGAMAN THE GOPVITAVVQRVETH LUTGOLVAROVGHL ARAGOMILITGH SIGNAGAMAN THE GOPVITAVAN THE GOPVITAVVQRVETH LUTGOLVAROVGHL ARAGOMILITA SIGNAGAMAN THE GOPVITAVA	1			CPWKEYKSDSGKPYYYNSQTKESRWAKPKELEDLEGYONTTVAG
EVTS IVATVVDNENTVI STEROAQLISTRAIODGSVEVSENTG ERTS KQETVADFTRKEE ESGOPAKUTINKERAKOA KIGLI KEKK VENNAS WEQMKMI INDERYSALAKLSEKKQAFNAYKVOT EKK 6334 17 644 GONFSGRAAGFAAAMPSSELWAVVCSKTYDQMYBDLLEKOK CEVYTONGILHMIDERKEIKERDER RQXCKOLFDLILTCEERVYD QUVELINSEQSTCOPPUVLVNUD IQDNEEATLGAFLICELCQC LUHTEDMERE IDELLQEFEEKSGRTYLHTVCYY ARARAFGVILCTELIGAALGDGSRVEMSY IPGGPVTAVQRVEIH KURGENILLGEFEEKSGRTYLHTVCYY ARARAFGVILCTELIGAALGDGSRVEMSY IPGGPVTAVQRVEIH KURGENILLGEFIGGGI IDDPSONPTSEBUTDMGIVYTRVSEG GPABLAGLQIGDKI MQVNONDMTMVTHQDAKREITKKSEEVVRL LUTRQSLGKAVQOSMUS 6336 1003 438 HEPASKGRAEVSNNRLSVAAAISHGRVFERMSLEGBERIHLLEN ADPHLEKCH IPRULAPRYKDOTGGYTRINLGI PNRSLDRAK MAVIEYKGKOLPPLEPERBEBIELLINOLLGGERQLEKOERGASA HEPASKGRAEVSNNRLSVAAAISHGRVFERMSLEGBERIHLLEN ADPHLERKOLIPKLFQVLAPRYKDOTGGYTRINLGI PNRSLDRAK MAVIEYKGKLPPLEPERBEBIELLINOLLGGRACDIKROLERGAGE HERASKGRAEVSNNRLSVAAAISHGRVFERMSLEGBERIHLLEN ADPHLERKOLIPKLFQVLAPRYKDOTGGYTRINLGI PNRSLDRAK MAVIEYKGKLPPLEPERBEBIELLINOLLGGRACDIKAGE LITGUSLGRACH ADPHLER ADPHLER ADPHLER ADPHLER ADPHLEPER ADPHLER ADPHLEPER ADPHLER ADPHLEPER ADPHLER ADPHLEPER ADP			l .	SLITKSNLHAMIKAEESSKQEECTTTSTAPVPTTEIPTTMSTMA
SETSKQETVADETPKKEEGESQPAKKITYTKNIKEGRAQAFKELLI KRKAVPSINASWEQAMKII INDRYSSLAKSKAQFRNAYKVOT EKK GONPEGRAAGFAAAMPSSPLVAVVCSINQBRSMEAHNI LISKE GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDQWAPBILLEKUK GFSVRSEGTGTHVKLI DEPAPOKPBNYVDFKTTYDGWAPBILLEKUK GFSVRSEGTTHVCFY GFSCRSEGTTHVCFY KLRGENLILGFSIGGGIDOPSCONFFSBOKTDGGITVTKVSEG GFABLAGLIGHGKIMONDMYNTHDDARKELTKRSEEVVRL LVTRQSLQKRVQOSMLS HEPASKGRSEGVORMUSVABATISHGRVFRRMSLGPBSRTHLLRN LLTGLVRHERIEAPWARVDENRGVAEKLIDVGKLGDTNREAMPM ADPHLTEKUL PIKLFQVLAPPKNOTGGALAKSKLI LLTGLVRHERIEAPWARVDENRGVAEKLIDVGKLGDTNREAMPM ADPHLTEKUL PIKLFQVLAPPKNOTGGALACSKLI BAPBMMRAKINVYHLLDCFACQLCNORPKVCOKPFJKNNMMILCQ TOLBEGLAKKGVAPQVR 6338 66 1349 APNESGTGJRJUFFRRMSTAGACNEKYKDYLLKALDKYWHEDCLKC ACCCCLLGVCSTLTYKANLILCRRIYYLLGGVTGRAACSKLI PAPBMMRAKINVYHLLDCFACQLCNORPKVOLKFFIKNNMANNY KNYKKYEVALLLYHEPPEDDKAGNQCPEGDFKLIKNINNAKNY KNYKKYEVALLLYHEPPEDDKAGNQCPEGDFFKJKNNMANNY KNYKKYEVALLLYHEPPEDDKAGNQCPEGDFKLIKLELLALAQOVLED KNYKKYEDDLASCHOPPERFELIKAVAQONTENPOLS ILIU AVENDERFEKYEDDLASCHOPPEFLIKAVAQONTENPOLS ILIU DEPOFFLIVPYNKKTEDIDLASPQLOVANDRAKPETUL BEJARAGNAKHTILKURIDFYE APPEBVENTIPKYNSEETUL SERVELOPEDIS ILIUGHENDED DEPOFFLIVPYNKKTEDIDLASPQLOVANDRAKPETUL BEJARAGNAKHTILLERNFTL VUSDOGTNIKARITYTELDEGDERTVELEGGDERQRSDFBOADTGGDTF SEPPIDDEFFROMEDTYTELBGGDERGOPEKTRAERGENIM DEPOFFROMENTATOKINGHENTYNINGENSY LEILAWTGLIAY INGYLITERSTAKRAGNAKHTHRELLEENFTL VUGDETNIKARTSTGKINGHGENTYNINGENSY LEILAWTGLIAY ILIUFRYSSORGAPTOKAGGGOPEKTARGKERIM DITMYNTHFLICHENFTL VUGDETNIKARTSTGKINGHENTYNTHELLEENFTL VUGDETNIKARTSTGKINGHENTYNTHELLEENFTL VUGDETNIKARTSTGKINGHENTYNTHELLEENFTL VUGDETNIKARTSTGKINGHENTYNTHENTHELLEENFTL VUGDETNIKARTSTGKINGHENTYNTHENTHELLEENFTL VUGDETNIKARTSTGKINGHENTYNTHELEGDEDIT SHILLEENFT	ļ		,	AAEAAAAVVAAAAAAAAAAAAANANASTSASNTVSGTVPVVPRP
6334 17 644 GONPSGRAAGPAAAMPSSPLRVAAVVCSSNQRSMARHNILSEK 6334 17 644 GONPSGRAAGPAAAMPSSPLRVAAVVCSSNQRSMARHNILSEK 65376 GSVRSRSGTGTHVILDEPADDKPNYVTPTTYDQMYMDLLEXDK 65376 CSVRSRSGTGTHVILDEPADDKPNYVTPTTYDQMYMDLLEXDK 6335 82 529 AARARPOVLCCELIGAALGDGSRVEMSYTPGGPVTAVVQRVEIH 6336 1003 438 HERASKGRAEVGNNRLSVAAAISIGRVFRRMGIVVTRVSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGDKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGHKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGHKIMQVNGMDMTWYTHDQARKRLITYRSEG 6781AGLQIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMQVNGMTUTTANAQARTHILDR 6781AGLGIGHKIMGTANAQARTHILDR 6781AGLGIGHKIMGTANAQARTHILTRITANAG	1	İ		EVTSIVATVUDNENTVTISTEEQAQLTSTPAIQDQSVEVSSNTG
6334 17 644 6GNPSGRARGFAAAMPSSPLEVAVVCSSNONESMEAHNILSKE GSVVRSGGGTHVKL PGPAPOKPRVYDFKTTTDQWANDLLIKUK EGFSVRSGGGTHVKL PGPAPOKPRVYDFKTTTDQWANDLLIKUK ELYTYNGILIHMDENKRIK KPPERFRQNCKLPDLILICEEERVVD QVVEDIMSREQETCOPVHVNNUT JODNHEBATIGAFLICELCQC JOVEDIMSREQETCOPVHVNNUT JODNHEBATIGAFLICELCQC JOVEDIMSREQETCOPVHVNNUT JODNHEBATIGAFLICELCQC JOVEDIMSREDETLOEIGEFERSGRIFHTVCYP. 6335 82 529 AARAFGVICCELIGAALGDGRUEMSYTPGGFVTAVVQRVEIH KLRQGENLILGFSIGGGIDQDPSCMFFSEBKTDGKTJVTKVSEG GPABIASIJGIGKI MQVNROMPUTVYTHDQARREITKRSEEVVRL LVTRQSIQKAVQOSMLS 6336 1003 438 HEPASKGRARGVONGRISVABATISHGRVFREMSLGPESRIHLLRN LLTGLURHERIEAPWARVDENRGVARKLIDVGKLGDERAKRAM ADPHLERKLIPKLIPKLAPPKDOTOGGARREITKRSEEVVRL LVTRQSIQKAVQOSMLS 6337 76 524 BEIGMLSVQPDTRFKGCACCNEK KORYLLKALDKVWHEDCLRC ACCCLLEGEVSTLYYKALDHEVRINGIPNEADRAM MAVIEYKGNCLPPLFLDREARRAM NAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDREARRAM MAVIEYKGNCLPPLFLDRAGRACHALLICHAD YLLKOLDARGARGARCH LICHADAVAHLICRD YLLKOLDARGARGARCH LICHADAVAHLICRD YLLKOLDARGARCH	1	1		BETSKQETVADFTPKKEEEESQPAKKTYTWNTKEEAKQAFKELL
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6335 82 529 ARARAPGUCCELLGALAGOGSTWEST JEGGVETTAVVQRVETH KLRQGENLILGFSIGGGIOQDESQNFFSEDKTDKGIYVTRVSEG GPAELAGLQIGDKIMQVNGNDMINVTHDGARKRLITKRSEEVVRL LVTRQSLQRAVQOSMLS 6336 1003 438 HEPASKGRAVCOSMLS ADPHLTRKOLIPKLEQVLAPRYKDOTGGYTRMLQIFNRSLDRAK ADPHLTRKOLIPKLEQVLAPRYKDOTGGYTRMLQIFNRSLDRAK MAVIEVRSNCLPPLEPLRPRDSHLTLLNQLLGORDLRQSGEAS NHSSHTAQTFGI PAFFMWARAKONVYHLDCPACQLCHQRFCUGKFFLKNNMILCQ ACCDCRLGEVGSTLYTKANLILCRRPYLRLGSGVTGNCAACSKLI PAFFMWARAKONVYHLDCPACQLCHQRFCUGKFFLKNNMILCQ TDYSEGGMKEGVAPQVR APNSESGTGGFLPTFANLFWTRRANPPPTTSMATDRMGFKAVP GLRLALLLLLGIGTPKSGVQGGGLDFFEVUONKVINVANANY KNVFKKYEVIALIYHEPPEDDKASQRFEMBELILLLAAQVLED KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFRGDEVITYDGEFS ADTIVERGINKEGVAPVELIRGRERESTLEKKLKPSMYTENDEFS ADTIVERFENTIPPKNSEERINFVERGSTLAFKRIKKENSMYTHDPTE BORDGIHIVAFAERADPDGFFFLETIKAVAQDNTENPDLSIIWI DPDDFFLLVPYWEKTFDIDLSAPQIGVVNVTIDARLAMMENDDES AFMEEPVTT PDKYNSEERINFVERGSTLAFKLKRESMYETH DPDDFLLVPYWEKTFDIDLSAPQIGVVNVTIDARLAMMENDDES UTTSPGRVITTEDDEBSTTVELEGGDENQEGFBDADTQGGDTE SEPTILVLVPGSVUSZAKFDDFSDEDIVEDDDDDDD VTTSPGRVITTSDDEBSTTVELEGGDENQEGFBDADTQGGDTE SEPTILVLVPGSVUSZAKFDDFSDEDIVENDDMDTAPLAMMENDDES VTTSPGRVITTSDDEBSTTVELEGGDENQEGFBDADTQGGDTE SEPTILVLVPGSVUSZAKFDDFSDEDIVENDDMDTAPLAMMENDDES VTTSPGRVITTSDDEBSTTVELEGGDENQEGFBDADTQGGDTE SEPTILVLVPGSVUSZAKFDDFSDEDIVENDDMDTAPLAMMENDDES VTTSPGRVITTSDDEBSTTVELEGGDENQEGFBDADTQGGDTE SEPTILVLVPGSVUSZAKFDDFSDEDIVENDDMDTAPLAMMENDED VTTSPGRVITTSDDEBSTTVELEGGDENQEGFBDADTQGGDTE SEPTILVLVPGSVUSZAKFDDFSDEDIVENDDMDTAVFAGFKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLALLIEMGEVDCMM DTMYHFFLTHADELSSVHFSDOFSFKMRDEMDTVYFAVGTKRAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLALLIEMGEVDCMM DTMYHFFLTHADELSSVHFSDOFSFKMRDEMDTVYFAVGTKRAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLALLIEMGEVDCMM DTMYHFFLTHADELSSVHFSDOFSFKMREKKRAKKERIM MEDDPERGRRLEBRALRRECKLEKKEKMMKNQLIKVRM SSSSTSSSARRALPAGDPPMEKALSHFSDSSSSSSSSSSSSSSSSSSSARRALPAGDPPBEFLAF PARPGGAGNIKTLGDAYEFBAUVRDFSSPDI UTTSNNHIEVRA EKLAADGVYMNNPAHKCQLDEBUDDTFSVTSARREDGSLTTRRRR HPHTEHVQQTFRTEIKI PALPKARAVAPKPSSSKGEVVAKLDDLWMARRSSSLWPMTFGSSTO PALPKARAVAPKPSSSRGEVVAKLDDLWMARRSSSTWP				OVVEDLNSREOETCODVHYDANIOTODNIERATI CARL TORI COR
ARARAPGULCCRILGAALGOGSRUEMSYIFGGPUTATVORVEIH KIRGGENLILGFSIGGIDODPSOM PSEDKTDKGIYVTRVSEG GFABIAGLQIGDKIMOVNGMDMTMVTHDCGARKLITKRSEEVVRL LVTRQSIQIRAVQOSMUS HEPASKGRAFVGMRKISVAAAISHGRVFRIMGLGPESRIHLLRN LLITGLVAHREI IEAPMARUDEMKGAEKLIDYGKLGOTHERAMRM ADPHIATRKOLIPKLEVOLAPPKADGTGSTYRMLQIPMRSLDRAK MAVIEYKSNCLPPLPLPRRDSHLTLINQLLQCLRGDLRQSGEAS NHSSHTAQTIFGI 6337 76 524 BGIQMLSVOPDTYPRGCAGCNRKIKDRYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLLKALDKYWHEDCLKC ACCDCRLGEWGSTLYTKANLILCRRDYLKALDKYWHEDCLKC CACCACANAWARKLGLICHENAATERAC KWYEKYYEVLALLYHEPPEDDKASQRQFEMEBLILELAAQVLED KWYEKYYEVLALLYHEPPEDDKASQRQFEMEBLILELAAQVLED KWYEKYYEVLALLYHEPPEDDKASQRQFEMEBLILELAAQVLED APMEEPVTIPDKYNESEEINFYPIDLSARQUNTENDELSILWI DEDBEJLLYWEWSTENTIPDLSARGUNYWYTDADRILMEMDDEE DLPSABEBLEDWLEDVLGGEINTEDDDDDDD DDBGIHIVAFAERADDDGGFFLETILKAVAQONTENDEDLSILWI DPDDFLLYWWEKTFIDIDLSARGUVWYTDADRILMEMDDEE DLPSABEBLEDWLEDVLGGESINTEDDDDDDD NRCHGGGGGAERQAGGCCTCGAGGFGGGFGFGFFFSTGGGAMKAFH TFCVVLLVFGSVSEAKFDDFEBEBIIVEVDUNDFABFEDUMEDS VTBSQRVI TITEDDEDSTTVELEGQDENQGEOFBADATOGGDTE SEPYNDEEFFGYENKYNDENHENTICHGSGEVCGGMLIQLRFIL KRQDLLNVLARMRPVSDQVQIKVTMNDEDMTYVFAVGTRKAL VRLQKEMGDLSEFCSDKYNKGAKYGLPDSLAILSEMGEVOTOMM DTMWHFITHTHYDKENTICLTHVOTGAGPSFEKKRAEKERIM NEEDPEKQRRJESPCSDKYNKANGHKYNTSTRAERSFTGSSSSS SSSSTSSSARADARDARDSWERKALDBLWHDTWYTANTHEELLESNFTI SSSSTSSSSARADARDARDSWERKALDBLWHDTWTANTHEELLESNFTI SSSSSSSSSARADARDORPMEKALBMYBDFSSFTARERSFTGSSSSS SSSSTSSARADARDORPMEKALBMYBDFSSFTARERSFTGSSSSSS SSSSTSSARADRADORPPBEKLARMSDDFSSFTARERSFTGSSSSSS SSSSTSSS				IQHTEDMENEIDELLOEFEEKSGRTFI.HTVCEV
KIRGESMLILGFSIGGIDGDPSONPFSEDKTDKGITYTRVSEG GPARIAGLGIGNKIMOVNONDMINTUTDQARKRITKRSEVVRL LVTRQSLQKAVQOSMLS HEPASKGRAEVGMMRLSVAAAISHGRVFRRMGLGPESRIHLLRN LLTGLVRHERIBAPMARVDEMRGYAEKLIDYGKLGDTHERAMRN ADVILTKKOLIPKLEQVLAPRYKDQTGGYTRMLGIPNSSLDRAK MAVIEVKSNCLPPLEPRDSHLTLLNOOLLQGLRQDLRQSQEAS NHSSHTAGTTGI 6337 76 524 EIGMLSVQPDTRPKGCAGCKRKKKDRYLLKALDXYWHEDCLKC ACCDCRLGEVGSTLYTKANLILCRIPYLKLEGVTENCAACSKLI PAREMWRARONVYHLDCFACQLCNORFCUGNKFFLKNINMILCQ TDYSEGIMKEGVAPOVR APNESSTGSPLPTFANIFYTRRANPEPTTSMSATDRNGFRAVP GURLALLLLLLGIGFTFSKSQAGQSGLDPPEVGUDNKFJLKNINAKNY KNYKKYSULALLYHEPPEDDKASQRQFEMEELILELAAQVLED KGVGFGLVDSEKDAAVAKKLGLTEVDSHVYKGDEVITSYDGEFS ADTIVSFLLDVLEDPVELLBGERELQAFFRIEDET KLIGYFKSK DSSHYKAFEDBAERFHYIIPFFATTFSKGAKKITLKLNEIDFYE AFMEEPVTIPDKNSEELIVNFVERGTLEKLAVADONTENPDLGIIMI DPDDFFLLVPWKENFFDIDLSAPGUVAVVTDADARLMMEMDDEE DLBSAEELEDWLEDVLEGEINTEDDDDDDD 6339 246 1813 NRCDRGGGGGGGRAERGAGGGFGFGFGFFFFGGAMKAFH TFCVVLLVVEGSVSEAKFDDFEDEBJVEVDUNDFARFEDVMEDS VTESPGRVITTEDDEDSTTVELEGGDENGEGFBDADTOGGDTE SPEYDDEFFEGYBLKPDTSSKNKDPTITVDVPAHLONSWES VY LEILMYTGLLAY INNYIIGKNKNSPLAQAWFNTHRELLESNFTL VRQKEMGDLSEFCSDKPKSGAKYGLPDSLALISEMGEVDGMM DTMMHFFLTHADKISSVHPSONGSPKIMGEGGOPLKJDTKR TLLUTFNVPGSGNTYPKDMEALIPLMMNVIYSIDKAKKPPLINRE GKKADAMRARVERBFHKLTHVVQROEAAQSRREEKKRARKREIM NEEDPEKQRRLEBBALRROKLIEKKOMKMCILKVKM GKKADAMRARVERBFHKLTHVVQROEAAQSRREEKKRARKREIM NEEDPEKQRRLEBBALRROKLEKKOMKMCILKVKM SSSSTSSSSARABLPAODPPBMEALLBFMGEGGDTTTRRRR PARPGGANIKTLGDAYEFRAUVRDFSSDDITTTSNIHIEVRA EKLAADGVWANPAHKGCLEBUNDFSDDGSTMPRSEPLAT PARPGGANIKTLGDAYEFRAUVRDFSSDDITTTSNIHIEVRA EKLAADGVWANPAHKGCLEBUNDFSSTOPSSTOPSSTOPSSTOPSSTOPSSTOPHSSPDITTTSNIHIEVRA HPHTENVQQFFREIKI HPHTENVQQFFREIKI	6335	82	529	AARARPGVLCCRLLGAALGDOSRVEMSYTPGOPVTANOOVETU
GPAETAGLGIGNKIMOVNGMDMINTMYDDGARRELTKRSEEVVRL LVTRGSLQKAVQGSMLS HEPASKGRAVGMRRIJVAAAISHGRVFRRMGLGPESRIHLLRN LLTGLVVRHERIEAPMARVDEMRGYAEKLLDYGKLGDYNERAMRA ADPWLTSKGLIPKLFQVLABRYTMOTGGYTRMLGIPNESDRAK MAVIEYKGNCLPPLPLDFRDSHLTLLINQLLQGLRQDLRQSQEAS NHSSHTAQTFGI 6337 76 524 EGIOMLSVQPDTYEKGGAGCNRKIKDRYLLKALDKYWHEDCLKC ACCDCRIGEVGSTLTYKANLILICRRDYLRLEGVUTGNCAACSKLI PAFEMWWRAKDNYYHLDCPACQLCNQRPCVGDKFFLKNNMILCQ TDYSEGIMKGVAPQOV GURLALLLLLGGTPKSGVQQGGGLDFPEYDGVDRVINVRAKNY KNVFKKYEVLALLYHEPPEDDNASGQGPEMEELILELAAQVLED GURLALLLLLLGGTPKSGVQQGGGLDFPEYDGVDRVINVRAKNY KNVFKKYEVLALLYHEPPEDDNASGGROFMEELILELAAQVLED ADTIVEFLLDVLEDEVELIEGGRELQAFEMEELILELAAQVLED DSERYKAFEDABERPHYIPPFATDSKGAKKLTIKLINELDFYE AFMEEPVTIPDKPNSEBEIVFVEDHSDARAKTIKLINELDFYE AFMEEPVTIPDKPNSEBEIVFVEDHSDARAKTIKLINELDFYE AFMEEPVTIPDKPNSEBEIVFVEDHDDDDDD 6339 246 1813 NRCDRGGGGABRAGNGCGTGGFGGFGFGFGFBFFSGGAMKAFH TFCVVLLLVEGSVSEAKFDDFSDEBDIVEYUDNDFAEFEDVMEDS UTSSPQNVIITEDDEDETTVELLEGQDENOGGPFBCADFLEGDETT VGDDGTNKEATSTGKINDENEHINUNGSGRVCEGMMLOGGBFFL KRQDLLNVLARMMRPVSDOVQIKVTMDEBMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLALLSENGETVDGMT DTMWHFLTHYADKLESVHSGOVGCGMLTQLEMTLESNFTL VGDDGTNKEATSTGKINDENEHINUNGSGRVCEGMMLTQLEFTE KRQDLLNVLARMMRPVSDOVQIKVTMDBEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPSLALLSENGETVDGMT TLLLTTNVFGGGNTERALLPLMMNVIYSIDKAKKFRLNEE GKKAADKNARAVERFFLKLTHVORGARACGGMLTQLEMT NEEDPEKGRRLEEAALREGKKLEKKQMKMKQIKVKAM SSSSTSSSASRALPAQPPPMEKAHSTSSTFRAEESFFISSSSS SSSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFISSSSS SSSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFISSSSS SSSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFISSSSS SSSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS SSSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSS SSSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS SSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS SSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS SSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS SSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS SSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS SSSTSSSSASRALPAQPPPMSHHTSSTFRAEESFFIRSSSSS SSSTSSSSASRALPAQPPPMSHHTTSSTFRAEESFFIRSSSSS PAPPGGAGNIKTLGDAYEFAVDVRDFSPED	1		•	KLRQGENLILGFSIGGGIDODPSONPFSEDKTDKGTVVTRVSEG
6336 1003 438 HEPASKGRAWGMRISVARAISHGRVFRRMGGPESRIHLIRN LLTGLVRRERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM ADPALTSKGLIPKLFQVLAFRYKDOTGGGYTMILGIPKNSLDRAK MAVIEYKGNCLPPLFLPROSHINTLINQLLQGLRQDLRQSQEAS NHSSHTAQTFGI 6337 76 524 EGIOMLSVGPDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC ACCDCRLGEVGSTLYTKANLILCRDYLRLEGVTGNCAACSKLI PAFEMWARAKDNYHLDCPACQLCNQRPCVGDKFFLKNNMILCQ TDYSEGIMKEGVAPQVR 6338 66 1349 APNSESGTQGFLDFPANLFWTRRANFDPTTSMSATDRMGPKAVP GLRLALLLLLLGLGTPKSGVQQGSGLOFPDSTONGVACKSKLI KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVKGDEVIEVDGEFS ADTIVEFLLDVLEDPVELLEGERELQAFENLEDEIKLIGYFKSG DSBHYKAFEDAAERFHPVIPPFATDSKGAKKLTLKLNEIDFYE AFMEEPVTIPDKPNSEELIVNFVEEHRSTLRKLKPESMYETKE DDMDGIHIVAFAEEADPDGFFFLETLKAVAQDNTENPDLSIINI DPDDFPLLVYYMKKTPDLDLASPGIGVNVYDADRLAMENDDE DLPSABELBCDMLEDVLEGEGTEDDDDDDD 6339 246 1813 NRCDRGGGGAERQAGGCRTQGAGFGFGFSFFFSGGAMKAFH TFCVVLLVYEGSVSEAKFDDFDDEDDTVUEDDDDDDD VTESPQNIITSDDEDETVELGDDDDDDDD VTESPQNIITSDDEDETVELGDDDDDDDD VTESPQNIITSDDEDETVELGUNGEDDATGGGDTE SEPYDDEFFEGYEDKPDTSSSKNKDPITIVDVBAHLQNSWESYY LEILMYGLLAYIMMYIGKNKNSTLAQAWFNTHRELLESNFTL VGDDCTNKEATSTGKLNQEMSHINNLNCSGRVCCEGMLIQLIFL KRQDLLNVLARMMRPVSDOVQIKVTMNDEBDMTYVFAVGTRKAL VRQKEMDLESFEGSDR KSGGALDFDSLAILSENGEVTDGM DTMWHFITHYADKLESVHPSDQFSGFKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTY KNMBALLPLMMNVIYSIDKAKKFRLNEE GKKAADKMRARVEENPLKLTHVOGRAAOSREEKKRAKKERIM NEEDPEKQRRLEEAALRREQKKLEKKQMKKACIKVKAM NEEDPEKQRRLEEAALRREQKKLEKKQMKKACIKVKAM NEEDPEKQRRLEEAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKQRRLEEAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKQRRLEEAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKQRRLEEAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKQRRLEEAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKGRRLEGAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKGRRLEGAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKGRRLEGAALRREQKKLEKKGMKKNCIKVKAM NEEDPEKGRREGEVAVAREDDFSTOTATRRE HHTEHVOOTFRTEIKI HHTEHVOOTFRTEIKL PARAGGAGNIKTLGDAYEFAVDVRDESPEDIITTTSNHIEURA HHTEHVOOTFRTEIKL	i			GPAEIAGLQIGDKIMQVNGWDMTMVTHDOARKRLTKRSEEVVRI.
LITCHVRIERT EAPWARVUBERGYARKILIDYGKLGDTIRERAMRM ADPHLTERDLIPKLFQVLAPRYKNOTGGYTRMLQIPARSLDRAK MAVIBYKSKOLLPPLPPHPRDSHLTLLNQLLQGIRQDLRQSQEAS NHSSHTAQTPGI 6337 76 524 EGIQMLSVQPDTKPKGCAGCNKKIKDRYLLKALDKYWHEDCLKC ACCCRIGEVSSTLYTKANILICRRDYLLKFGVTGNCAACSKLI PAFFMWARAKUNYHLDCFACQLCNQRFCVGDKFFLKNNMILCQ TDYBEGIMKEGVAPOVR 6338 66 1349 APNSESGTQGPLPTFANLFWTRRANPDPTTSMSATDRMGPKAVP GLRLALLLLGLGTPKSGVQGQEGLDFPETGGVDRVINVAKNY KNVPKKYEVLALLHYBEPPEDDKASQRQFEMEBEILBLIAQVIED KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVPKGDEVJEYDGEPS ADTIVEPLLDVLEDPVELIEGERLQAFERILICHIAGVIES KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVPKGDEVJEYDGEPS ADTIVEPLLDVLEDPVELIEGERLQAFERILGEIRKLKPSSMYETWE DEMERPVTIPDKNNSSEETVNFVEERRETLRKLKPSSMYETWE DEMERPVTIPDKNNSSEETVNFVEERRETLRKLKPSSMYETWE DEMERPVTIPDKNSSEETVNFVEERRETLRKLKPSSMYETWE DEPABRELEBVLEGBINTEDDDDDDDD 6339 246 1823 NRCDRGGGGABRQAGGGTGGGFGFGHSFFSQGAMKAFH TFCVULLVFGSVSEAKFDDFEDEDIVEYDUNDFARFEDDWEDS VTESPQRVIITBDBDETTVEEDGDENDEGDTE SEPYDDEEFFGVEDKDVSSEAKKDDITIVDVPAHLQNSWESYY LETLMVTGLLAYIMNYIIGKNNSNELAQAWFNTHHELLESNFTL VGDGGTNKEATSTGKLNQDENEILYHLMCSGRVCGGMLLQLEFL KRQDLLNULARMMRPVSOQVQIKVTMNDEDMDTYVFAVGTRRAL VRLOKKMQOLLSSFCSDKYKSGRQIDPDSLATLSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGFKIMGESGFLKDAFKREIN MCEDDEKGRRENEFNTILVFRQEARAGRGFKKARKFRIMRE GCKAADKNARAWEBFFLLITHVQRQEAAQSRREEKKPARKERIIM NEEDDEKGRREEBAALRROKKLEKKOMMMCQIKVKAM 1830 2 583 EACAHTLSCPAFARLGRARREPWMSHTSTSTFRAERSFFHSSSS SSSSTSSASRRALPRAQDPPMEKALSMFSDDFGSFMPHSSEPLIAF PARPGGAGNIKTLGDAYSFAVDVRDFSSEDIIVTTSNHIEVRA BCALABGTYMNNFAHKCQLPEDVDTSVTSALREDGSLTIRRRR HPHTEHVQQTFRTEIKI 1941 2 645 KWANLSAFGLRGFRILGERSSVSGPAVQARGVQSVATDGPSSTQ PALPKRARAVAPRESSGEFVAVAKLDDLVMARRSSLWFMTGOLA				LVTRQSLQKAVQQSMLS
ADPMLTRICLI PRILIPRIZARIA MAYTEYKONCEGYTRILQI PRISLIDRAK MAYTEYKINCL PPLPL PRISHLTLINOLL QGERQOLRQS (GEAS MASSHTAQTEG) 6337 76 524 EGIOMLSVOPDTKEKGCAGCNRKTKDRYLLKALDKYWHEDCLKC ACCDCRIGEVGSTLYTKANLI LCRRDYLRLEGUTGNCAACS KLI PAPERWARRAKUNYHLDCFACQLCNQRFCVGDKFFLKNINNI LCQ TDYEEGLMKEGYAPQVR 6338 66 1349 APNSESTQSPLPTPANLFYTRRANPDPTTSMSATDRMG PRAVE GLRIALLLLLGGTPKSGVGQGGLDFPEYDGDVRVINVMAKNY KNVEKKYEVLALLYHEPPEDDKASQRQFEMEBLI LELAAQVLED KGVGFGLVDSEKDAAVAKKLGLIEVDSMYVFKGDEVIEYDGEFS ADTIVEFLLDVLEDPVBLIEGERELQAFENI EBEI KLIGFFKSK DSERYKAFEDAAERFHEYIPFFATFDS KGAKKLTLKINEI DFYE AFMEEPVTI PEVENSEES IUNGERELQAFENI EBEI KLIGFFKSK DSERYKAFEDAAERFHEYIPFFATFDS KGAKKLTLKINEI DFYE AFMEEPVTI PEVENSEES IUNGERELQAFENI EBEI KLIGFFKSK DSERYKAFEDAAERFHEYIPFFATFDS KGAKKLTLKINEI DFYE AFMEEPVTI PEVENSEES IUNGERELQAFENI EBEI KLIGFFKSK DSERYKAFEDAAERFHEYIPFFATFDS KGAKKLTLKINEI DFYE AFMEEPVTI PEVENSEES IUNGERELQAFENI EBEI KLIGFFKSK DSERYKAFEDAAERFHEYIPFFATFDS KGAKKLTLKINEI DFYE AFMEEPVTI PEVENSEES IUNGERELGAFENI EBEI KLIGFFKSK DSERYKAFEDAAERFHEYIPFFATFDS KGAKKLTLKINEI DFYE AFMEEPVTI PEVENSEES TUNDEDHD TENDIS INI DPDDFFILVFYMSKTETOI DLSAPQIGOVINVITDADERISMEMDDEB DLPSAEELEDWINEDVINGES IUNGERDEFFGFGFFFFS GGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEI VEYDDMDFFAFFENVMEDS VTESPQRVI ITENDEDEBTTVELEGGDENGEGFFEDADTGEGTE SEPYDDEFFEGVEDKENDTSSSKNKDPITTVDVPAHLQNSWEGYY LEILMYTGLLAYIMMYI I GKNRSLADAAMPTHRELLESNFET L VODDGYNKEATSTGKLNQENEHI YNLUCGGRVCCEGMLI QLEFL KRQDLINULARMMRPYDQVQI KVITMINEDMDTYVFAVGTRRAL VRLQKEMQDLSFFCSDKEKSGAKYGI PDSLATLSENGEVTDGMM DTMVHFI.THYADKIESVHFSDQFSGPKIMQEGQPLKLPDTKR TLLLTFNVFGSGNTYP KOMEALLPILMNVI I SIDKAKKFRINRE GKQKADKBRARVEERFILKITHVQRQEAAQSREEKKRAEKREI M NEEDDEKQREEBAALRREGKLEKKOMMKGLKVKAM DETWAHFILHYADKIESVHFSDQFSGPKIMQEGGPLKKERIM NEEDDEKGREEBAALRREGKLEKKOMMKGLKVKAM SCHATTSCFFARAGRARREFWHSHETSTFFAERSFFSSSSS SSSTSSSASRALPAQOPPMEKALSMFSDDFOSTMPHISEELLAF PARPGGAGNIKTLGDAYSFAUDVDDFSSPDI IVTTSNHHIEVRA EKLAADGTYMINFAHKCQLEDEDVDPTSVTSALREDGSLTIRARR HHTTEHVQQTFRTEIKI AMAULSAAGLGKFRILGERSSVGFAVQARGVGSVATDGPSSTO PALPKARNAVAFNESSGEFVV	6336	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
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KNVFKKYEVLALLYHEPPEDDKASGRQFEMEELILELAAQVLED KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVTEYDGEFS ADTIVEFLLDVLEDPVELLEGERELQAFENIEDE IKLIGYFFKSK DSEHYKAFEDAAERFHPYIPFFATFDSKGAKKLTLKLNEIDFYE AFMEEPVTIPDKPNSEEBINTFVEEHRRESTLRKLKPESMYBTWE DDMDGIHIVAFAEADPDGFFLETLKAVAQDNTENPDLSIIWI DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRIMMEMDDEE DLPSAEBLEDWLEDVLEGEINTEDDDDDDDD RRCDRGGGGAERQAGGGCRTQGAGFGFGFGFSFFSQGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELBGQDENQEGDFEDADTOEGDTE SEPYDDEFFEGYBDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARNMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VKLQKEMQDLSFFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESUHFSDQFSGFKIMQEEGQPLKLPDTKR GKQKADKNRARVBENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEBAALRREQKKLEKKQMKMKQIKVKAM 1830 2 583 EACHHISCPAFARLGRARRFWMSHRTSSTFRAERSFHSSSS SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVMWARRSSLWPMTFGLA	l i			GLRLALLLLGLGTPKSGVOGOEGLDEPEVDGVDPVTNIMAVNV
ADTIVEFILDVLEIGERELQAPENIEDEIKLIGYFKSE ADTIVEFILDVELIEGERELQAPENIEDEIKLIGYFKSE DSSEHYKAFEDAAERFHPYIPFFATFDSKGAKKLTLKLNEIDFYEK AFMEEDVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE DDMDGIHIVAFAEEADDDGFFFLETLKAVAQONTENPDLSIIWI DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDD NRCDRGGGGAERQAGGCRTQGAGPGFGFGHSFFSQGAKKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVYDLONDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELEGQDENQEGDFEDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYINNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMIQLEFFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFILTHYADKIESVHFSDQFSGFKIMGEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFFLKITHVQRQEAAQSREEKKRAEKERIM NEEDPEKQRLEEAALRREQKKLEKKQMKMKQIKVKAM SECHHTSCPAFFARLGRARRRPWMSHRTSSTFRAERSFHSSSSS SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMPHSEPLAF PARPGGAGNIKTIGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFFILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPRPSSRGEYVVAKLDDLVWARRSSLWPMTFGLA				KNVFKKYEVLALLYHEPPEDDKASOROFEMERIJIJELAAOVI.ED
ADTIVEFLLDVLEDPUELIEGERELQAFENIEDEIKLIGYFKSK DSEHYKAFEDAAEBFHPYIPFFATFDSKGAKKLTLKLIGYFKSK AFMEEPVTIPDKPNSEESIVMFVEEHRBSTLRKLKPESMYETWE DDMDGIHIVAFAEEADPDGFEFLETLKAVAQDTENPPDISIIWI DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDD RRCDRGGGGOABRQAGGGRTQGAGPGFGFHSFSQGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDUNDFAEFEDVMEDS VTESPQRVIITBDDEDETTVELEGQDENQEGDFBDADTQEGDTE SEPYDDEEFEGYBUDTSSSKNKDPITIVDVPAHLQNSWESYY LETIMVTGLLAYINNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGBVTDGMM DTKMVHFLTHYADKIESVHPSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKOMEALLPLMNMVIVSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKBRIM NEEDPEKQRRLEEAALRREQKKLEKKOMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHLEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKRRAVAPKPSSRGEYVVAKLDDLVWARRSSLWPMTFGLA	1			KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS
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VTESPQRVIITEDDEDETTVELEGQDENQEGDFBDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAFGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA		2.20	10:13	MACURGOGG QALKQAGQGCRTQGAGPGFGFGHSFFSQGAMKAFH
SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIKKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHPSDQFSGPKIMQEEGQPLKLPDTKR TLLLIFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENPLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRLEEAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAFGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA			į	VIESPORULTURDEREUWEDE PROPERTIES
LEILMVTGLLAY IMNY I IGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHI YNLWCSGRVCCEGMILIQLRFL KRQDLLNVLARMMRPVSDQVQI KVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR TLLLIFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLITHVQRQEAAQSRREEKKRAEKBRIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMXQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSSS SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAFGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKESSRGEYVVAKLDDLVNWARRSSLWPMTFGLA		ŀ	ľ	SEPVIDEEEEGVEDVEDTOCGVANDO TOTAL OTTO TOTAL
VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTVYFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHPSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKBRIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA				LEILMVTGLIAY IMNVTTGKNKNGDI NON MENDUREL I COMMEN
KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLITHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQLKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRPWMSHRTSSTFRAERSFHSSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAFGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA		İ	ļ	VGDDGTNKEATSTGKI,NOENEHTVAT.WCccpbuccapout To
VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEBAALRREQKKLEKKQMKMKQIKVKAM 583 EACAHTLSCPAFARLGRARRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA				KRODLLNVLARMMRPVSDOVOT KUTMNDRDMDTVVERNUCTDERS
DTKMVHFLTHYADKIRSVHFSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAFGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA				VRLQKEMQDLSEFCSDKPKSGAKYGI.PDGI.ATI.SEMGEUTDGMA
TILLITATVPGGGNTYPKOMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLITHVQRQEAAQSRREEKKRAEKBRIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMXQIKVKAM EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI KMAVLSAFGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	1			DTKMVHFLTHYADKIESVHFSDOFSGPKIMOFFGOPI.KI DDWWD
GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKBRIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM 583 EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA		1		TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE
6340 2 583 EACAHTLSCPAFARLGRARRPWMSHRTSSTFRAERSFHSSSS SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA		ľ		GKOKADKNRARVEENFLKLTHVORQEAAOSRREEKKRAEKERIM
EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNPAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA				NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM
SSSSTSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	6340	2	583	EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSSS
PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAFGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA			1	SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEFLAF
6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	ŀ			PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA
6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA			1	EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR
PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	5363			HPHTEHVQQTFRTEIKI
PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA	034T	2	645	KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ
CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA	ł			PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA
		L		CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA

SEQ	Predicted	Predicted end	Daning
ID	beginning	nucleotide	
NO:	nucleotide	location	\n-nreliate, C=CVSCRing, D=lensy-ic laid =
1	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
ł	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	1	\=possible nucleotide insertion)
1			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
		1.	VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI
1	1		APLEGVKIDDLTRVLAGPFATMNLGDIGAEVIKUEPDCACDDDD
			I WGPPFVGTESTYYLSVNRNKKS I AVNIK DDVGUVI I VET A AVO
1			DVFVENYVPGKLSAMGLGYEDIDEIAPHTIVCGTTGVGOTGDIG
- (1	1	QRAGIDAVASAVSGLMHITGPEVACLSHIAANVI.TGOVER VONC
İ			IAGGSIVEYQAFKTKDGYIVVGAGNNOOFATVCKIIDIDER IDN
			SKIKINHLKVHNRKELIKILSERFEEFLTSKWI.VI.FEGGGUDVG
1	1		PINNMANVFAEPQVLHNGLVMEMEHPTVGKTSVDGDAVDVGVEV
6343	2	936	MSEARPPPLEGOHTTHILKEVLRYDDRATGET.T.CACTADOURGET
		936	GIAMVSDEDELNLLVIVVDANPIWWCKOALVEROPERIC CVCTCT
	1		MVLGNSHLFMNRSNKLAVIASHIOESRFT.VDGKNGDI CDEEGDD
1			GNPPERNISGSKDGKYELLTSANEVIVEEIKDI.MTVCDIVCOVIII
ł	1		ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
1			YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
1	1	1	POMPSILOYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL IBIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK
		1	VSA
6344	2508	147	TMPTATIGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
			QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSTTPNRKDSSS
i	1		WIMPYDUKSUPPEGSEEAAEPRMDTPEDODI.DDCDDDTX WRWDW
1		•	FAPEPEPCEASELPAKELRSSEEPTEKEPPCOLOUVE ODOADA
1	-1		I VENULUTED DEPENDENT PROPERTIES I
1	1		1 1 1 Q V Q PA D Q K Q A Q T Q T S P E H L V L Q O K O V O P O L O O P A E D O V O V O
1	i :		POVQPQAHSQGPRQVOLOOEAEPLKOVOPOVOPOAUGORDBOVO
1	1 1		LOUDQUO TOT YPQVHTQAOPSVOPOEHPPAOVSVOPPPOTUPO
			FRIQPOVSLLAPEOTPVVVHVCGLEMPPDAVEACCCMEVER DED
1]		VG1QVSMEETQNESACGLDVGECENRAPEMPGUMGACGGT 171777
1	1		LUSSUSKAI STVPLTPVPRPSDSVSSTPAATGTBCVOALORDON
	i i		ICKASCSSQQEPQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
ł		ľ	DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
l	1 1		PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
1	1		DHFITVDAVGCFEGDEEEEEDDEDEEEIEVEEBLCKQVRSRDIS REEWKGSSTYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
I	1 1		SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF
			TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
6345	2	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMREMTEOLOFY
	1	j	TELEKUNUTLKNRLISAKOOLOTOGYROTPYNNKOSPINTCPDV
	ļ	i	ANENAGLQECPRKGIKFODADVAETPHPMFTKVCNGLIFFRAGOR
	1		IRNUBRY TO SURGO I EELEHLAEILKTOLPRKENETET.CT.T.O.D.
	j		EQUATOURSNIRDNVEMIKLHKOLVEKSNALSAMEGVETOLOGY
		Į.	QRIDKISHDALMANGDELNMOLKEOPI, KCCCI, PVOT VCMCPOP
·	i		KIEELQDKINDLEKERELIKENYDKI.VDSAFCAAUEEOMYT VIIO
			VIAVOLAQUETALKSDLTDKTETI.DRI.KTEDDOMENT MORNING
1			QUQILEQKQQLDELKKRIKLYNOENDINADELGEALILITYAAND
i		1	QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
			LIMOHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA
		1	ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
J	ļ		ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSOYLVHVNDLELOVLOXVETT
		1	VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
		l i	RVPMDQAIRLYRERAKALGYITSNFKGFEHMQSLSQQAPKTAQL
	!		SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
- 1	1	1	DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
	<u></u>	1	OSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH
			HITEMANA

SEQ	Predicted	Predicted end	Amino poid gogment contribution
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ì	sequence	1 -	\=possible nucleotide insertion)
			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
Į	İ		LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
	1		TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
		İ	MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
		}	TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVIYVDK
1			ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
1		į	GVAHVDLADMFQEGRDLIBQNIDVFDARADGEGIGKLRVTVEAL
L			HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
1			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
I			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
l			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
I			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVO
1			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIOSENSASI
1			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETORRKHLAYL.
	1		IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
			KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSROLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
			ICVGLNEQVLHLWLEVLCSSLPTVEXWYQPWSFLRSPGWVQIKC
1			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6347	2921	533	
1		333	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDEFGFRVYKBEGDEPGSSLLANSPLME
			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
]			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1 1	i		QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
1 1			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
	ĺ		TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1 1	į	[DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIOSENSASI
			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETORRKHLAYL
]		ļ	IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
1 1		ì	KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSROLPGLL
, !			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
]			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
]		Į	ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
		İ	CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
	1	1	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6348	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
! !	-	1	KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
	į	ļ	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
ļ			DDDEDVOVENA PRIVORGE ODDEMONA PENNINGEN AND AND AND AND AND AND AND AND AND AN
		1	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLBECAITCS NSHGPCDSNOPHYNITYTEEEPENACTI MADDEGGADEGA
			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
1	j		ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKOOFENLKEKCELTOLAGELANGONKYKYEEGEDLIKENDA
1	Ì		EKKQQFRNLKEKCFLTQLACFLANQQNKYKYBECKDLIKFMLRN ERQFKEBKLAEQLKQAEELRQYKVLVHSQBRELTQLREKLREGR
1	İ		DASRSINEHLQALITPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ	Predicted	Predicted end	Amino noid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Stop
-	amino acid	sequence	Codon, /-possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
			EDAVHIIPENESDDEEEEEKGPVSPRNLOESEEEEVPOESWDEG
			YSTLSIPPEMLASYKSYSSTFHSLEEOOVCMAVDIGRHRWDOVK
ĺ	1		KEDHEATGPRLSRELLDEKGPEVLODSLDRCYSTPSGCLELTDS
]	Ì	CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
1	i		ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
i			SLDRCYSTPSSCLEOPDSCOPYGSSFYALBEKHVGFSLDVGEIE
1			KKGKGKKRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKBPEVLQESLDRCYS
1		·	TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
1	ļ		DQDPSCPRLSRELLDEXEPEVLQDSLGRCYSTPSGYLELPDLGQ
	1		PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
[VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
1			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHVPSVFV
6349			SFEEEHISFALYVDNRFFTLTVTSLHLVFOMGVIFPO
0343	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEB
			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
			EIILQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
			DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECAITCS
1	ĺ		NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
i			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
1			ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
ŀ			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
ł i			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
			EDAVHIIPENESDDEEEEEKGPVSPRNLOESEEEEVPOESWDEG
	!		YSTLSIPPEMLASYKSYSSTFHSLEEQOVCMAVDIGRHRWDOVK
i i	}		KEDHEATGPRLSRELLDEKGPEVLODSLDRCYSTPSGCLELTDS
			CQPYRSAFYVLEQQRVGLAVNMDEIEKYOEVEEDODDSCDDT.CD
1 1	Ì		ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1		i	QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
1 1	i		SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
			KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
-			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
1 1	•		TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
] [DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
j			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
[[LEVVEPEVLQDSLDRCYSTPSSCLEOPDSCOPYGSSFYALEEKH
[1		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGBEDONPPCD
1 1	1	1	RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHYRSVFY
6350			SFEEEHISFALYVDNRFFTLTVTSLHLVFOMGVIFPO
9330	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELOFKEE
j l	1	.	KLAEQLKQAEELRQYKVLVHSQERELTOLREKLREGRDASRSIN
] [}	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAOHLVOKLSPENDN
		İ	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
	1		NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
ļ .			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
	. 1		ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
	.	ľ	LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Trantonham V Thursday
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		 	FCATTCSNEUCRYDSNOTHRAND
1	1		ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
	I		EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
ł	i		YSTLSIPPENLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
1		1	KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
f	ļ		CQPYRSAFYVLBQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
İ	ł		ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1	}	ļ	QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
1			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
l .]	KKGKGKKRRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG
1] .		PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
1	1		DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
			TPSGCLELTDSCQPYRSAPYILEQQRVGLAVDMDEIEKYQEVEE
	. [DODPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEOPDSCQPYGSSFYALEEKH
i	1		VGFSLDVGETEKKGKGKKRRGRRSKKERRRGRKEGEEDONPPCP
	1		RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
6351	1291	319	SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
	1	010	REARRITERSQLGRMLVVEVANGRSLVWGAEAVQALRERLGVGG
l	ļ .		RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP
•	1		DSRHHSLALTSFKRQQEESFQEQSALAAEARETRROELLEKITE
	1		GQAAKKQKLEQASGASSSQEAGSSQAAKEDETSDGQASGEQEEA
	1 1		GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS
	ł ·]		KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD
			PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ PDGKVVYTSLQWASLQ
6352	235	923	WCRMI CDON'N NOVOLONG
	i .		WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSABGHVGQGAPG
	1		LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE
			PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP
			TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
			DDCVYIVVD
6353	65	672	RFAGAGAIPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
i	[VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
į			FLHHTRTLVEMKRDLDSIFRRIRTLKGKLARQHPEAFSHIPEAS
			FLEEEDEDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSLSPGFE
			DLSHVQPGSPAINGRSQTDDEEMTGE
6354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLRPVPDNQEVFC
ĺ	ĺ		HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVQGARAVHVE
			SVQPLSLENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLHQA
			LLRLPQYQTDLLLTFNQPP
6355	158	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
			WDGKVSEIKKKIKSILPGRSCDLLQDTSHLPPEHSDVVIVGGGV
ľ		ļ	LGLSVAYNLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ
			QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL
	1	j	LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
1			ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
1	1	1	SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA
İ		İ	WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
-	İ		ETPLVADTSGAYFREGLGSNYLGGRSPTEQEEPDPANLEVDHD
		1	FFODKVWPHLALBUDA FETT KUOCAMA CUMPINA PARALEVDHD
i	İ		FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
		i	PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF
]	•	INFIRMATION IN THE PROPERTY OF
6356	354	633	LFTRFYLGEKIQENNII
6356	354	633	TGLTSSCLPLQENNII TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEEEEEIEAREV ADSYAQNAKVIEKQLERKGMSKRRLQELAELEAKKAKMKGTLID

Designing nucleotide location cortesponding cortison cortesponding cofirst cofir	SEQ	Predicted	Predicted end	The same of the sa
Mociación cortesponding		beginning		The segment containing signal pantias
Cortesponding Coffee Cof	NO:	nucleotide .		Glutamic Acid E Deannie De Aspartic Acid, E=
L=Leucine, M=Methionine, N=Asparagine, profiler, occlustmine, R=Arginine, amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, S=Serin	1			Halietiding T Tables
to first amino acid amino acid amino acid amino acid amino acid and sequence 6357 2 915 GLERMALIVELENCISTIS VAUBLINE, VARIABLE, VALUE SEQUENCE 915 GLERMALIVELENCISTIS VALUE SECTION, **Stop COOM, *possible nucleotide cletion, Vapossible nucleotide providence OPPERINGET SEQUENCES SE	- 1	corresponding		L-Leucine, Manabiania, Kalysine,
amino acid residue of amino acid sequence sequen		to first		P=Proline O-Cluborine, N=Asparagine,
residue of amino acid sequence 6357 2 915 GLERMALINE RICHARD TO SEQUENCE COON, /-possible nucleotide deletion, /-possible n	1	amino acid		SeSerine Temperature in Walter
Codon, /-possible nucleotide insertion 6357 2 915 GLRRMALLVAVURNOTS ISOMOFOCSDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED INCIDENTRYISTRUSP FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED FOOGGDEAD. 8750PCMSSQOAGGSSEQIPED FOOGGDEAD. 8750PCMSSQOAGGSSQOAGGSSEQIPED FOOGGDEAD. 8750PCMSSQOAGGSSQOAGGSCADAUGTSCADAU	i	residue of		Watryptophan Vaturagine w Tuly
6357 2 915 GLERMALLVEWINGTSISQWPYCSRLIPSFTGGGDBALS RTSGNPGNSGSACGSSQIPGIDICINKYNTTRILSTTUSCEK RTSGNPGNSGSACGSSQIPGIDICINKYNTTRILSTTUSCEK TOPEEFFLECMOMDTFISSRLITLLHUMGLYEMKGEGRSGKYM CRITVHEMMEDVOGRGRWMSUPFLIKKSNIKHTALBUNTSCVEK TOPEEFFLECMOMDTFISSRLITLLHUMGLYEMKGEGRSGKYM CRITVHEMMEDVOGRGRWMSUPFLIKKSNIKHTALBUNTSCVEK TOPEEFFLECMOMDTFISSRLITLLHUMGLYEMKGEGRSGKYM CRITVHEMMEDVOGRGRWMSUPFLIKKSNIKHTALBUNTSCVEK TOPEEFFLECMOMDTFISSRLITLLHUMGLYEMKGEGRSGKYM CRITVHEMMEDVOGRGRWMSUPFLIKKSNIKHTALBUNTALLEV DEGILSDEGLAAALMETFENKCEDFRILELLVEVVEKGIOVL DEMMSGELLLIGEVSSRPLUENDSSILARDRYSCHUCTUVEIFEK GOSVLSFMRGHLANNVIRYFTGALMFAFRDYKGIFLGGVDRST AXSKTAVAPIERGVYKLLLOVOHASKOTJARGKYNGTUCTUVEIFEK EGGVLSFMRGHLANNVIRYFTGALMFAFRDYKGIFLGGVDRST GPRYFAGRILSGGAGASTSLCFVYPLDPARTRAM MGSGRKGADIMYTGTVDCWRKFFRDEGKAFFKGAMSNVLRGMG GAFVULVDELKKVI 0VRQFESKRKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- PROFILARDRYSCHULTURGKGAFFKGAMSNVLRGMG GAFVULVDELKKVI 0VRQFESKRKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- CRGESERKEDCLSSBVYSDBSSIOSESLIGLLKTYTCVTU- LINGKPINKTSVTTAVGSVTAVAVSTAVTTLOV- LINGKPINKTSVTTAVGSVTAVAVSTAVTLOV- LINGKPINKTSVTTAVGSVTAVAVSTAVTLOV- LINGKPINKTSVTAVGSVTAVAVSTAVTLOV- LINGKPINKTSVTAVAVSTAVTLOV- LINGKPINKTSVTTAVGSCTATAVTLOV- LINGKPINKTSVTAVAVSTAVTLOV- LINGKPINKTSVTAVAVSTAVTLOV- LINGKPINKTSVTAVAVSTAVAVSTAVAVSTAVATAVAVAVA 6360 1 345 6361 615 158 RPGGGOLDLAVCTTLAVASTLSVERNOGVTATAVAVA ARCHITATAVA FRENCAGOLDLAVCTTLAVASTLSVERNOGVTATAVAVA ARCHITATAVA ARCHITATAVA FRENCAGOLDLAVCTTLAVASTLSVERNOGVTATAVAVA ARCHITATAVA FRENCAGOLDLAVCTTLAVASTLSVERNOGVTATAVAVA ARCHITATAVA FRENCAGOLDLAVASTLSVERNOGVTATAVAVAVA FRENCAGOLDLAVASTLSVERNOGVTATAVAVA ARCHITATAVA	İ	amino acid		Codon. /=possible nucleotide deletide
GLIRMALLVRVIENCYSLIPVSPTOGOGDRALS RTSCHOMSOGACGGSGICPDIDICIANTKRUSTTKISTTOSP QVEEKVGAFTXIIRANGFTGFLKYSKKIKIAALRHYTSCVEK TDFEFFIKOCHOPTYNSNYHIILLKHWIKIVARKGERGKYKW CRIVHHMMEDUQORGRWASHYIILKKRMILMTHHFYAALLCY DEGISDBGLAALHRYFTFRKCEDPHELSVYHKHOGI DEMISEBLLITGEVSRYPLVEKNPOSILKPHSTYNDEGGL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL DEMISEBLLITGEVSRYPLVEKNPOSILKPHSTYNDEGGL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLELSSERSARPATTYETEGTVADGEOL ASSALHSISSPYLESSERSARPATTYETAGARPATTY COPHYTHAGALGALANCE THE TOLLAR TOLLAR TOLLAR ASSALHSISSPYLESSERSARPATTYETAGARPATALA TOLLAR COPHYTHAGALGALANCE THE TOLLAR TOLLAR TOLLAR MYGGAKADININ TOLLAR TOLLAR TOLLAR TOLLAR MYGGAKADININ TOLLAR TOLLAR TOLLAR TOLLAR CASFOLURINES CLIRCLE SPENGER TOLLAR TOLLAR TOLLAR CASFOLURINES CLIRCLE SPENGER TOLLAR TOLLAR TOLLAR TOLLAR TOLLAR CASFOLURINES CLIRCLE SPENGER TOLLAR	-	sequence	•	\=possible nucleotide deletion,
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ELGVPASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGGGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFFLIMILVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFIGVFLITRNERKPIPFEPYISMDAMPGMONMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE 6363 21 1201 RRTRLGSSFFRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMBHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVID SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS TIEIGPSRFRAPFELLFRPDLIGEFSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTMIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF CAMBERGALASLDTFKKMWVSKKEYEEDGARSIHRKTF DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDMNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS	1 1	ŀ		GHLVVSIALNLOKYCHIRLAGSKDPRAVEVEVEVEVEVE GT BI MI I G
ERRYVLSFVGGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDPIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE 1201 RRTRLGSSFFRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEFSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF OQIPKYCFPNYVGRPKHVRVMAGALEGDIPIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGYTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS	1 1			ELGVFASYAFAPLSLIVPLSAVSVIASATIGITETYEVWYDYDE
PFILYMLVEIILFCLLLYFYXEKNANNIVUILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYYMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLKREGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGESSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTNIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF OQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDGS				LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENUTPULLVGW
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RYPMEHGIVKOWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLEREGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGESRFRAPFELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF 6364 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGYTHAVPIVEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDGS	1		İ	DQIPKYCFFNYVGRPKHVRVMAGALEGDIFTGPKAEEHDGIT.ci
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TIEIGESRFRAPELLFRPDLIGE:SEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTHIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RTRLGSSFPRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAOYYLDGS		1	ļ	SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFI.RI.VI.REGV
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RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RRTRLGSSFPRREDSAMESYDVIANOPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIVEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDGS		f		PET HENTIN COCCUS THEORETE THE TENTIN COCCUS THEORETE THE TENTIN COCCUS THEORETE THE TENTIN COCCUS THEORETE THE TENTIN COCCUS THEORETE THE TENTIN COCCUS THEORETE THE TENTIN COCCUS THEORETE THE TENTIN COCCUS THEORETE THE
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DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSINRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS	6364	21	1201	PRINTING CONTRACTOR OF THE PRINTING CONTRACTOR O
RYPMEHGIVKOWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDGS	1	=	1201	DOLDKYCEDNYJCED PURINDING GO.
NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS	1			PVDMEHGIVKDWDMEDIWOWINGERING TO THE PVDMEHGIVKDWDMEDIWOWINGERING
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DFHSSSEFEIVKAIKERACYLSINPOKDETLETEKAOYYLPDGS	}		1	SGDGVTHAVPI VEGEAMBUGIMBIDIA CODUCTOR DI VILLE
TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR	į	ļ	1	DEHSSSEEETVKATKEDA OVI CTADOVDERN DERVE OVICE
			ł	TIEIGPSRERADELLEDDDLIGERGEGUEUR UED TOWN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	J .	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	1	\=possible nucleotide insertion)
İ			RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
ļ	ì ·		RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1939	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
			ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVA
	i		NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHOIAK
1	l		LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIRI
Į.			
l	İ		ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV
1			VNSCHROMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED
1			TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK
1			LDVTSVEDYKALQKYRKEKFEEMIQQIKETGANLAICQWGFDDE
1	ł		ANHLLLONNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL
}			GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE
ł			AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCP
1			TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVKEM
1			NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK
			IDDIRKPGESEE
6366	257	1898	GNKEGAHSSTFWVLLS1FLGAVAMLCKEQGITVLGLNAVFDILV
		1030	IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
			MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
	!	•	
{			WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC
{			QALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL
			YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV
)		LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI
			RYYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQ
			PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL
			GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
1			AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA
1			IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
			KENYGLLRRKLELMQKKAV
6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS
			QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE
			KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
			GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ
	l		SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
	1		CGKAFYFLNLCLIHERIHTGVKPYKCKQCGXAFTRSTTLPVHER
	1		THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV
			FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
	1		EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA
			SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
l	[[ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
i			YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC
i			GKAFIRASSCREHERTHTINR
6368	1	327	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE
	j		DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
			DOFVCGETVPAPSANKELVKC
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT
	_		PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMOET
·			
			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
ı			ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
J			TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY
I			DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL
Į	i		IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE
[CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM
1	ĺ		THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA
1			FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG
į	1		EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

SEQ	Predicted	Predicted end	l Amino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
	1		SSLHIHERTHTGDKPYECKVCGKAFTCSSSTRYHERTHTGEKPY
1			ECKHCGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE
6370	1711	329	HERTHTINR
	1 -7	323	FVLSEQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
1			ALVGGLRPVTMTTPANAQNASKTWELSLYELHRTPQEAIMDGTE IAVSPRSLHSELMCPICLDMLKNTMTTKBCLHRFCSDCIVTALR
1	1		SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSRBEYEAHQD
			RVLIRLSRLHNQQALSSIEEGLRMQAMHRAQRVRRPIPGSDQT
			TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG
ļ			SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS
1			PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
			LALRIALERRQQQEAGEPGGPGGGASDTGGPDGCGGEGGGAGGG
			DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE
6371	3		KFWKVSRPLELCYAPTKDPK
03,1	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC
j			LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG KSEAKK
6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH
			LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP
			LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM
l i	\$		VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
((EICTVDPCHKFTWCLDACIRERFVDSKRARELOGFLDGVKKGOE
			QVLGDLSMILCDPFAINTLALSTVRHLOELVGOETLPRDSPDIJ.
			LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
	1		DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY
1 . [1		YVLHITKQRNKNALLRLLPGLVETPGDLAFGDIFLHLLTGNLAL
[]			LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
]]			APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEOLDHRKPSPA QAAETPALELPLPSVPAPAPL
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
1 1	ĺ		DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA
			WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL
1	i		VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMODLTTIRGD
6374			GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
63/4	\$35	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
			CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
]			HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
1	[CPABLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
1		1	DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
1	1		IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR
1		•	VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL
			SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLONSTKII.
Ì			QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNTT
1		·	ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVARVI.
6375		4 2 2 2 2	EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTOSAKE
33/3	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT
			CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK
			PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY
ļ			FLEGOTAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSODYEVLLVCBALCCLGTALLBOADERAWY
1	1		SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP
	•		FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR
		i	RVLLLGTIQALFESVIFIFVFLWTPVLDFHGAPLGIIFSSFMAA
	1	j	SLLGSSLYRIATSKRYHLOPMHLLSLAVLIVVFSLFMLTFSTSP
			GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPETEQAGVLN
	-		

SEQ	Predicted	Predicted end	7
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown +_c+
	sequence	sequence	Codon, /=possible nucleotide deletion
	Doguetice		\=possible nucleotide insertion)
			WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
6376	380	1437	VGLFTVVRHDAELRVPSPTEEPYAPEL
1			ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
			NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC
-			GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
1			VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMARDDDGFKAD
1	· ·		ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKFIFGAKIMD
			PDEQLETCHEALKLLPPAHCETLRYLMAHLKRUTLHEKENTAMA
6377	2311	1048	ENLGIVEGPTLMRSPELDAMAALNDIRYORLVVELLIKNEDILE
1	2521	1845	SRIRRRSSRRPREPPGPSRRRRRRRPDPRTMPSEKTFKQRRTFE
İ	<u> </u>		QRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHV
-	Į.		NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE KDEDGFLYMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
1	1		DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
1	1		WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG
6379			I SMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6.3 /9	35	378	BRAGSPSPSRAALRRCAPORSOAPRWPDRAACRRSEOGSOGRAV
	Ì		LENSVVNVGCGPAEERVLLTGLHAVADTYCENCKTTLGNYVDDA
6380	1414		FESSQKYKEGKYIIELAHMIKDNGWD
1 200	7474	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
1 1	!	l	GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI
	·		LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
	ļ		CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSQGS PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
1 1			MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG
f			REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
6381			LALFTSLLC
0301	1668	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
!	İ		YLASCVQYRLVVRDVNTLQILOLYTCLDOIOHIEWSADSLETT.C
1 1	1		AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT
!	1		TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER
i l	į		RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIBWAPNGCVLAVWD TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG
	į		SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG
ŀ		1	LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLOTIKPVTDPAND
			KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDTOKI, PLANTEDI.
i		1	SPVRAFQWDPQQPRLAICTGGSRI,VI,WSPAGCMSVOVDGPGDPA
6382	2	1062	VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACPOLGGUT
	_		FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK
- 1			KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLYY
	1	1	TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS
	Ì	1	AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF
		i	HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG
1		į i	KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSUDURM
{			IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG
6383	3750	: 1:	Б
0000	3159	1061	SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK
j		1 (GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASOD
ĺ		} <u>-</u>	AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDV2KK
			PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS
	1	12	SSSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
		[]	GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA FFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI
			THE STATE OF

SEQ	I Dyndint-3	16. 41	
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid R-
1.0.	location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	sequence	sequence	Codon, /=possible nucleotide deletion,
		<u> </u>	\=possible nucleotide insertion)
1			LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
			TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS
ſ	1		AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD
			TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
			ESLESLISKSQEHEQRLAALQGRLEGIGSSEADQDGLASTVRSL
			GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQA
			QAARLFPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
6384	738	1904	SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
	1 /30	1504	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
1			AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ
1			NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
1			AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ
			HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ
1			QQQMQQMQQQLQQHQMHQQIQQQMFQHHMQQHLQQQQQH LQQQINQQQLQQQLQQRLQLQHMQHQSQPSPRQHSPVASQI
			TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
1 .	i j		LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
			ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP
i			PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
1			LHRQFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAQAP
			IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
			FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVI.
1 1	}		RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACOGOVETTER
			LRSLSPKIMQEAFLVQEVVELFVTERQIEREHLIOLRRWOETRG
	j		ELQCRSPPRLHGAKAILDAEPGPRPALOPSPSIRLPLDAPLPGS
1 1	,		KAKPKPPKQAQKEQRKQMKGRGOLEKPPAPNOAMVVAAAGDACD
6386			PQHVPPKDSAPKDSAPQDLAPQVSAHHRSOESLTSGESEDTYL.
0300	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWODKDOMDDI
1 1			RAQILGGANTPYEKGVFKLEVIIPERYPFEPPOIRFI.TPTVHDN
			IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIOLLMSEPNPDD
1			PLMADISSEFKYNKPAFLKNAROWTEKHAROKOKADEERMIDDIL
6387			PEAGDSRVHNSTOKRKASOLVGIEKKFHPDV
""	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
] !	j	i	KQELAETLANLERQIYAFEGSYLEDTOMYGNIIRGWDRYLTNOK
1			NSNSKNDRRNRKEKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
1			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
6388	<u>1</u>		STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
5500	*	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
1 1	1]	KQELAETLANLERQIYAFEGSYLEDTOMYGNIIRGWDRYITNOK
	Ì	1	NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
]	REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
6389	1074	497	STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
	40,7	43/	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
-		ļ	LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
		İ	QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
	f		EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
6390	158		LIGDDVKVERIEYKKP
	-30	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
•	!		LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
6391	5386	2000	SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
	2300	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
1		1	MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERIIAYLRDFNE
			DOKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

	0 1 2 2 1		
SE		Predicted end	Amino acid segment containing signal peptide
ID		nucleotide	
NO	: nucleotide	location	I WALLEY CELVSERING DELAGRANGE - 1 - 1 -
í	location		Targetting Actu, Pappent a langua of or areas
- 1		corresponding	/ ···································
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S-Serine W. Thursday, R-Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleofide deletion
<u> </u>	sequence		\=possible nucleotide insertion)
ł	i		LTENORKGHSDENSNAVIVONDUK MESELLION)
	i	I	LTENORKGHSDENSNAKIKONRVLVCAPSNAAVDELMKKIILEF
i	<u> </u>	}	I THE TOTAL CONTROL OF THE PROPERTY OF THE PRO
1	l	l	I PAREDESH VQAMHKKKEFLDYOLDEL QDODAL CDCCDBTODOD
ļ		1	1 DENTE NO VENTE PARTICIPATION OF THE POST TO COMP. OF
- I	į.	J	TSGGLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHRCN
ļ			KI-TI-VGDBYOL DDWYTCHYD CDYGO DEAGOSCEIETLTDTPLIHRCN
Į.	Į.	İ	KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVEHN
	1	ł	MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC
	1		OSDWEF QFILVEDVGDGSERRDNDSVTNDOFTET TOWN THE THE
Į	1		1 2000 ADLYMIGITIUIXAOKIMIOKOLDKEEDDRGDA EMPORTO
- 1	_ i		FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
- 1			ILGHLRTLMENQHWNQLIQDAQKRGAIIKTCDKNYRHDAVKILK
- 1	!		I.KDVI OBCI EUDOWAY BECCHE COKNYRHDAVKILK
	i i		LKPVLQRSLTHPPTIAPEGSRPQGGLPSSKLDSGPAKTSVAASL
i			I THE SUBJECT TO THE PROPERTY OF THE PROPERTY
1			TEAM PROPERTY OF THE PROPERTY
	1		1 DOGAREPYRGEPPAASPEASTCOSKONDERRY CHERRY DA DO 1
5000			GEQEKCGSETHHTRRNSRWDKRTLEQEDSSSKKRKLL
6392	972	186	GRTGVDL ACCMANDA OFFICE WAR THE QBDSSS KRRKLL
ŀ	1		GRTGVDLASSMAHRLQIRLLTWDVKDTLLRLRHPLGEAYATKAR
i	[]		AHGLEVEPSALEQGFRQAYRAQSHSFPNYGLSHGLTSRQWWLDV
1	1		VEQ 1 FROM VUDAUAVAPIAEOLVKDRQUBCTWOTT DOS TROTT
1	1 1		ECKIRGLELAVISNEDERLEGILGGI.GI.DEUEDEUE many
-	1 1		KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL
			VVGPQALDPVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
6393	2017	730	TGGSKMANNATGGGVANATGGSTAGLEPALDCLEGSTPGL
	1 1		TGGSKMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT
1	1 1		NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGTV
1	1		I DDIEDUKINI I ISPLEFKY PLAFCI WICHTI I WA CARDON ASSESSED.
1			EDPAPELEDDKCKKEFDEDVYNHKTDEGNITVMVIAMOVOLIA
	1 1		1 1GF VSSSREGHTYDASKRMPORT, TRACHINGCERT DRYTCOM
1	1		EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN
1	1 1		LGSPLWGDDICCAPMCCAGUGLERVER
	1		LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM
1	1 1		PTHLIQNKAIIARVTTLSDVVVGLESFIGSERETNPLYKDYHGL
1	l f		1 THE WATER DINNING COMES DAKEN DESCRIPTION OF THE PROPERTY OF
6394	1418		TYDEDDAMDLAESAKRIGPGCGMMAGGKKUT.DE
	1 1410	511	GAAAGGEGARRPAAMATVMAATAAFPAVILEPERDOLLY
ļ	1 1		VLKQLQDILKEASLRFTLPGSGTEGPAKQENFILGSCGTDQVKG
ł	i I		VLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQQIQDAR
Į.	1 1	j	NHVSOATVIJTSDDOGVOEPMOTER
1		1	NHVSQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLT
ļ	1		TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ
	1 1		THEOREM TANKERGGAVLHSPGAMFFWGGODI FUGITATION OF
6395	13		ATT TO THE TAIL ASPOPTOOF KDKL SALSSAMS AD DE
1	1 -3	658	PSGRPTRPLCCAARRGAARHGGSVSGWPAGPTPTETTCNTGGCLD
ı	1		ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP
İ	1		PCKPSCVSOT.COPARDVARDDOTT.DOTT.DOTT.DOTT.DOTT.DOTT.DOTT.DOT
l	1	1	PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ
İ	1	i	DLLEEASSRDMQMGPGLFLRMQLVPSIEERETPLTREDRPALQE
6396	1	1001	TINDESCIGNARIQIQROVIPOPTIGHRNDWUADDGGE
	} - }	1221	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFOUSSOSIDDE
	j	1	IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI
	1	į.	SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF
	, ,	1	INGLET.TVIAEEVENECUARI TRANSPORTATION TO THE
	1 1	1	INGLELIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
	j l	1	IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
]	ſ	GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLTEOFGWELDD
	1 1	1	PHUSHFIALLIFLSVVPLIKDACOVILLRI, PPEVEKET, HTATER
	į į	i	IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
į	1] ,	TGILKDAGVNNITTOURVEAVEOURGGI COGTUMENT CONTROL OF THE CONTROL OF TH
		l,	TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
6397	391		
i		144	GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
			KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY

SEO	D		
-		Predicted end	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	Leleucine, Memabbiomic, KeLysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	sequence	sequence	Codon, /=possible nucleotide deletion
	pedaetice		\=possible nucleotide insertion)
6398			Q
6398	353	1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
ŀ	i		RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK
	ĺ	l	DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN
ı	i	ł	SNVHSDETPAMACIAREDOCUEROCUEROCUEROCUEROCUEROCUEROCUEROCUER
i	1	į.	SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYLTSAIQLLRKD
ŀ			SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA
}	1	1	QEFGNQTLFT1FTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH
i	1	}	PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS
6399	75		VIIFSKSRV
	1 /3	1245	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
1	1	1	REGMADSLESTPLPSPEDRLAKLHPSKELLEVVOKKMARCEREN
- 1	1	i	EDUDKKLELYKEACEGOHKLECDIOOREERTARIOVALCDMOVG
l l	l .		LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT
ı			YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
1			ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED
1	1	•	RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR
]	i i		SENQNKEKSWMLEKDNLMSKIKQYRVQCKKKEDKIGKVLPVMHE
L			SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTMVCDEURVENGEN TI BIRTON
1			KTMKCDEVVYBVQSAILRHNCGYAMKTGKFFHNLMERKDFETWL
			DNISVTFLSLTDLQKNETLDHLISLSGAVQLRHLSNNLETLLKR
İ			DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW
			QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHEAFETS
1	1		SDIGHSARVYALYYKDGLLCTGSDDI.SAKT.WDVQTGOCVYGTOM
	!		HICAAVKFDEQKLVTGSFDNTVACWEWSSGAPTOUFDCUTTGALT
1	1 1		SVDINDELDILVSGSADFTVKVWALSACTCI.NTI.TCUTENTITICS
i	i		VLQKCKVKSLLHSPGDYILLSADKYETKTWDTGDETNGVGT VIII
			SVSEDRSICLQPRLHFDGKYIVCSSALGIVOWDFACUDIT BYTTE
1	1 1		TPETANLALLGFGDIFALLFDNRYLYIMDI.RTRSI.TSBWDIDBY
1	1		RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW
-			KEHG
6401	109	765	PGAAWSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG
]	1 1		PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL
{	í		VDEESOREDGASCARGOVYCOOCHGGATATATATATATATATATATATATATATATATATATA
1	1		VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSYLQRHSITHS
1			EVKPFECDICGKAFKRASHLARHHSIHLAGGGRPHGCPLCPRRF
6402	1196	279	RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRWKHP
	1	2/3	TTSQCGGTRQSSAIPVASMEPAAICLRNALLLLPEEQQDPKQEN
]		GAANSNOLGGNTESSESSETCSSKSHDGDKPTDADDOODT DVOD
	1		LENLKCS I LACSAYVALALGDNI MAI NHADKI TOODKI GOOT KE
i	1		LIGHLYAAEALISLDRISDAITHLNPENVTDVSLGTSSNEODOGG
l	1		DRGENEAMESSGKRAPOCYPSSVNSARTVMI.FNI.GCAVCI DCBV
ļ	1 1	J	DKARKCLHQAASMIHPKEVPPEAIIJAVVI.ELONGNTOLALOTT
6403			KKNQLLPAVKTHSEVRKKPVFOPVHPIOPTOMPAFTTYOPY
0403	2	1690	RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQ
	i l		RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL
	1		AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNLK
		[DI-ODI-HKDA FMETA TKENOT GERDOL GERMINITTI SQANEQNI K
' j		1	DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
1	1	Į.	LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR
		į	MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP
ļ		[PGPKGPKGDKGSQGPPGPTGNKGOKGEKGEPGPPGPACEPTC
i	i	ļ	PAGPPGERGGKGSKGSOGPKGSRGSPGKPGPOGPSGDPGPBGDD
ł			GREGLPGPQGPPGFQGLQGTVGEPGVPGPRGT,PGLPGVPGMPCP
J	ļ	1	RGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCVV
1			FSVEKEIFEDAKLFCEDKSSHLVFINTREEOOWIKKOMIGPESU
ŀ		!	WIGLTDSERENEWKWLDGTSPDYKNWKAGOPDNWGHGHGPGPDC
6404	1070		AGLIYAGQWNDFQCEDVNNFICEKDRETVI.ccai.
0404	1012	222	AAALAMAAFAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA
			ANAGORAL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
f	to first	amino acid	L=Deucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence		Codon, /=possible nucleotide deletion,
	 	-	\=possible nucleotide insertion)
1			RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
1			PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAAEDYA
Ī			KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQEREKI
1	Ì	}	VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGEGKAAVLKRI
6405	1	1456	LEDQEENPLPAALVQPHTGKLCWFLDEAAARLLTVPFEKHSPL
ł		1150	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
ĺ	1		TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYMSMELLQE
1			AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAQVLAGGRGKGT
Í	1		FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQ
]	Ī		VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE
]		TPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK
1	[]		LYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQK
	1		KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
1]		TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
1	1 1		VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
	l i		LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
6406	1036	167	
		207	HPRQMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
			DDDDDDHDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
1			VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
1 1			KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYQ
			SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
1 1	1		YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
6407	492	150	CRAALGSGMGRGKQRPVMERGCLTA
1 1		130	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
i I	1		SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	PGGITTESONUM PGGITTES
		700	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
			NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
]			SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
LI			LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
		:	GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS
	1		HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
	ļ		AISGLFNCITIHPLNIAAGVWMIMNAFILLLCEAPFCCQFIEFA
	İ		NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAFA
	ĺ		TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
6411	302	772	RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
		_	GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK
J			KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ
_ }	j		WENVSAMIEEVFEATDIKITVYTL
6412	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
	·		CONCLETIVENED NAVIGUES AND PROPERTY OF THE CONCLETION OF THE CONCLE
l l	i]	CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
J		Ì	LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQ
ļ		ĺ	GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKQN
	1	,	PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
ı	}	'	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
	İ		LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
1		ļ	PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
!			TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
1		j	RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
l		i	TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTOAVNMAGLPAVSID
1	1	1	VALSNOGLPIGLOFIGRAFCDQQLLTVAKWFEKQVQFPVIOLOE
			LMDDCSAVLENEKLASVSLKQ

SEQ	Predicted	Predicted end	Amino agid cognest as the
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
l	1		NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
	1		NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
1			GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
1			LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT
1			GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
	1		MEQSEELYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
1			SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
	j .		LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGFDRYKMVVQV
1	1		VIGEORGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
			FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
1]		FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
			LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATIOE
1			NMQIRTKVAGIYRELCLESVKNKYECEIOASROHCESEKIJIVD
i			TVQSELEEKIRRLEEDRHSIDITSELWNDELOSRKKRKDPFWPD
1			KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTRP
ŀ			PVKLEKHLHSARSEEGRLYYDGEWYIRGOTICIDKKDECPTSAV
6416	4.70		ITTINHDEVWFKRPDGSKSKLYISOLOKGKYSIKHS
0410	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
1			GLASKTAAWGTLGTLRTFLNFSVDKDAORLLRAITGOGVDRSAT
1	1		VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
			ALLQFTAQFDAQELRTALKASDSAVDVAIEILATRTPPQLQECL
	İ	ļ	AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
1 1		Ì	NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
1 1			TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
1			ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV KGDCQSALLALCRAEDM
6417	1	845	
	_	015	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
1 1	1	1	LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
			EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
1			GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
1	1	ļ	AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
		į	AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
1			TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQEAELVQ
ļ l			YFDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
	į	1	TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTEROVKIWFO
			NRRMKWKKENNKDKFPVSRQEVKDGETKKEAOELEEDRAEGI.TN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
! !		1	MARSISTSGPLDKEDTGRQKLISTGSLPATLOGATDSLGLEWHI.
1			PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV
			FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY
1		J	VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLOKSDNSF
] [ļ	l l	NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRORSLYRET
1 1		1	LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
 _		i	STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
	ļ	1	YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
	!] 1	NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
		1 (GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
		. [4	ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
LL			GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP

Γ	SEQ	Predicted	Predicted end	lamine and
- 1	ID	beginning	nucleotide	
- 1	NO:	nucleotide	location	1************************************
j		location	corresponding	Grutamic Acid, Fernandalanina Cocient
		corresponding	to first	
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ı		residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ł		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
.		sequence	sequence	Codon, /=possible nucleofide deletion
		1 - 1 - 1 - 1		\=possible nucleotide insertion\
		Ī	ľ	FAPMYGGFPVKLRTYLGDPIPYDPOITAEELAEKTKNAVOALID
-	6421	1844		MACKIPGNIMSALLERFH
		1044	362	WALSLRRQPERMSNKLLSPHPHSVVLRSEFKMASSPAVLRASRL
				I IQWSLKSSAQFLGSPQLROVGOIIRVPAPMAATT.TLEBACECCU
				DEPORTAVEGUAPEOPVTLRASLEDEKGALEGAHADVDAGTI CE
				DULERAPALGGSFAGLEPMGLLWALEPEKPIA/PIA/PDVPTPLA
				VELEVILIGHDPDPGRLLCOTRHERYFI, PPGVPDEPVPVGPUPCT
	ļ			HEDEPERGREPGIVDMFGTGGGLLEVDAGLAGVGDAGMALAUD
- [NIEDUPKTMETLHLEYFEEAMNYLLSHPEVKGDGVGLIGIGVGG
	ł	' I		ELCLSMASFLKGITAAVVINGSVANVCCTLDVKCETT DDVCVAD
	- 1			NAIKVIKUGYADIVDVLNSPLEGPDOKSPIDVPDAFGTELETVO
- 1	ĺ			QUDANWKSEFYANEACKRLOAHGRRKPOTICVDETCUVTEDDVD
		•		PLCRASLHALVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG
	6422			GREGTIPSKV
	0422	181	2133	EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE
				WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTQITY
	İ	Ţ		HQLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
	1			IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL
1	1			KELADEALQKCQEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI
-	1	ł		KRSCPDVQISWNQGIDLWWHELMQEAGDECEPEWCDAEDPLFIL
1	t	ł		YTSGSTGKPKGVVHTVGGYMLYVATTFKYVFDFHAEDVFWCTAD
	ı,	i		IGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK
-	1	ł		VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTVGEPINPEA
	i			WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT
1	i			FPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE
	1	1		RFETTYFKKFPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL
		1		LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT
	1	1		FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV
├	403			LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ
1 °	423	614	1237	ANLKEIPRDLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLS
				ANGLE FIDERAFKGVAETLOTLDISDND TOCKUVNA CARRE VADA
j	i		ĺ	RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
ı				FLNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQN
-	424			QEDARRHLEYLKSLPSROKKADEPDDTSmin
1 °	424	1	1188	KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL
		1		GGEGGREGDVWVVAHNRMTI.KOI.KDRVDDKDEVAGVGAMGVZGA
		ł	1	DAGS RGRDWEI PVPVGISVTDENGKTIGELNKENDDIT TVA COCT
	ĺ	1		GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC
1	Ī	i	1	VSHAKPATADYAFTTLKPELGKIMYSDFKOTSVADI DOL TEGALI
	1			MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII
				LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP
	}			KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL
<u> </u>	125			DBQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII
۰۹ ا	±25	1850	1144	LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG
		1	1	LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR
l			1	CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA
	- 1	1	1	WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE
1	- 1	ď	ĺ.	RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE
				KRPCTSMHFQLPIQA KRPCTSMHFQLPIQA
64	26	30		SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR
		i		LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG
	- 1		1 :	PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI
	1		í i	IRRRYPAHT.ADSSCREVITED DUGA TOTAL
			13	WRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT
64	27	145		AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK
				VIREYVRWMMYWIVFALFMAAEIVTDIFISWFPFYYEIKMAFVL
	_			THE TAXABLA TOTAL TAME A LA TENEMA PART

SEQ	Predicted	Predicted end	1 minor
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Ĭ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
- 1	sequence	1	\=possible nucleotide insertion)
		 	WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVQAKERSYETV
			LSEGERGINIA SANGARTEGORAL ROPLESCO.
į.			LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDA
i	1	Ì	PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA
	j		VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT
6428	1982	444	·
1		•••	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR
			EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDLLKGTEAST
	<u> </u>		KNIFGRYSSQRMKDWQEIIALYEKDNTYLVELSSLLVRNVNYEI
			PSLKKQIAKCQQLQQEYSRKEEECQAGAAEMREQFYHSCKQYGI
ĺ	1		TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGF
			VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
	ļ	, ,	PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
1			KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY
1		1	TETRNQFLDELMELEIFLAQRAVELSEEADVLSVSQFQLAPAIL
			QGQTKEKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK
L			TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
			VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
			NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS
			GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR
			VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
1			PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
1			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
1 1			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV
1			QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH
			TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH
	1		ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
			VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
1			LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
1 1	1	i	ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
1	1		VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
			TYIHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG
[AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVI.A
1 1			YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
1 1	İ		QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLOAPDSATLLEKM
] [KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSOGDLS
I		1	HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
1 1		1	KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEERRRMA
1	1	ĺ	TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
1 1	1	ŀ	TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR
1	1		PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG
			GPPKSGEP
6431	3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR
	ĺ		LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEERGEKU
			RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV
		1	IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTORAIAELTRED
			LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE
1			DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR
1		1	FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
!	İ	į ·	WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
	1	1.	LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
j	[1.	AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
			MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT
			TOUR THE PARTY OF

SEQ	Predicted	Predicted end	l Drive noted
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=H1Stldine, I=Isoleucine, K=lygine
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
ł	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
i	residue of	residue of	S=Serine, T=Threonine, V=Valine.
i	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	sequence	seducince	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
1			TGDGVARAFLKAQAAFFGSYRNALKIEPEEPITFCEEAFVSHYR SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVFEEEINM
ĺ			GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
1			AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
			PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
6433			THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
1			PTTPPQPGWCLCGKDFKSSCOTPGREKERRIATMHGSCSFLMI.T.
1	1		LPLLLLVATTGPVGALTDEEKRLMVELHNLYRAOVSDTASDMI
1			HMRWDEELAAFAKAYAROCVWGHNKERGREGENLEATTDECMDU
Ĭ			PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
			SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
	}		SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
6434	40	2002	AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
1			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
1 1			TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
•			DGGRIKELEKGKEEKEIKMEKTDETRLQKEAEFEKSAKENLRDS
1 1			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHEDDEGV
			SASSKIIISDVPSRKDHMCHPHGIMIIEDPAATNKDERT.VVVVV
	!		KSKMDRHGNDKSTPKKTCKKROSSESDIESVIVTIEAVAVCDWC
	1		IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSPEKKMSKEKS
j	1		SDTTKESRPPDFISISASKNISGETPEGIKAEPI TPMEDALDDG
. 1	ļ		LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
1			LRANVDRGKRSSGKGNSSDHEGCWNBESWTFSQSGTSGSKKFKK
			TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
[,	MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
			DIQRAGYHHEEVLWMTNLMNNCGGVYLKOLRHTAMTNA
6435	2227	657	ALQRDAAAAYAHPEYEERFLOEETVSOOINSIELLOTPDLALDE
			VVKSQRPLQRQVHLRGRPASOPTVIRGITYVKAKUSEEENDIEE
ĺ			QQDEFFSGDNGVDLLIEDOLLRHNGLMTSVTRRDAATDOGUGTA
- 1			VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
- 1	!	}	PTRESVLOPSPOVPATTVAHTATQQPAAPAPPAVSPREALMRAM
- 1	1	1	HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
- 1			GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
[AFTRNI I KYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
ļ		ì	VDBNGLWLIYPALDDEGFSOBVIVLSKLNAADI.STOKETTWDTG
ı			LRRNFYGNCFVICGVLYAVDSYNORNANISYAFDTHTNTOTUDD
6436	1295		LLFENEYFYTTQIDYNPKDRLLYAWDNGHOVTYHVIFAY
0130	1495	341	GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
- 1		Ī	YPIDCVKTRMOSLOPDPAARVRNVI.EALWDTTPTEGLWPDWG.
- 1	1	į	NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
ł	[l l	VATLUMDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWONEGAG
		1	AFYRSYTTOLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL
1			SGACAGAVAAAATTPLDVCKTLLNTQESIALNSHITGHITGMAS AFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
			KRQEEWRAGK KRQEEWRAGK
6437	1828		PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
[, ,	LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
	j	[]	SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
	İ	j t	MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAOSYKLYRCC
1		[5	SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH
1	ļ	j I	DLGITCCDFSSQPVSDGEQGLOFFRLASCGODCOVKIWIVSFTH
			ILGFELKYKSTLSGHCAPVLACAFSHDGQMLVSGSVDKSVIVYD

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
1	sequence	sequence	Codon, /=possible nucleotide deletion
	1 3	 	\=possible nucleotide insertion)
1			TNTENILHTLTQHTRYVTTCAFAPNTLLLATGSMDKTVNIWQFD
			LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
1	1	İ	nnidgkellnltkesladdlkieslglrskvlrkieflrtkvks Lssgipdeficpitrelmkdpviasdgysyekeamenwdpakrn
			RTSPP
6438	109	901	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV
1			NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
1			GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP
}			DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKIDITARTIAVED
]			KQERIHLVLGDCTHSPGSLOISLLDGLGPLPTOGLLDGLTGTIN
6439	23		KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLTHGLOFUTKV
	43	412	SIQTASAITTEMASOSOGIOOLIOAEKRAAEKVADARVEVADET
ļ			RQAKEEAQMEVEQYRREREHEFOSKOOAAMGSOGNI.SARVEOAT
6440	3	517	RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
i i			RARWINSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRFGQNRT
	ļ	•	IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF
			YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
6441	234	1373	KSGGLRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY
			KNVCKENSTVGMKIOEELORSGGLDHI.VI.SPGEWDVSDNTIMUT
			ATAKALTIDYWCLDDLYREMVRCYVETVEKI, PERPPDDATTECT
1			AQLKPNNYLLAWH'I'PFNEKGSGFGAATKAMCIGI.RYWKDRDI.rr
1	Į.		LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAOGKDIJJOUGDD
	ŀ	i	MLKAVPLAEEYCRKTIRHTAEYOEHWFYFEAKWOFVLEEBUIGV
1	i		DSENKAIFPDNYDAEEREKTYRKWSSEGRGGRRGHDAPMIAYDA
			LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDPAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS
1			LOROSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
j			DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD
f	1	ł	GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
		j	QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGAPPGDC
6443			EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
0443	2	555	MASPAASSVRPPRPKKEPOTLVIPKNAAEEOKT.KI.ERI.MKNPDK
1	İ		AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVVPHIDDD
1		1	EYQRQDYMDAMAEKQKLDAEFOKRLEKNKIAAEROTAKBBKKDA
		[KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE VPSFTMGR
6444	390	899	
			GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
	ŀ		PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA
			RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
6445	2	753	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
1]	J	SEEQFWEACAELQQPALAGADWOLLVETSGISTYPI.Drvmcrv
1	1		EYKVEGVLEDCSPTLLADIYMDSDYRKOWDOYVKELVEOFONGE
1	ļ	. 1	TVVYWEVKYPFPMSNRDYVYLRORRDLDMEGRKIHVILAPGTCM
j	ļ	1	PQLGERSGVIRVKQYKOSLAIESDGKKGSKVFMVVFDNpggotp
6446	1		SWILLNWAAKNGVPNFLKDMARACONYLKKT
	*	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENERDI.DET.C
		1 -	DSGDEAAWEDEDDADLPHGKOOTPCLFCNRIFTSAERTESUCVE
			EHQFN1DSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSTVNDV
		1.	PWEKEEILKPVLEDDLLLOFDVEDLYEPVSVPFSYPNGI.SENTS
	i	1 '	VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT
ļ	i	1.0	CSSTSVIADIOEDEDGE
		1.5	CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI

SEQ	Predicted	Predicted end	Amino acid company
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Grucdmic Acid, F=Phenvlalaning C-Cl
ŀ	location	corresponding	n=nistidine, l=isoleucine K-Lugine
	corresponding to first	to first	D=Leucine, M=Methionine N=Nconvocine
1	amino acid	amino acid	P=Proline, O=Glutamine D=Apprinted
	residue of	residue of amino acid	Serine, Tethreonine, Vevaline
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	sequence	Dagactice	Couon, /=possible nucleoride deletton
			\=possible nucleotide insertion)
			LYQAMDIIRLNKLEDTITLIKGKIEEVHLPVEKVDVIISEWMGY FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
			DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
	İ		IDENTISTS DEFSSOFTLK ITRTSMCTATAGVED I VERVICINI
ł			RVVFSTGPQSTKTHWKOTVFLLEKPPSVKAGFALVGVJFTIJIZDIV
6447	1554		KDPRSLTVTLTLNNSTOTYGLO
5117	1554	1068	RLGPAEWHLSGPCHATLGAANRGRALGVPAAWPCARLGODIAME
	ĺ .		SKINLATGIPSSKVKYSRLSSTDDGVIDLOFKKTDDVIDVVAIA
			HAIVLE LIGARLIIIGSLLLSGYISKGCADD AVDVITTCTT VIDY
6448	74	559	PGFIHLKIAYYASKGYRGYSYDDIPDPDD
1		333	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLQK
			FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
			AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER QFIVRKVHYDPEKDVHIYEAQKRNQKEDL
6449	597	1876	EYGVCBNLRKLEITGVSCRDVYAKLLHRYRHILGLWQPDIGPYG
			GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
			ATVECMIGHKGPHHGHIOIVKKDEFSTKCNOTDHUDMCCGDORE
1 1			FRINLREEWGRTLEDIFHEHMORLTIMKRIVTSOVDNOLTUNDI
1 1			111PPSRPDDLIKPGLFKGTYGSHGLETVMLSFHGPPAPGTY 100
			DPNIPAGQQTVEIDLRHRIOLPDIENORNERE, CRIVIEWERN
[ROBUGERGEGROGPRESOPSPAODPAFADGUCADCARDO
	ŀ		BUGGEPGDAVAAAEOPAOCGOGOPFVI.DVCVSSDNEDVDD TOOM
	1		CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY
6450	848	269	SRVQATFRNADAPSPQAFDEMLKNIQSLTS
	Ì		FVPAPRTVSGKRSLFGEWEERGEGORTGREFSGNGGRAVEAAR MRLLCGLMLWLSLLKVLQAQTPTPLPLPPPMQSFQGNOFQGEWF
1			VIGHAGNSERPEHRALLNAFTATERI,SDDCDERUMINAMIDOOLO
1			DIWSIVE PAAOPGOFTVDHRVWTHEOAGDDODODAGODT HAR A
6451	232		RDAGPVHLPGQSSGPLG
	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMQE
1	1		ILPGLELGPYSSAMKSKLPVLOKHGTTHTICTPONTERNETURN
			FQQDFKILVLDIADNPVENIIRFPPMTKEFTDGSI.OMGGVVIIVI
1	j		GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF
			VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE EEDDFGTMQVATAQNG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
1			LKFLKPKINSFYAFEVKDAKGRTUSI.EKVKGKUSI VIDBURGEGO
.	j		LIDRNY LGLKELHKEFGPSHFSVI.AFDCMOFGPGFDDDGVBVB
1			FARKNIGVTFPIFHKIKILGSEGEPAFPFIJIDGGVVFDDWITTING
6453	827	223	*LVNPEGQVVKFWRPEEPIEVIRPDTAALVROVTTKVVPD1
	4 2.	223	HRRWLPGLSMSPRRTLPRPLSLCTSLCTCLAAALGSAGGGG
1			RDKKNCKVVFSQQELRKRLTPLOYHVTOEKGTESA FEGEVELING
1			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
		1	FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
			RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
		1	DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
1			FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
6/55			PADSSGTAEGGSGVASPAOADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMOGSTRRMGVMTDVHRPETOL
1	1	1	LITTHGVLEEWDVKRLOTHCYKVHDRNATVDKI,EDFTNNTNCGT, P
		i	SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAFNELDIR
	ĺ		KALELIIDSETGFASSTNILNLVDOLKGKKMRKKEAFOULOVR
i	ł		VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	†		LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK
ł			VFDPEKERESGVLKSNKKSLRSRQH
6456	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
l	1		TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
į	i		RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
	ľ	1	KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
			DIFQNFSV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
i		,	KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
Ì	ľ		IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1	}		DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
L.			SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
}			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
ŀ			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
i			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
6459	23	892	SFLTLSSQLKPKPVGKENICLDLKS
1	2.5	632	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
i			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET IILGKQYSLNIILSVPAIILGAPIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
		•	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAPIAAGSDLAFNLEGYIFVFLND
1			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
[[•	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
	I		TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
	ļ		LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS
	ļ		LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
	1		DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
			YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
	ļ		GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
ŀ	1		APLEVQFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
1	ł		GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
	·		STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI
6462	3	773	QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
	-	,,,,	PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIO
l			YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
1.			KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
İ			PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
	ľ		GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
6463	2	350	VILCILGGWIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD
.	į	-	LHQAEEDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYELL
			NKRRSVRFISNEQVPMEVIDNVIRTAGL
6464	12	1154	GILROKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVOTVLG
			

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	[-	\=possible nucleotide insertion)
			LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
1			YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
1	ł		GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL
1			TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
1	l .		AQAQLGCPVIIHPGRSSRAFFQIIRILQEAGADISKTVMSHLDR
1			TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR
			IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
			PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
1			QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTI.FEKNAADI
1			LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGDGTLOEV
1	1	i	VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVOHT
1	(TDATLAIVKGETVPLDVLQIKGEKEOPVFAMTGLRWGSFRDAGV
	[KVSKYWYLEPLKIKAAHFFSTLKEWPOTHOASISYTGPTERDDN
1	[]		EPEETPVQRPSLYRRILRRLASYWAOPODALSOEVSPEVWKDVO
l			LSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFITIGSP
1			KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSERVFAMDU
6466			EVKLLPRKLQFFCDPRKREQMLTSPTO
0466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETOETC
1			PFCNHEKSCDVKMDRARNTGVISCTVCLEEFOTPITYLSEPVDV
6467			YSDWIDACEAANQ
0467	301	2571	GELRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
1 1			IKCVVVGDNAVGKTRLICARACNATLTOYOLLATHVPTVMATOO
	ì		YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
]			VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILUGCOLDLDV
1	ĺ		ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYVETSV
			VAQFGIKDVFDNAIRAALISRRHLOFWKSHLRNVORDI.LOADET.
1			PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI
1 1			FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
1 1			SDQHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
	}		SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
ļ · [i		LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
1 1	1		LEVFOLRMMVANILNNEAFMNQBITKAFHVRRTNRVKECLAKGT
			FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
1 1	1		FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
]	i		CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
1	1	i	EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
L!		j	SPSSSSAVV
6468	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
		1	KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
; i	.	1	SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQBPNVNPASAGN
	J	j	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
		ļ	TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
		[GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
l		İ	PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
	1	j	ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
ſ			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
			GKGKFSRAHFVLLSLL
6469	3		DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
e.			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
ł	ł]	KDVTIGFSLDRTXNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
	ĺ		SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1		1	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
			INTERNATIONAL TERRETORIESA

SEQ	Predicted	Predicted end	I Amino anid annual
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence	"	\=possible nucleotide insertion)
			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
1			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
1	i		ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
ł			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
L			GKGKFSRAHFVLLSLL
6470	2726	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAFRS
		1	GPI-PPEDGCPTPGPOLL BL DGRALL BREET A GOLDEN
l			GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT
1			QHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE
			ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG
[]			SLOKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEAIKFY
			RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
! !			YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS
			SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYRAWHQ
			VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLRTR
6471	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALRRRRR
			GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLSEAPN
	İ		EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILENTSK
İ			VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGBLPREVRRAQAR
ì			LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDEFFLE
			QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS
			AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE
Į.			ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQQRRREKA
ſ	ĺ		VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR
			ROARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG
			NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL
6472	3	897	SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRPGTTTP
- 1			ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY
			ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL
- 1	1		DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKF
			LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA
	1		AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN
			RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
6473	22	912	SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK
1		İ	NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ
j	İ		LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ
- 1			LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW
(1		DAPATEPSGTQQPAPSTESSGLAOPEHGPNTDI.LGTQDKAQI DI
1			KSSIIGKKRPAAAKKGLGAKKGLGAOKVSSOSESETEPOAOVAE
			KLREQQAADAKKQAEESMVASMRLAYOELOIDR
6474	3	462	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSDFNTFGVDCC
- 1			KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKTSPCA
ļ		1	KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
			PSTLSVKGQIETVRVKGTEN
6475	3	462	LOROROHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
		Ì	KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
1	1		KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
			PSTLSVKGQIETVRVKGTEN
6476	106	1090	ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL
i			KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE
ſ		1	RQLAKROHLEEQRLQQERQREQEORRERKEKISCLSFALDDLDD
Į.			QADAAEARRAGNIGKNPDVDTSFLPDRDREEEENRLREELRQEW
ı		1	EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL
1			QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK
,	1	i	
. 1	l l	1	SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	
j	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ľ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
-		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
6477	227	915	LOGHLMGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVL
	·	ł	SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHELELGVVMGKRCR
i	ł	i	AVPEAAAMDYVGGYALCUDMTARDVQDECKKKGLPWTLAKSFTA
1	Į.		SCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPY
1		ļ	IISYVSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM
			TFKVEKPEY
6478	2	1495	FVSSRILPESLASSEASTLEAMGRKEEDDCSSWKKQTTNIRKTF
Į.			IFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLEN
1	į	l	
í	1		EIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILE
i	1		RGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPE
1	1	Ī	ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA
1			VDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFW
			DDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDI
			YPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRP
	!		EVENRPPETOASETSRPSSPEITITEAPVLDHSVALPALTQLPC
1	ĺ		QHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC
İ	<u> </u>		SSCLNIGSKGKSSYCSEPTLLKKANKKONFKSEVMVPVKASGSS
	}		HCRAGQTGVCLIM
6479	3	949	SCRGPGWHPAGGQAGAMELLSALSLGELALSFSRVPLFPVFDLS
1			YFIVSILYLKYEPGAVELSRRIIPIASWLCAMLHCFGSYILADLL
			LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL
			IFVAMKEVVRVRKIAVGIHHAHHHYHHGWFVMIATGWVKGSGVA
	ĺ		
1			LMSNFEQLLRGVWKPETNEILHMSFPTKASLYGAILFTLQQTRW
			LPVSKASLIFIFTLFMVSCKVFLTATHSHSSPFDALEGYICPVL
			FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK
6480	192		KKAKKAD
0400	192	514	DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY
1 i			QIFPDPSDFDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL
			VQEDEQDNCEETAKENKEQ
6481	110	1131	KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWPSALIRIYYWY
			WRRTLGMQVRYVHHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD
			MWLSVVKFLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH
			QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLWLVCP
			AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC
1.	· ·		SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ
1			NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG
1			HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD
6482	2517	568	EPVSKVSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFQA
1			ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE
1			RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVRLAVIEFHLGV
1			
		İ	NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI
1			LWSEREEIETAQAYLESSEALYNQYMKEVGSPPLDPTERFLPEE
1 1			EKLTEQERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHYCHSTL
1 1	İ		KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI
, 1	1		FGQTGKISATEDTPEAEGEVPELYHQRKGEIARCWIKYCLTLMQ
		ļ	NAQLSMQDNIGELDLDKQSELRALRKKELDEEESIRKKAVQFGT
(/	ĺ		GELCDAISAVEEKVSYLRPLDFEEARELFLLGQHYVFEAKEFFQ
1 1	J		IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE
i i	ļ		PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD
Į ,	ļ		SHIVKKINNLNKSALKYYQLFLDSLRDPNKVFPEHIGEDVLRPA
[]	İ	İ	MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP
1	İ	,	EAAQEIEVELELSKEMVSLLPTKMERFRTKMALT
6483	3	633	
0 203	3	623	NSHLLCGLRARAPLSANGREARAMEQRLAEFRAARKRAGLAAQP
1	1	!	PAASQGAQTPGEKAEAAATLKAAPGWLKRFLVWKPRPASARAQP
		!	GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW
LL			LVLLGLFVELEFGLAYFVLSLFYWMYVGTRGPBEKKEGEKSAYS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			VFNPGCEAIQGTLTAEQLERELQLRPLAGR
6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF
	1		MILWLKGVKFNVTTVDMTRKPEELKDLAPGTNPPFLVYNKELKT
- 1		•	DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAKFSAYIK
		İ	NTQKEANKNPEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVS
	1		RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW
1			RYLHNAYAREEFTHTCPEDKEIENTYANVAKQKS
6485	6	1091	FVDLVRAVEFLPCPDSQKLEKECQSSEESMGSNSMRSILEEDEE
-		2002	DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRQRDK
i			KASVLYIEGHMNPKMKGFTVSLKSLKHFDCKEKQTLLNQAREDF
ľ			NQDIGWCVSLITDYRVRLGCGSFAGSFLEYYAADISYPVRKSIQ
			QDVLGTKLPQLSKGSPEEPVVGCPLGQRQPCRKMLPDRSRAARD
1	1		RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQYVT
	!		CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD
			VLLPEAIICAISAGDEVDYKTAEEKYIKGPSLSYREKEIFDNQL
	1		LEERNRRRR
6486	10	581	LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA
1			GGTGRFSGPLHRAWRMMNFRQRMGWIGVGLYLLASAAAFYYVFE
Ì			ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV
			IFLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV
			KASNQISRLQLIDT
6487	352	863	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN
1 .			YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYSEYL
	ĺ		KHNVRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID
			GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAO
6488	878	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP
1 1			MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH
1	1		KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYI,
			SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP
6489	1467		SEVLSTPFGQALRPLLDSIQIQFPGGSSVGRPNGQS
0409	1457	375	KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML
1 1]		YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR
1	. 1		GLEMEGWEVVERRRTPAEIREEFERLQREREERRLQQRTNPKGT
1			ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL
1			TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG
1 1			DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR
1 1	j		NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP
] [TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR
6490	3	1183	SKRTGGG
	-	2200	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
			KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
		Į	HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
] [1	APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
} I		Į	DSSPNAMAKVQIFEYNENTRKYAKARTLMTVTDPVHDIAFAPNL
]	i i	İ	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
	İ	İ	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
		j	KGNGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS
6491	3	1183	HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH
1	1		KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
] [ľ	HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
1	į		QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
1 1	}	i	APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
1			DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
Į I			GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
	ļ	1	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
			Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
Ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
j	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ţ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence		Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
6492	34	2573	KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
]			IPFLKSCCCCLFDFPPPPLDQVQEEECEVERVTEHGTPKPFRK
1		}	FDSVAFGESQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI
1	1		KRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSPSELRK
1			IFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSG
1	!	ł	PGEEKLKHAAATFCSNQPFALEMIKSRQKKDSRFQTFVQDAESN
1			PLCRRLQLKDIIPTOMORLTKYPLLLDNIATYTEWPTEREKVKK
1	1		AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN VBELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL
1	ì		QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDN
1	ſ		KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS
J	1		TKPIPLPQSTPGEGDNDEEDPSXLKEEQHGISVTGLQSPDRDLG
			LESTLISSKPQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK
	į i		EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT
1			EKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP
1	1		FRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQASNILVMDH
l			MIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNK
İ	1		EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLQPMTGIP
j	1		AVESTHOOOHSPONTHSDGAISPFTPEFLVQQRWGAMEYSCFEI
l	1		QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTILCQRLAGS
L			ALTDKHSDKS
6493	557	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
1	,		KEQNIGHNNINGVVQPSGTSKTLYSTNMALSSSPGTSAVOLUDE
1			VGHTTNHLI PALCTSSPOTLPMNNSCI, TNAVHT MMVCGUCCDIDI
Į į			VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIAPENU
6494	2405		EPERLGLINGIAETTVAMEVT
0434	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSDILDUGG
			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVOVFSEVEVEVE
			SEESIKDNFVIIYELLDELMDFGYPOTTDSKTLORVITORCHVI
			BIGAPRPPATVINAVSWRSEGIKYRKNEVFI.DVIRGUMI.LUGAM
	i		GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
	1		VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
	1		PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
i	İ		DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ
6495	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
l	1	_	LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
ĺ		ļ	VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
1			EBESIRDNFVIIYBLLDELMDFGYPQTTDSKILQEYITQEGHKL
	Ţ	!	ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN
1	i	j	GNVLRSEIVGSIKMRVFLSGMPELRIGINDKVI.FDNTGBGKGVG
1		ŀ	VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSVPLMTHUV
j		ł	PULWIESVIEKHSHSRIEYMIKAKSOFKRRSTANNUFTHTDUDM
ŀ	i		DADSPREKTTVGSVKWVPENSEIVWSIKSFPGGKEVI MDAUECT (
ļ	ļ		PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
6405			PWVRYITQNGDYQLRTO
6496	247	559	LRAVSLLPLQLVLPEYSIHSLFCIMFLCAOEWLTIGINVPLLEY
	ļ		HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL
			SFFYYLYCMIYTLVSS
6497	1053		ANTQICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
		1	GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
1		[.	TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY
1		1.	DHAEATIVVMLVGNKSDLSOAREVPTEEARMFAENNGLLELETE
			ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	Sectine, leinreonine, vevaline,
l l	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	seductice		\=possible nucleotide insertion)
			EPGPGEKRACCISL
6498	2636	272	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL
i			LRVSWICGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI
1	!		VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL
i			AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLM
ı		Ī	CETT.DULUTUECADVENEETMODERINGS PET 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
ŀ		1	SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGHLSINQD
1	1		LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
i		1 .	DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPE
		i	KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQL
ł	1		QAQIRNLTVLTPEGEAGLSWPVGLPAPFTFHSRFEVLGWDYFTE
			QHTFSCADGAPKCPLQGASRADVGDALETALEOLNRRYOPRLRF
		İ	QKQRLLNGYRRFDPARGMEYTLDLLLECVTORGHRRALARRVSI.
1	1		LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAA
ı	1		NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRY
			PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPG
1	1		PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGP
ŀ	i i		DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG
1		•	ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRD
1	1		CSDDL SEEL VIDGOL ON BOL GOD OF THE TRAVEPGLVQKFSLRD
6499	3	2040	CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST
1		2040	SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETPQVACLP
			GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEHLKLAGM
· I			ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAG
ł	1		GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDC
	1		LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIATTAHERM
1	1		PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEOGTYALSLIVG
1	i		KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKADGLIYC
1	1		LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT
			PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL
			LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTE
	1		EMMREAQIMHQLDNPYIVRLIGVCQABALMLVMEMAGGGPLHKF
	1	i	LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL
1	f I		VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINF
1	}	I	RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR
İ	Į į		MECODECODEL ANT MODORITARIADO DO DE MINICOPERA LEGGRA
1	1		MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLA SKVEGPPGSTQKAEAACA
6500	1773	726	
1	1 -113	120	TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK
1	1		MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL
ŀ			QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE
1	, I	1	TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
1		l	YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSG
1	1	• [DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEOGGMIWKISED
1		1	KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN
L	<u></u>	!	QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ
6501	1	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE
1	1		IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE
	[]	}	TNEHTL DECENTABLE COM OR OF SEARCHREIM DENLKNMIHE
1	1		TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI
!	1	j	HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ
6502	-373		YAEMEKDLAKFSTF
1 0302	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWNRSWLQQSYQAVKE
ł			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
l	ţ l	1	SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
[1	1	AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
	l f	1	KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ.
	1	1	EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
		0	AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
		. 1	QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
			Z

SEQ	Predicted	Predicted end	Amino noid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
· ·	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=Ston
	sequence	sequence	Codon, /=possible nucleotide deletion
 	Bequence		\=possible nucleotide insertion)
Ì		1	IHSKPLTPAGHTGGPEPRPFARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
6503	213	1650	EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
ł		1030	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEPTQVVQHDTACTIAATASVVKEKLATEGS
		1	SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
1			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
			EQARRDALKORAEOSISEEPGWEEEEELLMGISPISPKEAKVPV
i			AKISTFFEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
			QIANPATAPEARVLPKDLSQKLLEASLEEOGLAVDVGETGDSDD
	j	•	INSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTREEVOMALSKIDASC
6504	2131	1004	EVSGPGGSEGSEPNGPGCESSPOPAOLSPOEGPCSCLR
0301	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
1 1			DRVASSHISDANLANTIIGKAVEHMPEGEHGSKDEWRGMVLAQA
			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1 1			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
	i		SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
	1		WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
1			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
1 1	į		PIMKAWFYITYEKDPVLYMYOLLDDYKEGDIRIMPESSREDDTD
1 1			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHOVEAKPSVYFIKF
6506	1		DDDFHIYVYDLVKKS
0300	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
1 1			ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLREVTYSR
ł			STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQQAY
1 1			RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
1	1		LDVPSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFQASPSV PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
			WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA
1 1	1	1	EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGIABVET
1 1	!		REKEPPGWGQGQGEGEVGNNSLGLPQGKRPASPALLLPPCMLKS
	1		PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
6507	1070		QAATSVPNPP
550,	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA
		1	ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD
		ļ	IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMQRNASVPNLR
1			GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS
			ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE
		ł	VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
			EDISRKGN
6508	862		WEARKRPQRWPSERREVRVPPPHLQRGRSGLEPGTFRKMAAARP
		I.	SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
			DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
			ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
6509	2	1053	FVWNPRGGRKRRQAAVTQAATRASGTPSPRDGTMTQGKLSVAN
		ſ i	KAPGTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP
1		į i	APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTPSWDDOKV
1		į 1	RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVOANPGWYW
	<u></u>		ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML

SEQ	Predicted	Predicted end	
σι	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
- }	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptopian, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
- 1	1	1	LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
		}	LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRB
6510	37	1156	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
- (1	GLVINFVQLCTLALWPVSKOLYRRLNCRIAVSIMSOLUMI I BUIL
	1		SCIECILFIDOATVERFGKBHAVIILNHNFFIDELCGUTMCEDE
f	1	l	GVLGSSKVLAKKELLYVPLIGHTWYFLETVFCKPKWFFDDDMIN
	ł.		LGURRUSDYPEYMWFLLYCEGTRFTETKHRYSMRYDDDDYCH DYG
	1		A THELPHIKGFTTAVKCLRGTVAAVYDVTLNFRGNKNDSLIGTI
1	-1		IGKKYEADMCVRRFPLEDIPLDEKEAAOWI,HKI,VOFKDALOFIV
1			NOKEMPPGEQFKPARRPWTLLNFLSWATTI.I.SDLESEW.CUEAG
6511	2541	1425	GSPLLILTFLGFVGAGNGHCR
	-544	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
ŀ	{		THATMESDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGBOBLE
	1		KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
			SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV
1	1 1		QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
	1		LVSWPLCSLRRYGRDATRFTFBAGRMCDAGEGLYTPQTQEGEQI YQRVHSATLAIAEQFKRVLLEMEKNVRLLNKGTEHYSYPCTFTT
1	1		MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI
6512			LLKPKPSQGDSSEAKTPSQ
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLG-GGYTGSGPGFGFDDDGGA
i			EVPSGSGRATGCERGGVRGAROGRAPGSSIWPKEDDMUCTPVTV
ı	1		TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGOEDADDVVT
			EEDKGDTLKIIERLDHLENVIKOHTORADAKDERARARDEWDGG
6513	2	756	LEAHWGQELSPEGRRVALKOFOYYGYNAVI.chpt.hthph
1	1	/56	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA
	[LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV
1			AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
1	1		GVPLTGNVTTSOMANEQGLFDVHSILRVVLGANGTYSCLVRNPV LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
1	1		SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
]	[1	PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA
İ	1		PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
1			PLIGNVITSQMANEOGLEDVHSII.RVVI.GANGTVSCI.VDNDVIT.O
1	1		QUARISSYTITPORSPTGAVEVOVPEDPWALAGEDATERGERGE
6514			EFGF5TAQLINLIWQLTDTROLVHSFTEGR
0314	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSPAKMCPPACOECA
	}	İ	UAENHUNGKNSSLTLTGETSSAKI, PRCROGGWAGDGWKAGVEDD
1 1		ļ	KASEKI EDFRLRPOSLNGSDYGGDI PI I PDI EFUOPEDEUL OVA
]]	· .	1	APPSIQIARVMTYRDLDNDLMKYSATOTLDGETDLKLLTERG NO
		1	EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLOTEKEDP
6515	1345		AGQARHT
1 1		303	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
	ľ		VAGGGAGPI SADKKERVHOGMVRAATVGYGTI RECCCAIMAIDA
) i			AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
(I	1	ļ	VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
]	1.		LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
1 1		[]	KVNLARLTLFHIEQGKTVBEAADLSLGYMKSRVKGLGGLIVVSK
		1.	TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
6516	1	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL
	j	[]	KGRRSEHRNENQBMPYSTNKELILGIMVGTAGISLLLLWYHKVR
	1		KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
	ļ	1.	LEKLNELLTNMEELKEEIRFLKEAIPKLEEYTODELGGKTTMUV
		:	ISPQHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS

Γ <u></u>	SEQ	Predicted	T 200 - 37	
,	ID	beginning	Predicted end	
1	10:	nucleotide	nucleotide	I Washing, CECVSTRIBE Datements as a second
[]		location	location corresponding	TOTALCHUIC ACIG. PEPPANGISTANIAN A AS
-		corresponding	to first) ···································
		to first	amino acid	D=Deucine, M=Methionine N=According
1		amino acid	residue of	F=Froline, O=Glutamine D=Arginine
		residue of	amino acid	S=Serine, T=Threonine V=V=line
1		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	bequence	(Codor, /=possible nucleofide dolonia.
			 	-possible nucleotide insertion)
1	- 1			FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
			1	DATE ADDITIONAL PROPERTY OF THE PROPERTY OF TH
- 1	Í			INRAPMNGHCHLWYAVLCGYVSEFEGLQNKINYGHLFKEHLDIA
- [ı			IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSTV
<u> </u>				QEALHNFLKAEELCPGYSNPNYMYLAKCYTDLEENQNALKFCNL ALLLPTVTKEDKEAQKEMQKIMTSLKR
65	17	3	1414	GRVWGGS SEI NAMUTURGUA GRUNGGS SEI NAMUTURG GRUN
- }	1			GRVWGGSSSLNAMVYVRGHAEDYERWOROGARGWDYAHCLPYFR
	- 1			KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLEATQQAGYP
			}	LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA
- 1	- 1		l	EAETLVSRVLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN
j	- 1			SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLEIYIQQ
- 1	- 1			ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
	- 1			GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE
	- 1			ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
- 1	- 1			PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA
651				EKAADIIKGQPALWDKDVPVYKPRTLATQR
627	۱ ۳۰	242	1098	PAWNPGSEPRTRVRPRARSEDT DDDDADDDDDDDDVDV
- 1	Į	i		RHRCRRAPPPPSTMGDAGSERSKAPSLPPRCPCGPWGSSKTMN
1	- 1			1 ACCRETANT VAROPININGAPSTISMSOCRIT. PORTERMANNAME
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	- 1	İ		ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
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				VPPTLLHAQPHHLLLPAAAAASANAKSRRPKBKREKERRHGL GGARBAGGASBEENGEVERI
1			ſ	GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKERKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKHK
	1	1	i	ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
1	1			KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
6521				HIMAGENGGASVIHCLO
0321		184	1798	KLFKMATDTSOGELVHPKALPLYVGAQLTVADVT GUV
1	- 1	ļ	1	TANKE THE ENDINGREE KEEKPEPHICCEPCUCHUPACHAN
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1	- 1		ļ	VALLESWATUSASOLARAOKOTDMASSDDDDVMDATI DDD TIER -
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		1	I	DURAY ERGULEOLTG KGASGTFOI. KYSCEVDI I CCCI VDVI
		1	1 -	ALAAMINEPATCSTTALKKYVLENHPGTNSNYOMULLEVERI OVOR
	1	ļ	i i	MIGHIEQISGRGFSGTFOLCFPVVDCDGM.FDVVFDDDGDDDD
	1	ĺ	4	DEDESSEEDSEDEEPPPKRRLOKKTPAKSDGKAAGUVORGGKDA
	1		1 '	FRVSAMORGKARPLPKKAPPKAKTPAKKTRPSSTVITKVBCGGCC
6522	+	1043		RRPAISARRE
0322		1042	391 1	NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED
				THE CHEED

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PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid common
ar	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	į	\=possible nucleotide insertion)
j			ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
	1		SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
1	1		RKRRRPVSPERYSYGTSSSSKRTEGSCRRRQSSSSANSQQGSP
		1	PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
1	}	1	RSRKLGIFRRCWLVFKKASSKGPRRLEKPPDEKAAYFRNFHKVT
ı		·	ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
		}	KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
1			LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
1			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
			MDTSTCKVVHDLE
6524	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
	1		RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
l			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
]			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
1			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
l	1		LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGB
1	1		IYSLQGNHENRHSDLTGKSCKTSENRFLBENAPLVMYGITHHLP
			MDTSTCKVVHDLE
6525	1	1859	GESPFSEEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
			PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIOSSRYK
			KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKPSSSSP
]		NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNOLSDVNTHD
			SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
			EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSOLAR
	4		MREDWIEEECHRVEAQLALKEARKEIKOLKOVIETMRSSLADKD
			KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
	1 . 1		PEKSLTLNPPLDTMADGLSLEEOVTGEGADRELLVGDSTANSTD
			LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGGFFGSVAA
			ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
			MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
			LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
			PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
6526	2	2024	IKT
	~	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
			GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
			NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
İ		İ	KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
}			LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK
}		j	KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH
. [ł	FINDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK
		ı	CONCINCULT COLIT EDIT MANAGEMENT
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNTVMDOGD
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLOKIGID
			GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMELTVPGI
			GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVFFPMLI
			GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESBFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTPAPV
		i	GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESBFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRRRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETBAEPESTSEKPSDVNTEETSVAVKFRULDINV
		İ	GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYSTRKNSMGIKRPAPQPASGANIPKESBFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRRRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
6527	1		GGVSIAGHSLGSLILEPILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRRRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ
6527	1	922	GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS
6527	1	922	GGVSIAGHSLGSLILEPILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRRRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ

Doginning	SEQ	Predicted	Predicted end	
No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence				Amino acid segment containing signal peptide
Cocation Corresponding Coffree				A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of residue of residue of amino acid residue of amino acid sequence acid sequence aci				Glutamic Acid, F=Phenylalanine, G=Glycine,
bo first amino acid residue of amino acid amino acid amino acid sequence Percentage	Ì			National Management Rallysine,
residue of amino acid sequence				P-Proline O-Glutamine, N=Asparagine,
amino acid sequence Sequence	1	amino acid		SeSerine T-Threenine W-Walter
Sequence Codon, /=possible nuclectide deletion, -possible nuclectide insertion -possible nuclec	1	residue of	1	Wetryptophan Yetropian V Wetre
LUESRKREENELBEELTLINKHAMESISKOSMINEONFEPTRRC SLTPPPQNTITWEYYISAENGKAPHLORELVCKESKKTFKATIA MSOSPPLOIBELLUNLUKUVAPKHENKLEEVUKESKKTFKATIA MSOSPPLOIBELLUNLUKUVAPKHENKLEEVUKESKKTFKATIA MSOSPPLOIBELLUNLUKUVAPKHENKLEEVUKESKKTFKATIA MSOSPPLOIBELLUNLUKUVAPKHENKLEEVUKEPSPYKAT DIPVPFTITATVITOSPFKYDSTOGSITTIPDVKEDSFRYDSTOGS TITODVKEDSFRYDSTOGSITTIPDVKEDSFRYADSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDVKEDSFRYDSTOGSITTIPDSFRYDDAGSFTATASTORDOPPHAL SSUNDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDDAGSFTAGSFRYDAGSFR		amino acid		Codon. /=possible nucleotide deletion
LVLESKARREKLISEED ILRNKAIMESISKOON HEONDEP IRRO SLIPPPOON TINEEYISABANGAPHLORELUKSES KATEKATIA MOOSPELGIELLINVLEWVAPPKHENIKREYVONKLPPGFPVKL DIPPPTITATVTPGEFYAPPOGS IPTIPPOSSPPPLL LTGBAAAEPRCAADAGMKRALGREKGWURLEKTLEFULGYTA LOPEBUVIGWKTVPAWKKANGOKOOMWEDDALGSHPT LIV LOPEBUVIGWKTVPAWKKANGOKOOMWEDDALGSHPT LIV LOPEBUVIGWKTVPAWKKANGOKOOMWEDDALGSHPT LIV LHONAGTKOOHNVEHISCPHUTUNGTUNGUNGVOPPEDALGSHPT LIV LHONAGTKOOHNVEHISCPHUTUNGVATURUNGUNGVOPPEDALGSHPT LIV LHONAGTKOOHNVEHISCPHUTUNGVATURUNGLOS RETTPDALLIESS PTHINEERSLEPH SVITYAYETLOSS ROMTDALHVEDWIKKESPHOVATINGVATURUNGLOS RETTPDALLIESS PTHINEERSLEPH SVITYAYETLOSS ROMEDALHVENOON PERSON PUTUKKI GOPURDALGSHP PILOK RETTPDALIESS PTHINEERSLEPH SVITYAYETLOSS REASFRDEKVOYFPENDLOYRHKYTYKSPELPRILOKSE PENOH 6529 363 2215 HIETAYKAGVVKTMSCONPEVETLIKKI GOPURDALGSEDPOWLP GOVEDSSPLIKHFOONWOONVLSURELBERFS ILQKSGRPILBOA ALBEAKINCTISSLESS PHINEERS PLOKSGRPILBOA ALBEAKINCTISSLESS HINEERST LOKSGRPILBOA ALBEAKINCTISSLESS HINEERST KIKUPEN LOO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORGOLIBATION SINESSPERIKUTOS ICO NOELLEBRULEMBALGOATH VORG		sequence		\=possible nucleotide insertion\
SITPPPQNTITWERY ISAEMGRAPHLORESUVCKESKKTFKATIA MSOSPPOLGELLELLNULWUNDPREPHENKLERFULEPOPPVAL DIPYPETTTATUTFOSFRYDSTOGS I FITPDDYKEDSREPPDL TOTAL TOTAL TOTAL AND THE PROPERTY TO THE PROPERTY I THE PR				LVLESRKRREHLSEEDTI.RNKATMESI.SKGGNTMEONERDTERO
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LHONAGTROGDBRYELTKURSLGYHVVTTDVRGGGGSVGTPSE RGMYTDALHVEDMIKARSGGNEVTIMGEGTGVATRILVERICE RETFPDALILES PTNIREBAKSGNEVTIMGEGTGVATRILVEKS TAA FARSFRDFKVOFVPFHSDLGVRHKYIYKSPELPRILREFIGKSE PENGH 6529 363 2215 THIEYBKIGVVKTWSCGNEFVETLKKIGYPKADNINGEDFDWLF ECVEDESFLKWFCGNVNGCNVLSERGLEAFSILGKOSKEFILBGA ALBEALKICKTSDLKTPRIDDKELBILGHEDEVOTLLKKINKIGR RINKCQLMASVISHKSLRINAKSEBATKKLKOSGGILMAMITKIS NELGALITDEVTQLMMFRISHLGGGTFWLSGFSLEKKYLSGE EGSTAALTLYTKKOFFOGIHEVVESSNESGFFNFLKKOFFSICO NGGELIEBEREBRARGLAN ICAGOLIHASMISMSMISSIKNBE ESLHSITSKAPVBKENLDARISSLTSEIMKLEKEUTOJKORSLPA VWERNGLILMPVVKGDFDLGIAKGVYTAGELVINGVLKOKA SFELLGLSYBIELRKURDIYRGLENLVQELGGSNMMLYKQLEML TDPSVSGQJUPPRTTLOTRYSTHRLYQVLEGGSNMMLYKQLEML TDPSVSGQJUPPRTTLOTRYSTHRLYQVLEGGSNMMLYKQLEML LEBEVAEKLKONISLUODGLAVSAQEHSFLSKNKEUDMLCOTL YCGGNGLLLSQBEITERGKRRDIYRGLENIKVGELIKOKA SFELLGLSYBIELRKURDIYRGLENILVQELGGSNMMLYKQLEML TLANNKLHQMEREFYVYVLKOEDYLLDVLETGGSKIKANSLED LEVYAEKLKONISLUODGLAVSAQEHSFLSKNKEUDMLCOTL YCGGNGLLLSQBEITERGKRRDIYRGLETGSKIKANSLED BAHRGAIVQVHPLLPGSSTIMHDLCLVFPAPAKAVVYVSDIQ ELYIRVDKVEGIGKTVKAYVEVLDLHKKFFLAKYFFPMDLKURA ASPIITLVALDEALDNYTITTLIRGVGISLTASVTHKAGOR INSAPQGIEVFPPFRLMFRKVTILIGATMQVISGGOPDGONIL FSISMESVALVSAGALGKALAINGVALDABETKVVI SQDLVQVEVLLHRAVIRAP-MMRTGTGMFIVYTITHHONPF SFGNAVPGLAFFRWSVTKADVLDLRGKHRASIRVDSGVPPAMW LGRVKGRTGLRAVVKAVDPTSGGLARE-SDEIQVQVPPELQ LLNFRIERBGILMSNESVILLQONDFOALSIRVDLOTPERVYV VAVDEKGFLAGGSMIGTSTIEVIAQEPFGANOTILVAVVSPPS YLRYSMS PULFTONKSALVAVRAVGSTVALUTSLEGLSGT RSSSANSILTHFRWSVTKAVRANVSSVVVSULTLAKVNDAKH PGLASDFPPLVLQAISEELGGAMVGDVLCLARVLSEGGSTGTTUFFSSD VINGALAIPETLISCGSCRYKAVSTPPSGDVFTVEPGTPTALG QYFCSITMIRLDTKQRKHLSMKKTALVVSASLSSSHFSTEQVCA EVPPSPGLAPGALFELLISTYTSEBIRVSGERVLENDERVINGS PAVLAPAKKERFGWPSFITTTTGVLDAPAGSCGPLGSTTLFFSSD VINGALAIPETLISCGSCRYKAVEDPSGOVETVEPGTPTLAFSSD VINGALAIPETLISCGSSEKCTISSS SLGMLYDARASSPPGOLFSPROGRENTERDSGGGERGEKCTISS SLGMLYDARASSPPGOLFSPROGRENTERDSGGGERGEKCTISSS SLGMLYDARASSPPGOLFSPROGRENTERDSGGGERGCHANTERPSGAL ALLGGTAVMILAYHTVCTRRDLAVALDFRSGGISGSEKCTISSS SLGMLYDAGALLTHPRS	Ì			LQPEEDVTIGVWHTVPAVWWKNAQGKDOMWYEDALASSHPIILV
RGMYYDALHVPDW/KARSGGNEV/YIWGHSIG/TGVATKILVRILCE RETTPDALILES/PINIREAKSHPFSVI/KYPDGFOMPILDI TSSGIKFANDENVKHISCPLLILHAEDDPVUFFOLGRIKLYSIAA PARSFRDERVOFVFHSDLGYRHKYIYKSPELPRILREFIGKSE PEHOH 6529 363 2215 THIRYNKIGVVKTWSGNEFUETLKKIGYPKADNINGEDFDWLF ECVEDSSPILKMPCGNVEGNVLSRELEAFSILOKSGKPILBGA ALDEALKTCKTSDLKTPRIDDKELEKLEDEVQTILIKLKNILTOR RNKCQIMASVISHKSIRINAKEEBATKOSGGILMAMTIKKS NELOALTDEVYQLMMFFRISNIGGTNPLVFILSOFSLEKYLSOG EOSTAALITYTKKOFFOGHEVVESINGSGILMAMTIKKS NELOALTDEVYQLMMFFRISNIGGTNPLVFILSOFSLEKYLSOG ESSTAALITYTKKOFFOGHEVVESINGKESGIFNLATICKSIADA VVERNAGLINMPVVKGDPDLQIAKQYYTARQELVINQIIKORSIAP VVERNAGLINMPVVKGDPDLQIAKQYYTARQELVINQIIKORSIAP VVERNAGLILMPVVKGDPDLQIAKQYYTARQELVINQIIKORSIAP VVERNAGLILMPVVKGDPDLQIAKQYYTARQELVINQIIKORSIAP VVERNAGLILSOPSTERPHVVSGIAKKHLITDILADVKTRK TLANKLHQMERSFTVYFLKDEDYLKDIVELGENKKKELITHGIN LEEVAEKLKONISLVQQLAVSAQEHSFFLSKRINDDMLCDTL YQGGKQLLLSOSLTERPHVVSGIAKKHLITDILADVKTRK TLANKLHQMERSFTVYFLKDEDYLKDIVELGESKIKAVSLE D 6530 128 2986 GAAHHGAIVQWHPLLGGSSTIMHDLCLVPFPDARAVVVYSDIQ ELYIRVVDKWEIGKTVKAYVRVLDLIKKRPILAKYPPMDLKLIRA ASPIITUVALDRALDNYTITPLIRGVAIGQTSLTASVTNKAGQR INSAPQIEVPPPRIMPKKTULLIOATMQVTSEGPOPQGNILL FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETEKVVI I SQDDLVQVSVLLLRAVIRAPLMEMRGTGOMPIVTITINHONPF SSGNAVBALTFHRSVTKNDVDVLDLGRHHEASIRLPSQVYPAMNV LGRVGRTGLRAVVKAVDPTSGQLVALARELSDEIQVQVPHKLQ LLNEBISERGIIMSNSTILVLORDFSGLVVQVDHKLQ LLNEBISERGIIMSNSTILVLORDFSGLVVVLIGATVLTSLEGUSGT MSSAMSILHIDPKTGVAVARAVGSVTVTYEVAGHARTYKEVVV SVPQRIMARHLHPLGTSFQBATASKVTLVAGGDERSURGECTPT QREVIGALHPEPLILAGSGGFKAVEDPFSQDVETUEPQFDTALG QYFCSITMHRLIDKQRKHLSMKKTALVVSASLSSHFSTEQVGA SSVPGRIGHPAVTVAVVRROPPSGOVTUEPGFTDTALG QYFCSITMHRLIDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA SVPSPGLEJADABILLANITYSSEIRVDLOGGFULSVRCUSGG PAVLAFAKEKEFGMPSFITTTGVLDPAAGSGGPLSTLLTRSSP VINQALAIPVTAFVVDRSGOPQTASTROLTSGVLLGRYDTYREVWYQA LGGTAVMILAYHTVCTPRDLAVPAALTFRASPGHS PHYFARS SCHUNPAGSSFOLQSSLEPPHDRELIDSQDQTMSPTQAL ALLGGTAVMILAYHTVCTPRDLAVPALTFRASPGHS PHYFARS SCHULPPAGSLEPPHOFTLISHGGGOQVISKCCELRINTYREVWYQA CQCQYDYCKMSSFOLQSSLEPPHORFLIDENGQUFLOSGOLFVQAL NLSLPLP				LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE
RETPOALILES PTNIRERAKIPFSVITKIPFGFOMFILDI TSGGIKPANDENVAHISCPLLIHAEDDPVYPFOLGKUKYSTAA PARSFRDFKVGFVPFHBDLGYRHKYIYKSPELPRILREFIGKSE PEHOH 6529 363 2215 THIEYRKIGUVUKTUSGNEFUETLKKIGYPKADNINGEDFDWLF ECVEDESFLKWFCGNVRSGNEFUETLKKIGYPKADNINGEDFDWLF ECVEDESFLKWFCGNVRSGNEFUETLKKIGYPKADNINGEDFDWLF ECVEDESFLKWFCGNVRSGNEFUETLKKIGYPKADNINGEDFDWLF ECVEDESFLKWFCGNVRSGNEFUETLKKIGYPKADNINGEDFDWLF ECVEDESFLKWFCGNVRSGNEFUETLKKIGYPKADNINGEDFDWLF ECVEDESFLKWFCGNVRSGNEFUETLKKIGYSGGLAMMTKIS NELOALIDEVYGLMKFRIDDVELEKLEDEVYTLIKLKINKIGR RNKCQLMASVISHKSLRIMAKEEBATKKIKOSOGILMAMTKIS NELOALIDEVYGLMKAPKISHIGGGIHEVKISOFOENTKIKTOTESICD NGEILSEREREMBRIGLAJA ICAQQUILHIKASNISMKSSIKMAE ESIHSITSKADVKSNILDAKISSLTSEIMKLEKEUTQIKORSIPA VVRENAQLINMPVVKSDFDLQILAKQDYYTPARQELVUNQLIKOKA SFELLQLSYBIELRKKRIDIYRQLENGSSMMMINKGLEML TDPSVSQQIMPRRTIDTKDYSTHRLYQVLEGENKKKSELFLTHGN LEEVAEKKKRNISLUQDQLAVSAQERISKRIKDVDMLCDTL YQGGNQLLLSDQBITEOPHKVESOLMKIMHLITDILADVKTRKK TLANNKLHOMEREFYVYFLKDEDYLKDIVETOSKIKAVDVLDTL YQGGNQLLLSDQBITEOPHKVESOLMKIMHLITDILADVKTRKX LANNKLHOMEREFYVYFLKDEDYLKDIVETOSKIKAVVYSDLQ ELYIRVVDKVEIGKTVKAYVEVLDHKKPFLAKYFFPMLKIRA ASPIITUVALDEALDNYTITFLIRGVAIGGTSITASVTNKAGQR INSARQQIEVFPFPRIMRERVATLILGATMQVTSEGGPQPGONIL FSISMESVALVSAAGLVQGLAIGNGYSSLOVADAETGKVVI LGRVKGFTGLRAVVKANDPTSGGLVCALARE-SDBIQVUPFRKLQ LLNPBIZAEQIIMSPNSYIKLQTNRDGAASISTRVLDGFERVPV VHVDEKGFLASGSMIGTSTIEVIAGEFFGANDTIVTVGTITHON PF SFGNAVPGLIFFWSVTKRDVLDLRGRHHEASIRLPSQYNPAMNV LGRVKGFTGLRAVVKANDPTSGGLVCALARUSDBIOUVPFRKLQ LLNPBIZAEQIIMSPNSYIKLQTNRDGAASISTRVLDGFERVPV VHVDEKGFLASGSMIGTSTIEVIAGEFFFGANDTIVTVAVKVSPWS YLRSMSSYLHTDPKTGVAVARAVGSVTVYEVAGHRITYKEVVV SVPQRIMARHLBPIOTSGRATASKUTAGATVITSLEGISGT MSSSANSILHIDPKTGVAVARAVGSVTVYEVAGHRITYKEVVV SVPQRIMARHLBPIOTSGRATASKUTAGAPESNILGEGCTPT QREVIOALHPETLI SCQSQYKDAVFDPSQDVFTVPQFDTDTAG QVFCSITMHILDDKQTRKHLSMKKTALVVSASISSHTSEQUGA EVPSSCLEPADQABILLSNNYTGSEINVFGAPEVLENLEWKSGS PAVLAFAKKERGFGWSFITTTTGVLDPAAGSQOPLSTTLIFSSB VTNQATALFYVAVEVURREPGPYGAALTFRASPGHSPHYFAAS SPSTPRALPPARKSPPSGLMSPADATPLDSQQTOMFTTAEWWYQA LCQCYDYCNSMSSPQLQSSLEPPHORPLINDSGQDTLOSTGGENTY		1		RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNIVRRICE
TSSCIKFANDENWHISCPLLIHAEDDPVUFFCIGKELYIAGA PARSFADFVCVFVFFSBEDGVRHKYIYKSELPRILRFIGKSE PENGH 6529 363 2215 HIRYNKIGVVKTMSGGNEFVETIKKIGVPKADNINGEDDDWF EGVEDESFILMFCCONNEGNVUSERELEAFSILQKSKFILBGA ALDEALKICKTSDLKTPILDKREHLEKLEDEVVTLIHLKINTLOR RINKCQIMASVISHKSIRINAKEBERYKKLKOSGGILMAMITKIS NELQALIDEVYQLMMFFRISNIGGTINPLVFISGPSLEKKISGE EGSTAALITYTKKOFFOGHEVVESSIRKKKRSFOFFNIKTOTPSICD NGEILEERRLEMARLQLAYICAGHLVUKASINSKGSIKVABE ESLHSITSKAVDKENLDAKISISITSETHLKEVTOTKURGSIDA VVERNAGLIMPVVKGDPDLQILAKQDYYTARQELVINQLIKQKA SFELLQLEYBEILEKKRIDIYRQLENLVQLSGNMMLYKQLEML TDPSVSQQINPRNTIDTKDYSTHRIVQVLGENKKKELLTHGN LEEVAKKKKNISLIVQDQLAVSAQEHSFFLSKRINDDMLCDTL YQGGRQLLEBQELTEGPKWESGINKKHLELTDILADVKTRK TLANKKHQMEREFTVYYLKDEDYLKDIVELETGSKIKAVELD D 6530 128 2986 GAAHRGAIVQVHFLLEGSSTIMHDLCLVFPAPAKAVVVXSDIQ ELYIRVVDKVEIGKTVKAYVRVLDLIKKPFLAKYFPMDLKIRA ASPIITLVALDEALDNYTITPLIKGAIGGTSLTASVTNKAGGR INSAPQGIEVPPPFRIMFRXVTLICATMQVISEGGPQGGNIL FSISMESVALVSAAGLVQGLAIGNGTVSGIVQAVDAETKKVII SQDLVQVSVLLLRAVVRAVPEVDLUDLGRHRVSTUNDVTSGGGPQGGNIL FSISMESVALVSAAGLVQGLAIGNGTVSGIVQAVDAETKVVII SQDLVQVSVLLLRAVVRAVPPTSGGLVSLARELSDEIQVQVPEKLQ LIMPEIERGCIMSVNSVIILQTNDRDASISTVULDGEPKYPV VIKVEKGFTLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS YLRYMSMSVLHTONKEALLAVPLGHTVTHHENDSGIDVPHAM SSVLINFATNEDDFVQIGKGFTNNTCVVRTVSVGILTLLRAWDAKH PELSDFMPLFVULQAISPELGGAMVVGAUTPHSDVTHENDSGIPTAGG QYFCSITMHRIDTBKQRKHLSMKKTALVVSASISSSHFSTEQVGA SVSPGRIUARHLBPIGTSFQBATASKVIVAVGGDEVLIENEVKGG PAVLAFAKKKSFGWPSFITTTGVLDPAAGSQCPLYENLEVKGG PAVLAFAKKKSFGWPSFITTTGVLDPAAGSQCPLYENLEVKGG PAVLAFAKKKSFGWPSFITTTGVLDPAAGSQCPLYENLEVKGG PAVLAFAKKKSFGWPSFITTTGVLDPAAGSQCPLYENLEVKGG PAVLAFAKKKSFGWPSFITTTGVLDPAAGSQCPLYENLEVKGG PAVLAFAKKKSFGWPSFITTTGVLDPAAGSGCPLYENLEVKGG PAVLAFAKKKSFGWPSFITTTGVLDPAAGSGCPLYENLEVKGG SPTSPRALDPARKASPPSGLWSPACHEPSVGAL SCHULPPARSSPDOLDSFUFFDRETUFFLDSFQQVFFTAFS SLCMUTTYVDVKVRETURGCQVISKTCCEKNTYAFEVWYQA QCQYDYCNSSSPQULSSLEPPHORFILDPSDQTQMEYQAL NLSLPLPHRHAGTERDOLDPWTLSINIGLSFAELRRMVLFINS	-			RETPPDALILES?FTNIREEAKSHPFSVIYRYFPGFDWFFLDDT
6529 363 2215 THIRYNKIGVVKTMSGGNEFVETLKKIGYPKADNINGENFDWLF BENGH EGVEDESPLKMFCGNVEGNVLGERELEAFSILQKSGKPILBGA ALDEALKTCKTSDLKTPRIDDKELEKLEDBVQTLIKLKKILKIGA RINKCQLMASVISHKSLRINAKEEEATKKLKSGGILNAMITKIS NELQALTDEVTQLMMFRHSHLIGGELHKARSSSMKSSIKVAB EGSTAALTLYTKKOFFGGIHBVVESSNESOFFMFLKIOTPSICD NGSILEERIEMARIGLAYICAQHLIHKARSSSMKSSIKVAB ESSLHSLTSKAVDKENLDAKISSLTSELMKLEKBVTQIKORSLPA VVERNQLLMPVVKGOFDLQIAKQDYYTARQELVINDLIKGKA SFELLQLSYEIELRKHRDIYRGLERIVQELSGSNMMLYKQLEML TDPSVSQQIMPRNTIDTKDYSTHRLYQVLESGRSMMLYKQLEML TDPSVSQQIMPRNTIDTKDYSTHRLYQVLESGRSMMLYKQLEML LEKVARKLKQMISLVYTYFLKDEDYLVENLETGSKIKKELELTHIGN LEKVARKLKQMISLVYTYFLKDEDYLVENLETGSKIKKELELTHIGN LEKVARKLKQMISLVYTYFLKDEDYLVENLETGSKIKKEKELELTHIGN LEKVARKLKQMISLVYTYFLKDEDYLVENLETGSKIKKELELTHIGN LEKVARKLKQMSREYVYFLKDEDYLVENLETGSKIKKAVSLS D 6530 128 2986 GAAHRGAIVQVHPLLDGSSTIMHEDLCLVYPAPAKAVVYVSDDIQ ELYIRVDKVSIGKTVKAYVRVLDLHKKPFLAKYPFFMDLKIRA ASPIITLVALDEALDMYTITLIRKVAIGGTSITASVTNKAGGR INSAPQQIEVFPFRIMFRKYTLLIGATMQVTSGGGPQOSNIL FSISMESVALVSAAGLVQGLAIGMOTYSGLVQADAETGKVVII SODLVQVSVLLLRAVKAUPTSGGULARLSGDEIQVYPFKL LGRVKGRTGLRAVVKAUPTSGGULARLSGDEIQVYPFKL LLMPRIERAGILMSPMSYIKLOTMRDGAASLSYRVLDGPEKVPV VAVDEKGFLASGEMIOTTSTIEVIAGLEFSDEIQVYPFKLV UVLDEKGFLASGEMIOTTSTIEVIAGLEFSDEIQVYPFKLV VAVDEKGFLASGEMIOTTSTIEVIAGDEPSGAMTITVARVSPYS YLRVSMSSYLHTONKEALVAVPLGMYTTTVHFHDMSGDVPHAH SSVLNFATNREDDFVQIGKSPTNNTCVVRTVSVGLTLLRVNDAKH PGLSDFPPLEVLQAISPELSGAMVVQTORSSNINGGCTPF QREVIOALHPETLISCQSQFKPAVFPPPSQDVFTVPQFDTALG QYFCSTIMHLTDKQKRHLSMKKTALVVASGRSSMINGGCTPF QREVIOALHPETLISCQSQFKRHISMKKTALVVASGRSHTERVGGA EVPFSPGLFADQAEILLSNHYTSSEIRVASGRSHFTTYKESSP VTNQALAIPVAKENSFGWPSFTTTVGVLDPAAGSQGLSTTLTFSSP VTNQALAIPVAKENSFGWPSFTTTVGVLDPAAGSQGLSTTLTFSSP VTNQALAIPVARKSFGWPSFTTTVGVLDPAAGSGGLSTTLTFSSP VTNQALAIPVARKSPGWPSFTTTVGVLDPAAGSGGLSSTKTTSSS SLCMVITYYDVKVPFLVRGCGYLSYRGGSKKTISSS SLCMVIDPPARKASPPSGUMSDAVAGSFGREFTSSS SLCMVIDPPARKASPPSGUMSDAVAGSFSSGKTISSS SLCMVIDPPARKASPPSGUMSDAVAGSFSSGKGTISSS SLCMVIDPAGALTHPINSTERVLAGASSGGLSTTLTSSS SGLLVVPDAGALTHPINSTERVLAGASSGGUMPTOAL NLSEPPNPHAGTEPDGLDDMVTLSINLGLSFA				TSSGIKFANDENVKHISCPLLILHAEDDPVVPFOLGRKLYSTAA
6529 363 2215 THIRYNKIGUVKTMSCGNEFVETLKKIGYPKADNINGEDEDWLF EGVEDESPLKMPCGNVNEGNYLGERELEAPSILQKSGKPILEGA ALDEALKTCKTSDLKTPRIDDKELEKLEDEVOTLIKKLKNIKT QR RINCQLMASVTSHKSLRINAKEEBATKKLKOSGGIJNAMITKIS NELQALTDEVYGLMMFFRISHLGGGTNFLUVFLGSFSLEKYLSGE EGSTAALTLYTKKOFFGGIHEVVESSNESDFFNFLKIOTPSICO NGEILEERRLEMARIGLAYICAQHGLIHLKASNSMKSSIKNAB ESILSITISTKANDKENLDAKISSITSEINKIKEKEVTQIKORSLPA VVRENAQLINMPVVKGDFDLQILKQDYYTARQELVINGLIKQA SFELLQLSYBIEBRKHRDIYRGLENLVQELSGSMMLVKQLEML TDPSVSQGINPRRITIDTKDYSTHRIYQVLSGENKKLEKELFTHRIN LEEVAEKLKONISLVQDCLAVSAQEHSFFLSKRKNDVMLCDTL YGGNGLLISDGELTEGPHKVESGLINHLHLTDILADVKTKKK TLANNKLHQMEREFYVYFLKDEDYLKDIVENLETGSKIKAVSLE D GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFFAFAKAVVYVSDIQ ELYIRVVDKVSIGKTVKAYVRVLDLHKKPFLAKYFFFMLKIRA ASPIITIVALDEALDNYTITFLIKRYGGTSLTASVTVKAGGR INSAPQGIEVFPFFRIMPRKVTLLIGATMQVTSEGGPOPQSNIL FSISNESVALVSAAGLVQCILAIGNIGTSLTASVTVKAGGR INSAPQGIEVFPFFRIMPRKVTLLIGATMQVTSEGGPOPQSNIL FSISNESVALVSAAGLVQCILAIGNIGTSLTASVTVKAGGR INSAPQGIEVFPFFRIMPRKVTLLIGATMQVTSEGGPOPQSNIL GGNGRIGGRAVVKAVDPTSGGLYGGLARELSDEIQVQVPFKLQ LLNFSIERGGILNSNNSYLKLQTHRDGAASLSVRLDGPEKVPV VAVDEKGFLASGSMIGTSTISVILOGEFGANOTIIVAVKAYPVS VLRVSMSSVLHTONKSALVAVPLGMTVTTVVIHENDRGHVPHAH SSULNFATNEDDPVOIGRSPINNTCVTVSVGLTLLRVWADRH GGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGISGT WSSSANSIHIDPKTGVAVARAVGVSVVYZYKVGHERTYKSVVVV SVPQRIMARRHHPIGTSQGAFRAVFDFPSGDVFTVEPQFDTALG QYFCSITMHILTDKQKKHLMKNTALVVSALSSSHTSTGVCA SVPPSPGLFADGAEILLENHYTSSEIRVFGAPEVLENLEVKGGS PAVLAFAKKSFGWPSPITTYVGVLDPAAGSGGLSTTLTFSSP VTNQALNIPVTVAPVVDRRGGFYGASLFQHFLDSYGGMSFTQAL SPTSPMALPPARKASPFGUMSDAVALSSSHTSTGVCA SVPSPGLFADGAEILLENHYTSSEIRVFGAPEVLENLEVKGGS PAVLAFAKKSFGWPSPTTYTVGVLDPAAGSGGLSGKKTISSS SLAWATTYYDVVDRWFTLFFCLVEDDSVGGISGSEKCTISSS SLAWATTYYDVDVRWFTLFFCLVEDDSVGGISGSEKCTISSS SLAWATTYYDVDVRWFTLFFCLVEDDSVGGISGSEKCTISSS SLAWATTYYDVDKWFTLFFCLVEDDSVGGISGSEKCTISSS SLAWATTYYDVDKWFTLFFCLVEDDSVGGISGSEKCTISSS SLAWATTHYDDFRAGTEDGIDDMVTLSINLGLSFAELRRMYLFINS SGLLULPGAGLTHPHS	1	1		PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE
ALDEALKTCKTSDLKTPKTLKKIGYPKANNLNGEDFDWLF EGVEDBSFLKMFCONVEQNVLSERELBAFSILQKSKPILBEA ALDEALKTCKTSDLKTPKLDDKELEKLEBEVOTLLKLKKIKTOR RNKCQLMASVTSHKSLRINAKEEBAFKKLKOSQGINNAMITKIS RNEQALTDEVTOLMMFRHSHSULGGTNPLVFLSGFSLEVILSGE EGSTAALITYTKKOFFGGIHEVVESSNBSGPFBFLKIGTPSICD NGELLEERRLEMRALQLAYICAQHLIHLKASNSSMKSSIKWAE ESLHSITSKAVDKENLDAKISSLTSEINKLEKEVTGIKOFFSICD VVERNAQLLIMPVVKGPFDLQIKAQCHSILVKLEKEVTGIKORSLPA VVERNAQLLIMPVVKGPFDLQIKAQCHSQENMALYXQLEML TDFSVSQGINPRNITITKMYSTHRIVINENLOGKIKAVSLE LEEVARKLKQNISLVQQQLAVSAQEHSFFLSKRNKUVDMLCDTL YQGGNQLLLSDQELTEGPHKVESQLINKLHILDILDADKYTKRK TLANNKLEQMBREFTVYFLKEDDTLVSTNETGSKIKAVSLE GAAHHGAIVQVHPLLFGSSTIMHDLCLVFPAFAKAVVVVSDIQ ELYIRVVDKVSIGKTVKAVVRUDLHKKPFLAXYPFFMDLKLRA ASPIITLVALDEALDANTITPLISCHQTSLTASVTNKAGGR INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQFOSNIL FSISMESVALVSNAGILVQLIGKGNTVSGLVOAUDAETGKVVII SQDLVQVEVLLLRAVRAPTSGQLYBARSLSGDEQVOYFMKLQ LLNFSIERGGILMSPNSYIKLQTNRDAAASLSTRIDGOVPFKLQ LLNFSIERGGILMSPNSYIKLQTNRDAAASLSTRIDGOVPFKLQ LLNFSIERGGILMSPNSYIKLQTNRDAAASLSTRIDGOVPFKLQ VIVUEKGFLASGMIGTSTIEVIAGERSLSDEQVOYFMKNQ VIVUEKGFLASGMIGTSTIEVIAGERSLSDEQVOYFMKNQ VIVUEKGFLASGMIGTSTIEVIAGERSLSDEQVOYFMKNQ VIVUEKGFLASGMIGTSTIEVIAGERSLSDEQVOYFMKLQ SVINFATNRDDFVQIGGPTNNICVVRTVSUGTLLRVMDAHH SSVINFATNRDDFVQIGGPTNNICVVRTVSUGTLLRVMDAHH SSVINFATNRDDFVQIGGPTNNICVVRTVSUGTLLRVMDAHH SSVINFARNRHLBFILTSTGORATASKVAVAGPRSSNIRGECTFT QREVIQALHFETLISCQSQFRAVFPPPSQDVFTVEPQFDTAIG QYFCSTIMHLTDKGKRHLSNKTRJAVAGRSSNIRGECTFT QREVIQALHFETLISCQSQFRAVFPPPSQDVFTVEPQFDTAIG QYFCSTIMHLTDKGKRHLSNKTRJAVAGRSSNIRGECTFT ALLAGTAVMILAHTVCTPRDLAVFALJEPRASGGSPLSTTLTFSSP VTNQALAIPAPRAKSPFUBSGLSSPLFHDFLASSLSSSFSTEQUCA SPTSPRALDPPARKSPFSGWSPSTTTVVGVLDPAAGSGGLSTTLTFSSP VTNQALAIPAPRAKSPFORSSLFSHFTPLASFGSPHYFAAS SPTSPNALPPARKSPFORSGLSSSLFSHPBFLALFLSSGGOPKFTLSSS SLCMVITYYDVVRFULFCCQVILSYRCOKKNTYFAEVWQA QCQYPYCNSMSSQLQSSLFSHPBPRLALFLSSGGOPKFUFINS	6520	363		PEHQH
ALDEALKTCKTSDLKTPRLDDKELEKLEDBUQTLLKLINLKIQG RNKCQLMASVTSHKSLRINAMERTKKLKDSGCLINAMITKIS NELQALTDBUTQLMMFFRHSNLGGTNFLVFLSGFSLEKYLISGE EQSTAALTLYTKKQFFGGIBEVVESSNESSJFNFFLKIGTPSICD NGEILEERRLEMARIQLAYICAQHQLTHLKAGNSSMKSIKME ESLHSLTSKAVDKENLDAKTISLTSEIMKLEKEVTQIKORSLPA VVERNAQLINMPVKGPDDQLJAKQDYTARQELVINQLIKQKA SFELLQLSVEIELRKHRDIYRQLENLVQELSGSNMMLKQLEML TDPSVSQQINPRNTIDTKDYSTHRLYQVLESGNKKKELFLTHGN LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL YQGGNQLLLISDQELTEQPHKVESQLMKLMHLITDLLADVKTKRK TLANNKHCHMEREFYVYFLKDEDYLKDLVENLETOSKIKAVSLE D GAAHHGAIVQVHPLLPGSSTIMHDLCLVPPAPAKAVVYVSDIQ ELYIRVVDKVSIGKTVXAYVAVLDLHKKPFLAKYPFPHDLKLRA ASPIITLVALDEALDNTTITFLIRGVAIGOTSLTASVTNKAGQR INSAPQCIEVPFPPFRIMPRIVTLIGATMQVTSEGPQPQSNIL FSISNESVALUSAAGLVQCLAIGNGTVSGLVQAVDABTGKVVI SQDLVQVEVLLLRAVRIRAPIMMRGTGMPIYVTGITNIQNPF SGRANVPGLTFHMSVTKRDVLDLAGRHHEASIRLPSQNFRAMV LGRVKGRTGLRAVVKAVDDTSGQLVSLARELSDBIQVQVPEKLQ LLNFBIERABGILMSPNSYIKLOTHGAASLSYRVLDGPBKVPV VHVDEKGFLAGGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS VLRVSMSPVLHTQNKEALVAVPLGFTVTTVHFIDNSGDVFHAM SSVLNFATNREDDFVQIGKGFTNNTCVVXTVSVGLTLLRVMDAHH PGLSDFPPLEVLQAISPELSGMWVGDVLCLATVLTSLEGLSGT WSSSANSILHHIPKTGVAVARAVGSVTVYZVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFGBATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFFSQDVTTVERQFTTALG QYFCSITMHRLTDKQRKHLSMKTALVVSASLSSSHFSTEQVGA EVPFSPCLFAQAELLLSNHYTSSEIRVFGABFULENLEVKGGS PAVLAFAKERSGEWSPFTTYTTQULDPAGSQGGLSTLTFFSSP VTNQAIAIPPTVAPVVDRRGGPFYGASLFQHFLDSVQVMFFTLF ALLAGTAVMIIAHTVTCTPROLAVPAALTRASFGRSPHYFAAS SPTEPNALPPARKASFPSGLUSPAYASH 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDDSVGCISGSEKCTISSS SPTEPNALPPARKASFPDGULDSVAYASH NLSLPIPPNHAGTEPDGLDWVTLSINLIGLSFAELRRMYLIFINS SGLLVVITYDVAKVRIVRGCQQYISYRCQESKGEKCTISSS SPTEPNALPPARKASFPDGULDSPAYASH NLSLPIPPNHAGTEPDGLDWVTLSINLIGLSFAELRRMYLIFINS SGLLVYLTIYYDVAKRIVRGCQQYISYRCQEKGSGSEKCTISSS SCLLVYTIYYDVAKRIVRGCQQYISYRCQEKGRSFRYFYFAAS SGLLVYLTIYYDVAKRIVRGCQQYISYRCQEKGGSGSKCTISSS SCLLVYTIYYDVAKPRIVRGCQQYISYRCQEKGRSFRYFAENS SGLLVYLTIYYDVAKPRIVRGCQQYISYRCQEKGRSFRYFAENS SGLLVYLTIYYDVAKPRIVRGCQQYISYRCQEKGRSFRYFASHAND	1 3323	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLF
RNKCQLMASVTSHKSLRINAKEBRATKKLRSGGILNAMITKIS NELQALTDEVTQLMAFFRHSLLQGTMPLUFLSQFSLEKYLSQE EQSTAALITYTKKQFFQGIHEVVESSNESQFRPFLKIQTPSICD NQEILEBRIEMARIQLAYICAQHQLIHLKASNSSMKSSIKMAB ESLHSITSKAVDKERLDAKISISEIMKLEKEVTQIKDRELPA VVNENAQLIMPVVKGDPDLQIAKQDYYTARQELVLNQLIKQKA SFELLQLSVEIELKHRDIYRQLENUVQELSQSNMMLIKQLEML TDPSVSQQINPRNTIDTKDYSTHRLWQLUGSSNKKELFLFHGN LEEVABKLKQNISLVQQQLAVSAQEHSFFLSKRNKDVDMLCDTL YQGGNQLLLISDQEITEQPHKWESUKKHHLITTLADVKTKRK TLANNKLHQMEREFYVYFLKDEDYLKDIVENLETOSKIKAVSLE D GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ ELYIRVVDKVBIGKTVKAYVRVLDLHKRPFLAKYPFPMDLKLRA ASPITLVALDEALDNTTITPLIAVAIGGTSTASVTNKAGQR INSAPQQIEVFPPFRLMFRKVTLLIGATMQVTSEGGPQPOSNIL FSISMESVALVSAAGGIVQGLAIGNGTVSSCUVQVDPAKAVVYVSDIQ LGRVKGRTGLRAVVKAVDPTSGCLVCARELSDEIQVQVPEKLQ LGRVKGRTGLRAVVKAVDPTSGCLVCARELSDEIQVQVPEKLQ LLNPEIEAEQILMSPNSYIKLTNRDGAASLSYRVLDGPEKVPV VHVDEKGFLAGSMIGTSTIEVIAQEPGANQTIIVAVKVSPVS VHVDEKGFLAGSMIGTSTIEVIAQEPGANQTIIVAVKVSPVS VHVDEKGFLAGSMIGTSTIEVIAQEPGANQTIIVAVKVSPVS VHVDEKGFLAGSMIGTSTIEVIAQEPGANQTIIVAVKVSPVS VHXDEKGFLAGSMIGTSTIEVIAQEPGANQTIIVAVKVSPVS VHXDEKGFLAGSMIGTSTIEVIAQEPGANQTIIVAVKVSPVS VHXDEKGFLAGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS VHXDEKGFLAGGSMIGTSTIEVIAQEPFGANGTIFTYTHAGGSGUFTTHFGSSP VTNQALAFAKERSFOWSPFTYTYTUYLDARAGSGGFLETTHFGSSP VTNQALAFAKERSFOWSPFTYTYTUYLDARAGSGGFLETTHFFSSP VTNQALAFAKERSFOWSPFTYTYTUYLDARAGSGGFLETTHFFSSP VTNQALAFAKERSFOWSPFTYTYTUYLDARAGSGGFLETTHFFSSP VTNQALAFAKERSFOWSPFTYTYTUYLDARAGSGGFLETTHFFSSP VTNQALAFAKERSFOWSPFTYTYTUYL				EGVEDESFLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA
NELQALTDEVTQLMMFFRHSNLGGGTDFLVFLSQFSLEKYLSQE EQSTAALITYTKKOFFOGIHEVGESSNESQFPNFLKIQTPSICD NQEILEERRLEMARLQLAYICAQHQLIHLKASNSMKSSIKWAE ESLHSLTSKAVKKEHDLAKISSLTSEIMKLEKEVTQIKORSLPA VVRENAQLLMMPVVKGDPDIQKQDYTARGGLVANQLIKOKA SFELLQLSYEIELRKHRDIYRQLEMLVQBLSQSNMMLYKQLEML TDPSVSQQINPRNTIDIKDYSTRLYQVLEGENKKKELFLTHGN LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRKKDUPMLCDTL YQGGRQLLSDQELTEGPHKVESQINKKHLLTDILADVKTKRK TLANNKLHQMERFFYVYELKDEDYLKUTUENLETOSKIKAVSLS D GAAHKGAIVQVHPLLEGSSTIMHDLCLVPPAPAKAVVYVSDTQ ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA ASPIITLVALDEALDNYTITFLIRGVAHGGTSLTASVTNKAGQR INSAPQQIEVFPPFRLMFRKYULLIGATMQVTEGGGPQPOSNIL FSISMESVALVSAAGLVGLAIGKGTVSGLVQAVDABTGKVVI SCDLVQVSVLLIRAVRIRAPICHAPHAVRTGTOMPIVVTGITNIQNPP SFGNAVPGLTFHWSVTKRDVLDLGRRHHEASIRLPSQYNFAMMV LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVERLQ LLNFBIEAEQILMSPNSYLKLOMTVTFTVHFHDNSGDVFHAH SCVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRWMDAKH PGLSDFMPLVVQAISFELGGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHTDKNKEALVAPATOSVTVYTEVAGHRTKKEVVV SVPQRIMARHHPIQTSFQRATASKVIVAGGRSSNLGGCTPT QREVIQALHPETLISCGSQFKPAVTDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKLISMKTALVVSASLSSSHFSTEQVGA EVPFSPCLFADQAEILLSNHYTSSEIRVGAPEVLENLEVKSGS PAVLAFAKEKSFGWFSFITTVAVUDDAASGCGDLSTTLTFSSP VTNQAIAIPTVAFAVENSFGWFSFITTVAVUDDAASGCGDLSTTLTFSSP VTNQAIAIPTVAFAVENSFGRSPSTLWSGASPSGLSGEKCTISSE SLCMVITIYYDVAFVUDRGCPGFYGASLFCHFLDSYQVMFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTRRSPGCHSPHYFAAS SPTSPNALPPARRASSPSCLUSPAVASH 845 1425 PSASIPPSASPPDVPDITTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVAVRIFUNGGCISYRCCEKNTYFFABYWQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLAILISDSQIOWFYQAL NLSLPLPPNFHAGTEPDGLDPMTTLSINLGLSFAELRRMYLFINS SGLLUPPQAGLIPPHS				ALDEALKTCKTSDLKTPRLDDKELEKLEDEVQTLLKLKNLKIQR
BOSTAALITYTKKOFFOGHHEVVESSNESOFPNFIKIOTPSICO NOSILEERRIEMARICLAPITOAQLIHIKASNSMKSSIKWAE ESLHSLTSKAVDKENLDAKISSITSEIMKLEKEVTQIKORSIPA VVRENAQLIMPVVKKOFFLOQUITAKOPYTARQEIVINQLIKOKA SFELLQLISVEIBIRKREDIYAGDIYTARQEIVINQLIKOKA SFELLQLISVEIBIRKREDIYAGDIYTARQEIVINQLIKOKA LEEVAKKKKQNISLVQDQLAVSAQENSFILSKRKKDUPMLCDTL YQGGQLLLSDQELTEQPHKVESOLNKLHHLITDILADVKYKKK TLANNKLHOMEREFYVYFIKDEDYLKDIVENLETOSKIKAVSLE D GAAHHGATOVVHPLLFGSSTIMIHDLCLVFPAPAKAVVYVSDIQ ELYIRVVKVEIGKTVAYVRVDLHKKRFLAKYFPFMDLKIRA ASPIITLVALDEALDNYTITITIKRVATGOTSITASVTNKAGQR INSAPQOIEVFPPFRLMPRKVTLLIGATMQVTSEGGPOPOSNIL FSISNESVALVSAAGLVQGLAIGTVSGLVQAVDAETGKVVII SODLVQVEVLLRAVRIRAP MRWRTGTQMPIVVTGITNIQNPP SFGNAVPGLTHWSVTKRDVLDLAGRHHEASIRLPSGYNFAMWV LGRVKGRTGLRAVVKAVDPTSGLOGLGLARELSBEIQVOQVPBKLQ LLINPBIRAGQILMSPNSYIKLQTMROGASLSYRVLDGPEKVPV VHVDEKGFLAGSGNIGTSTIEVIAGPGRANOTII TVAKVSPPVS YLRVSMSSVLHTQNKCALVAVPLGMTVTFTVHHDNSGDVPHAH SSVLNFATNRDDFVQIGKGFTNNTCVVRTVSVGITLLRWDAHH GELSDFMPLPVLQAISFELGGANGVGDVTVYEVAGHLRITKKEVVV SVPQRIMARHHPIQTSFGRATASKVIVAVGDRSSMLRGECTPT QREVIQALHEBTLISCGQS(PKPPFPSQDVFTVPPQDTDLIG QYFCSITMHRITDKQRHLSMKTALVVSASLSSSHFSTEQVGA EVPPSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGGS PAVLAFAKERSFGWPSFITTIVAVLDPAAGSGGPLSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRGPGFYGASLEQHSTTLTFSSP VTNQAIAIPTVAFVVDRRFTLFGCLVERDSVGCISSSEKGTISSS SLCMVTITYDVBVRFTLYGGVJESVGCISSSEKGTISSS SLCMVTITYDVBVRFTLYGGVJESVGCISSSEKGTISSS SLCMVTITYDVBVRFTLYGGVJESVGCISSSEKGTISSS SLCMVTITYDVBVRFTLYGGVJESVGCISSSEKGTISSS SLCMVTITYDBVRRFTLFGLDSPDVGCISSSEKGTISSS SLCMVTITYDBVRRFTLFGCLBEDBYGGISGSEKGTISSS SLCMVTTTYDBVRRFTLFGCLBEDBYGGISGSEKGTISSS SLCMVTTTYDBVRRFTLFGCLBEDBYGGISGSEKGTISSS SLCMVTTTYDBVRRFTLFGCLBEDBYGGISGSEKGTISSS SLCMVTTTYDBVRRFTLFGCLBEDBYGGISGSEKGTISSS SLCMVTTTYDBSS				KNKCQLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS
NGEILEERRIEMARLOLAYICAGHQLIHLKASNISSMKSSIKMAE ESLISLITSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA VVRENAQLIMMPVVKGDFDLQIAKQDYYTARGELVINQLIKQRA SFELLQLSYBIELRKHRDIYRQLEINVQELSQSNMMLYKQLEML TDPSVSQQINDRRITIDIKDYSTHRLYQVLSGENKKKELFLTHGN LEEVABKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL YQGGNQLLISDQELTEQFHKVESQIKKINHLILIDILADVKTKRK TLANNKLHQMEREFYVYFLKDEDYLKDIVENLETOSKIKAVSLE D 6530 128 2986 GAAHHGAIVQVHPLLEGSSTIMHDLCLVFPAFAKAVVYVSDIQ ELYIRVVDKVBIGKTVKAYVRVLDLHKKPFLAKYPFPMDLKLRA ASPIITUVALDBALDNYTTTFLIRGAIGGTSLTASVTNKAGQR INSAPQQIEVFPPFRIMPKYTRUDAIGGAGGTSLTASVTNKAGQR INSAPQQIEVFPPFRIMPKYTRUDLAGHHEASIRLPSGYNFAMMV LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQUQVFEKLQ LLNPEIEAGQILMSPNSYIKLQTNBGAASLSYRVLDGEEKVPV VHVDEKGFLASGSMIGTSTIEVIAGEPFGANGTIIVAVKSPPVS YLRVSMSSVALTONKEALVAVPLGMTVFTVUHFHDNSGDVFHAH SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRAWARH PGLSDFMPLPVLQAISPELSGAMVVGDULCLATVLTSLEGLGGT WSSSANSILHTDPKTGVAVARAVGSVTYYZVAGHLRTYKEVVV SVPQRINARHLPJQTSFDGATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQUGA EVPFSPGLFADASELLSHAFTSERRYVLSGG PAVLAFAKEKSFGWPSPITTTVGVLDPAAGSQGLISTLITESSP VTNQAIAIPVTVAFVVDRRGGFPTGASLFQHFLDSYQMFFTLF ALLAGTAVMILATHTVCTPRASPGHSPHSHYFAAS SPTSPBALPPARASPSPSGLWSQALGHFLDSYQMFFTLF ALLAGTAVMILATHTVCTPREDLAVPAALTPRASPGHSPHYFAAS SPTSPBALPPARASPPSGLWSPAYASH 6531 845 1425 PSASTPFSASPDPVDTTCTCFCFCLVEDFSVGCISGSEKCTISSS SLCMVITIYYDVXRVFLYRGCGQVISYRCQBKRNTYFABYWQA QCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQQMFYQAL NLSLPPHRAGTEPDGLDDMVTLSLNLGLSFABLRRMYLFINS SGLLVVPQAGLLTPHS				MELOAL THE VIOLENT FRHSNLGQGTNPLVFLSQFSLEKYLSQE
ESLHSLTSKAVDKENLDAKISDITSEIMKLEKEYTQI KORSLPA VVRENAQLIMPVDYKOFDIQIAKQDYTARQELVINQLI KQXA SFELLQLSYEIELRKHRDIYRQLEMLVQELSGSNMMLYKQLEML TDPSVSQQINPRNTIDTKDYSTHRLYQYLEGENKKKELFLTHGN LEEVABKIKGNISLVQDQLAVSAQEHSFISKRNKDUDMLCDTL YQGGNQLLLSDGELTEQFHKVESQLMKLNHLLTDILADVKTKKK TLANNKLHQMERFFYVYFIKDEVYLKDIVENLETGSKIKAVSLE D 6530 128 2986 GAAHHGAIVQVHPLLFGSSTIMIHDLGLVFPAPAKAVVYVSDIO ELYIRVVDRVEIGKTVKAVYVVLDLHKKPFLAKYFPFMDLKLRA ASPIITLVALDEALDNYTITFLIRGVAIGGTSLTASVTNKRAGGR INSAPQGIEVFPPFRLMFRKVTILLIGATMQVTESGGPQFQSNIL FSISMESVALVSAAGLVGGLAIGNGTVSGLVOADDABTGKVVII SODLVQVEVLLLRAVRIRAPLMEMRGTGMPIYVTGITNHQNFP SFENAVPGLTFMSVVTKRDVLDLRGRHHEASIRLSGYNFAMMV LGRVKGRTGLRAVVKAVDPTSGQLVGLARELSDEIQVQVPEKLQ LLNFBIEAEQILMSPNSYIKLQTNRDGASLSYRVLDGEEKVPV VHVDEKGFLAGSSMIGTSTUIAQEPFGANOTIIVAVKVSPVS YLRVSMSPVLHTQNKEALVAVPLGNTVTTVHFHDNSGDVFHAH SSVLNFATNRDDFVQIGKGPTNNTCVURTVSVGLTLLRAVWDAKH PGLSDFMPLPUQAISPELSGAMVVGDVLCLATVLTSLSGLSGT WSSSANSILHTDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQRATASKVIAVGBSSNLRGECTPT QREVIQALHPSTLISCOSGFRAVVEDFPSQDVFTVEPQFDTALG QYFCSITMHRITDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPPSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITTYVGVLDEAAGSGGELSTLITESSP VTNQAIAIPVTVAFVVDRRGGFBYGASLFQHFLDSYQMFFTLF ALLGGTAVMILATVHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASEDEVPDIRTCHFCLVEDFSVGLISGSEKCTISSS SLCMVTITYYDVKVFFLVRGCGQVISVRCOKRMTYFAEYWYQA QCCQYDVCNSWSSPQLOSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNPHAGTEPDGLDEMVTLSLNLGLSFAELRRMYLFINS SGLLVVPQAGLLTPHPS	}			WORLD PERDI ENABLO IN ANTICO CONTROL OF THE PERDI ENABLO IN ANTICO CONTROL OF THE PERDICAL PROPERTY OF THE PERDICAL PROPE
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LEEVARKIKONISLVQOQLAVSAQEHSFIJSKRINKDVDMLCDTI. YQGGNQLLSDQELTEQPHKVESQLNKLNHLLTDILADVKTKKK TLANNKLHQMEREFYVYPLKDEDYLKDIVENLETOSKIKAVSLE D GAAHHGAIVQVHPLLPGSSTIMIHDLCLVPPAPAKAVVYVSDIQ ELYIRVDKVEIGKTVKAYVRVLDLHKKPFLAKVFPFMDLKLRA ASPIITLVALDRALDNYTITFILRGVAIGGTSLTASVTNKAGQR INSAPQQIEVFPPFRLMFKVTLLIGATMQVTSEGGPQPQSNIL FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDABTGKVVII SQDLVQVEVLLIKAVRIRAP_MMRRTGTQMPIYVTGITNHQNPF SFGNAVPGLTFHWSVTKRUVLDLRGRHHBASIRLPSQYNFAMNV LGRVKGRTGLRAVVKAVDPTSGQLVGLARELSDEIQVQVFEKLQ LLNFBIEARQILMSPNSYIKLQTNRDGAASLSVRVLDGPEKVPV VHVDEKGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKUSPVS YLRVSMSSVLHTQNKEALVAVPLGMTVTTVHPHDNSGDVPHAH SSVLNFATNRDDFVQIGKGPINNTCVVRTVSVGLTLLRVWDAKH PGLSDFMPLPVLQAISPELGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQBATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITHHRLDTXGCKRHLSMKYRALVVSASLSSSHSTEGVCA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITTTVGVLDPAAGSQFLSTTLTFSSP VTNQAIATPVTVAFVVDRGGGFYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRRSPGKSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH BASIPPSASPPSASPDVPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKWRFLVRGCGQYISYRCQEKRNTYFAEWYQA QCCQYDYCNSMSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDFMVTLSLNLIGLSFAELRRMYLFINS SGLLVUPQAGLLTPRPS			ĺ	TDPSVSOOTNPRNTTOTKDVSTUDI VOU BOSSWITTER
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VHVDEKGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVPHAH SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQBATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKKKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGFGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASFDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKVRFLVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPWTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	1		Ì	LINERIERECTI MODIFICATION OF THE PROPERTY OF TH
YLRVSMSPVIHTONKEALVAVPLGMTVTFTVHFHDNSGDVPHAH SSVINFATNRDDFVQIGKGPTNNTCVVRTVSVGLITLLRVWDAKH PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQRATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGEGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFINS SGLLVLPQAGLLTPHPS	i i			WHYDRYCEL ACCEMICITED THE ACCEMICITED AND ACCEMICITED ACCEMICAL ACCE
SSVIMFATNRDDFVQIGKGPTNNTCUVRTVSVGLTLLRVWDAKH PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQBATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLISNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS]	ì	ì	VI.PUSMSDIJI. UTONKENI UNIDI CIMUMBUMININI UNIDI CIMUMBUMINI UNIDI
PGLSDFMPLPVLQATSPELSGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQBATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQABILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGGGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQLQMFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS		j	ł	SSVINFATNEDDEVOTORGENATORGENETICS
WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQBATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTYGVLDPAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGFGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSPQLQSSLPEPHDRPLALPLSDSQIQMFYQAL NLSLPLLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS			j	PGLSDFMPLPVLOATSPELSGAMMGDWGCLATMTTCLTCC
SVPQRIMARHLHPIQTSFQEATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTUGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFCHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKVRFLVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPWTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	1			WSSSANSILHIDPKTGVAVARAVGSVTVVVEVAGULDTVVEVAG
QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAGSQGPLSTTLTFSSP VTNQAIAIPVTVAPVVDRRGEGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKVRFLVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPWTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS			j	SVPORIMARHLHPIOTSFORATASKVIVAVGDRSSNIAGECTDT
QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLISNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAGGSQGPLSTTLTFSSP VTNQAIAIPVTVAPVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPWTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS			1	QREVIQALHPETLISCOSOFKPAVFDFPSODVFTVEPOFDTALC
EVPFSPGLFADQAEILLISHNYTGSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAGGGPLSTTITFSSP VTNQAIAIPVTVAFVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQVDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS			ł	QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEOVCA
PAVLAFAKEKSFGWPSFITYTUGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS				EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLRUKSGS
VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYHYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	j			PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSOGPLSTTLTFSSD
ALLAGTAVMI IAYHTVCTPRDLAVPAALTPRASPGHS PHYFAAS SPTSPNALPPARKASPPSGLWS PAYASH PSASTPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS			1	VTNQAIAIPVTVAFVVDRRGPGPYGASLFOHFLDSYOVMFFTT.F
SPTSPNALPPARKASPPSGLWSPAYASH PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSE SLCMVITIYYDVKVRFLVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS		}	1.	ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQNFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	653.			SPTSPNALPPARKASPPSGLWSPAYASH
SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	0531	845	1425	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS		ļ	1 :	SLCMVITIYYDVKVRFIVRGCGQYISYRCOEKRNTYFAEYWYOA
NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	!	1		QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSOIONFYOAT.
SGLLVLPQAGLLTPHPS	ļ		1	NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
954 AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGLIKGVAPPTL	6532			SGLLVLPQAGLLTPHPS
			954 2	AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGL1KGVAPPTL

SEQ	Predicted	Predicted end	Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
- 1	sequence		\=possible nucleotide insertion)
		 	TTDSTGTHING TUTTING THE TRANSPORT OF THE TOTAL OF THE TOT
i		1	ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
	1		QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
		j	QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
1	1		PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
]		DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
1	Į.	ļ ·	LQLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
1	1		ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
			GAKLCSKLKAELKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES
1			AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
1			KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
1			FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES
	'		ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
			LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD
			KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS
-			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGEVPA ANNO
			GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLOTLSFLFSGDLA
ŀ			EKSLQCFPCSAMLLELIPLLGIHFVLRTARAOSVTOPDTHTTVS
			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
1	!		LEKKEKEDESFOLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
6535	250		PHCPQGL
6555	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
1 1	ſ		ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKT.
			TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD
1 1	ſ		LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW
1 1	J		DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
6536	242	1174	SEINFSFSRSFASSGRWA
		/-	SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
1	i i		LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS
1 1	ľ		LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
]	i		GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
1 1			IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
j]	1		DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC
		ł	bi
6537	1638	921	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
†	1		FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV
1	İ	l	DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
]]	1		LALFGEPQWAVVGDTFPVGCRPOASVVFCDSTFODNPDIODDPV
		!	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
L			AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEOLRRLTKOVOE
1			ARHNRDDEAIKKAVNEYDETMEKYIPVLMAOAKIYWNLENYDMV
j		1	EKIFRKSVEFCNDHDVWKLNVAHVLFMOENKYKEAIGFYEDTUK
1	ł	1	KHYDNILNVSAIVLANLCVSYIMTSONEKAEELMRKIEKEEEOI.
		i	SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPVN
1 1	1	1	KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIOECVOFLGHC
			BLYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
6539			NK }
	218	339	FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
6540	3	391	LERLWLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDR
I	}	Į.	KQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLP
			IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	1	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
1		i	RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
1			RSSSLQGMDMASLPPRKRPWHDGPGTSBHREMEAPGGPSEDRGG
l	Ì		KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
f	ĺ	i	SRGGRSGSNWGRGSNWNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
1	_		KRGFLSKKTAEASRWHEKWPALYQNVLFYFEGEQSCRPAGMYLL
	i		EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE
	1		
	İ		LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLVQIVET
1	1		EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
1	ł		DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
			NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
]		VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
i .	į .		LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
			LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
			ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQG
			SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
ł	ŀ		SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
			KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
!			TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPOIR
1			YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
1	ĺ		IXKRPFTSIPVRSLELFFATSONNRGEHLVDGKSPRLCRKFSSP
1			
	ļ. :		PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS
1			PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRVDLCNK
		:	LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
			YROPGGOTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC
1			DKEFIIRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE
i			EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
			MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGWMKLDK
1			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
	l j		ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD
l			KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
1			PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
1			LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
1 1			LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
			YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
]			TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
1			SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
[•	SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
			LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	79	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS
		, ,	
j l	. 1		EPSDTDPEPRTLNPSPAGWFVQQHPBLELMSSFRERFGRNWLQY
			RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQEEAR
[İ		GPQESPQKMSEEVRAEPQEEEEEKEGKEEKEGEMAPLPEAHLG ,
			EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAYNGDN
ļ	Ì		CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
<u></u>			SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
6546	1657	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
	i		SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICANPCKQ
	ĺ	Í	IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
	ļ	İ	
	1		HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
			PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
1			EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAPTVAVSIIA
			KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP

SEQ	Predicted	Predicted end	7
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- [location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Walter Territorian, Vavaline,
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
L	sequence	i -	\=possible nucleotide insertion)
	1	 	TPILOKYPETFORY VOICE MARKET TON)
1			TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRRQLMAA
			EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLADAL CCODCMMDCODD CCCC
ĺ		Į.	LHSKYLAPALCSQPGMMRCCRRRCCCRQPPHALRPLLLLPLVLL
Ì		[PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
	ļ		NDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA
			PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL RPLA
6548	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAYVPIETDAEDG
L	ļ		IKGCGITFTLGKGTEVGELKILSRFQNA
6549	73	1490	ETGRYCEDARDACCCRCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
1 !			ETGRVCEDARPACGSRSRRRRKEAAPGIPTPSPSSSSPTSSRPA
			ARAFSKAPARLSRPRAREEPPDPGRRYTQBEIIQARKHKLIKMC SSVAAKLWFLTDRRIREDYPQKEILRALKAKCCEEELDPRAVVM
			DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVQSDSDIT
1 1			VLRHLEKMGCRLMNRPQAILNCVNKFWTFQELAGHGVPLPDTFS
			YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA
			DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST
1 1			DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSNILGMDVCGIDLL
1			MKDDGSFCVCEANANVGPIAFDKACNLDVAGIIADYAASLLPSG
1 1			RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
L CEES !			PESTERELLTKLPGGLFNMNOLLANEIKLLVD
6550	2293	922	FRVSRDGAPDCGIEOMGLAMEHGGSVARACGSSDGCWVVIDVE
1 1			LEVSLIGHTILGLVLFMVYGNVHVSTESNIOATEDDARGIVGO
1			LLGLTASQSNLTKELNFTTRAKDATMOMWI.NAPPDT.DDTMAGED
i i			QCQGDRVIYTNNORYMAAIILSEKOCRDOEKDMWKGCDXLLEMT
1 1	1		NORVETLEVELAKEKTICTKDKESVLINKRVAREOLVECTVPDE
1	ĺ		LOHQERQLAKEQLOKVOALCLPIDKDKFEMDI.PMI.WDDGTIDDG
i 1	1		LUNLGINLYHPLGSELASIRRACDHMPSIMSSKVEET.ADGLDAD
1 1	ĺ		IBRVARENSDLQRQKLEAQQGLRASOEAKOKVEKEAOADEAKLO
1	I		ABCSROTOLALEEKAVLRKERDNLAKELEEKKREAEOLDMELAT
1 1			KNSALDTCIKTKSQPMMPVSRPMGPVPNPOPIDPASLEEFKRKI
6551	157		LESQRPPAGIPVAPSSG
""	13/	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
			ADIVOLNWCVISDMEVIELNKCTSGOSFEVIIKPPSEDGUPPEN
		Ì	ASLPRREDPSLEEIOKKLEAAEERRKYOEAELLKULAEKDEUED
			EVIQUALEENNNFIKMAKEKLAOKMESNKENRRAHI, ADMITTIO
6552	157	746	EKDKHAEEVRKNKELKEEASR
	-37	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
	1		ADIVOLNWCVISDMEVIBLNKCTSGOSFEVILKPPSFDCVPFFN
ļ		i	ASLPRERDPSLEEIOKKLEAAEERRKYOEAELLKHIAEVDBURD
ſ	Į.	1	EVIQKAIEENNNFIKMAKEKLAOKMESNKENREAHLAAMTERTO
6553	2		EKUKHAEEVRKNKELKEEASR
1	- ,	100/	FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD
1			EYLTGPFGLIAQYSLLKEHEVEKMFTI.KGNDI.DADWWWXXXEEL
1		1	RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD
1		1	LGVLGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS
ļ	l		LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG
. 1	}	[]	SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS
·		j ,	YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN
1	ļ		FNAVGSVLSKKAKI ISAAFEERHNAKTVGEIKOFVSOI.DUMON N
ļ	1	1.	RGSLANHTSIABLIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN
4	· · · · · · · · · · · · · · · · · · ·		
1	1	1	YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT
			IGYEHILTLHNLEKAGLLKPOTGGRNNYPTTRKTI.PLWMDDIAE
			YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAOLLSRPGWRSIEEVLRTLPGPUF
			IGYEHILTLHNLEKAGLLKPOTGGRNNYPTTRKTI.PLWMDDIAE

SEO	Predicted	1 5-232 1	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cvsteine
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ı	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	_	\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
			KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFDOGLAMGID
i	İ		LKNQMVLLQGGEALPFSHLILATGSTGPFPGKFNFVSSOODATO
1			AYEDMVRQVQRSRFIVVVGGGSAGVEMAARIKTEVDRKEVTT.TH
1		j	SQVALADKELLPSVRQEVKEILLRKGVOLIJSERVSNIREIDIN
1			BYREYIKVQTDKGTEVATNLVILCTGIKINSSAVRKAFESRIAS
			SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANTAV
1			ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
6555	3,550		VRLTKSRDLFVSTSWKTMRQSPP
0333	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
f			TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANTI.FVVVG
	1		LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
ļ			LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVQGDIQELYDTTLA
1	i		LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG
			ISPSTCSFNPGVIVANMTEWKHQRITKQLEKWMQKNVEENLYSS
1			SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
6556	241	1449	QEAKLLHWNGRHKPWDPPSVHNDLWESWFVPDPAGIFKLNHHS
1		7447	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
i			PAALKAFRRLVNSQGQLRVPVVFVTNAGNILQHSKAQELSALLG
1			CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR
1			NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
			WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
			YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
1 1			LQKATHDGAPBLGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
1 1			STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
			KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
1			KSPQSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
1 1			SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWORC
1 1			QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
1 1	1		MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPATI.DC
1 1	į		EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
1 1	Í		PECLAPVDLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
ĺ	i		ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP YSO
6558	21	1138	
1			FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEFAS VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
1			SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
			GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
i i			NYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
1	İ	1	VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
	1	1	ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCOYTWD
1	1		TOMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
			DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANOTPIAMDCCASRSCSVPTGPATTICSS
1		1	DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPQPCVPTCF
			LLNSCOPTPGLETLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLQVRDTSSRIAKG
1			GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESQLTPC
İ	ļ		IRNVTSPTRQHHVEREKDHSSSRPSSPRPQKASPNGSISSAGNS
ļ		1	SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
1			NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAR
l		f	GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
ł	1		TIKCRDLSALMHELSNDGARROFEFYLEEMILPLMVASAOSGER
			ECHIVVLTDDDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE

S	EQ	Predicted	Predicted end	I Produce the second se
) :	ID	beginning	nucleotide	
N	o:	nucleotide	location	Managarine, Cattle on Danagaria hada n
		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>		sequence	-	\=possible nucleotide insertion)
1				NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
				YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
				QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
65	61	3	1086	PGRRFRRKESSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
	l			PCPMAALTDLSFMYRWFKNCNLVGNLSEKVVFTTGCDCGROWT
	- 1		1	ARQUVURGMQVLAACFTEEGSOKLORDTSVRIOTTII.DVIIIVORG
	ł		İ	I LAAAQWVRDKVGEQGLWALVNNAGVGI PSCPNEWI TVDDETVVI
- 1	- 1			INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGVG
- (f]	VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNVRTATI.GVENT DO
				RMRKLWERLPQETRDSYGEDYFRIYTDKIKNIMOVAFDDURDUR
	j			NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKI,PTPVTDETI.CDV
656	52	1		LPRPADSV
	-	_	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
	1			LIEWFLGKRSEGVPVSGPMLIEKAKDFVEOMOLTEROUVEGGGWT
				WAT KARHGI KKLDASSEKOSADHOAARORCA PEDGI A DEVOT CO.
	- 1			EQVINADETGLFWRCLPNPTPEGGAVPGPKOGKDPI TVI MCDATA
1				I GSARLAPLAIGKCSGPRAFKGIOHI, DVAVKAOGNALIUDVETEG
				DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
1	- 1	1	•	SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEEE
1				LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG
	- 1			REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE
1	- 1			VAAVAFDAVLRFAEROPCFSAOEVGOLRALDAVERSOOVERDER
656	-	1319		GALGAVVKVEALQEGPGGCGATAOSPI,PCSSTACDN
1	٠. ا	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLOGGHLPPPAUDOTEX
	ĺ	Ĭ		HEHPLPCDQMFWRQMGGHLRMVEANSRGVJWGTGVDUTALTDVTG
	- 1		i	GIGGGLEQGLASSTSNIYTOSDVKCVHTVENODUNDUTCVTGDG
			i	LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG
1		į		TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
ļ		j		EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
1				ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV YPSQPAGDCWYHIPSPROPEN YOUNG GOVERNOON TO THE PROPENCY OF THE PROP
1			1	YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDENGNLWYRQ GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
1	1		1	RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
				SQEQEPSAPPEAHGPVCC
6564	•	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE
1			1	REALETHF GFETVSEEEKGGKVYOVFESVAKKVDVMMDMMCT.CT
j				HRVWKULLUWKMHPLPGTOLLDVAGGTGDTAFRFI.NVVOCOUOD
i .		1	1	AURROLRAGONLSWEEIAKEYONEEDSLGGSRVVVCDTNVPMT.V
			ľ	VGRQRAGAQGYRAGLAWVLGDAEELPFDDDKFDTVTTAFGTDNI
į			1	THIDQALQEAHRVLKPGGRFLCLEFSOVNNPLTSPLVDLVCFOU
ł			i	1PVLGEVIAGDWKSYQYLVESIRRFPSOEEFKDMIEDAGFHKVT
6565		1464	999	YESLTSGIVAIHSGFKL
ĺ	ı		333	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
			1:	AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT
	_	1	1,	VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS
6566	T	3	1385	LLPAFPVLLVSLSAALATWLSF
1		.		KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAWAQG
	- 1			HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF
	-	J] [STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
		1	15	TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP
	-		16	CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
			1 1	LITATSVAIWVVWIVMYTYGNKOHNSPTWDDPTIATALANAW
			i P	WVLFYVIPEVSQVTKSSPROSYOGDMYPTRGVGYETTI.KEOKG
				SMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL

SEQ	Predicted	Predicted end	lamino agid gogment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA
L			ATPPKDGKNSQVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDGDFN
1		1	YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD
1			LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL
1			AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMOTAESESA
			MESHSLLNPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
L		l	ALLSLGIAYYVSGVLPFVENQPBLVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTELFHPTLASISSPM
Ì			LEGAELYFNVDHGYLEGLVRGCKASLLTQODYINLVOCETLEDL
		•	KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGEFRYFRNHS
}	ĺ		LEPLSTFLTYMTCSYMIDNVILLMNGALQKKSVKEILGKCHPLG
			RFTEMEAVNIAETPSDLFNAILIETPLAPFFQDCMSENALDELN
i		•	IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF
1			IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAQAEDFDQMK
1			NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNRQF
6569			HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPQRLGHGRPTPLLCRWRTAGPSHWEKQARAFQGLRPVDPR
1			RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
1			AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
Į.			HHLMDKQGVYVTSPLVNNFTMHSDLGKI1QSLLDEFWKNPPVLA
			PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV
1	ł		ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSQNG
			FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK
1			QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM
			KSTFEKKMOROHELSESCSASALQARLKVAAHEAEEESDNIAED
			FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA
6570	330	1304	ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP
		230%	PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG
	J		LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGLVDARF
			PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ
ļ	.		EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE
!	1		FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRODHL
j	ł		RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA
L			SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLQKLTDTLTKNCKHLFRGFDXDNDGCVNVLEWIHGL
	Ì		SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKOP
			SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYELAVREETLLL
			EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM
6572	49	1646	TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN
			LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNENDNRV
			QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELOLKOEEKI.AM
l i		İ	BLAKLKHESLKDEKMRQQVRENSIELRELEXKLKAAYMNKERAA
	Ì		QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA
		1	KAQYYLDLEKQLEEQEKKKQEAYEQLLKEKLMIDEIVRKIYEED
			QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII
			EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLEEMLRQRED
			LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA
		1	LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE
1	1	İ	HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE
ļ	ĺ		RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI
CEE-			CEEK
6573	767	275	GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK
- 1		1	LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL
			TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR
		· · · · · · · · · · · · · · · · · · ·	

SEQ	Predicted	Predicted end	Amino agid as
ID	beginning	nucleotide	This was acquent containing class and a
NO:	nucleotide	location	Managarde, Cacvareine Dalameria x - 12 -
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	n=nistidine, l=Isoleudine, K=Tareine
l	to first		L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
ì	residue of	residue of	(S=Serine, T=Threonine, V=Valine
ŀ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Hnknovm + Ch.
		sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
1	}		LAREROAOLEECKIKERREEL AGEGREE AGEGREE
Į.	1		LARFROAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK
ļ			KVAQIQNAGLGEFRIRDLNDEINKLLREXGHWEVRIKELGGPDY
1	1		GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
	}	į	PRKTRAELMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
1	1	1	AWAABREARLARGEKEEEEEEEEEINIYAVTEEESDEEGGOEVO
ſ			GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLOKYASETLOAO
6575	772		SEEARRILGY
1 03/3	117	820	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFPPFPPP
	İ		ASPERQUEETEPDEESGNGAPVPVPPKPTVKPNTDVLDAODI +
	1		SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
1			LQFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
i			AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQQRIER
	1		NKQLALERRQAKLP
6576	1	1060	PEPOALVGOKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
[1 1		RETPALADOUEDGI GUDUNGUGO DE COMPANDO DE CO
	1		RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
1		•	GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV
	[VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
ļ.	1 1		YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
1	1 1		AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPPGOEEALRDR
i			HGNLPYDVTSPALCDTHLHPRNOLAGPPLETTOEAGEMUEUDSG
	1 1		WHRQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPFLGWNGVAH
6577	2271	987	G
	/-	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
	1	j	TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSPSPSPGPGCPUP
ł		i	DESWORKINGSESRSRDHRREDRVHYRSDDI.ATGVDVCUCVCDIV
1	!		REKSPYREPVDNLSPBERDARTVFCMOLAARIPPDDLEDEEGAL
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i i	1		VP11VQASQAEKNRLAAMANNLOKGNGGPMRT.VVGGT.UENTTDD
1	i i		MERGIFEPFGKIDNIVLMKDSDTGRSKGYGFTTFSDSFCARDAT
1 1	' !		EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
i i	1		RFQLMAKLAEGAGIQLPSTAAAAAAAAAAAAQAAALQLNGAVPLGA
		j	LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
1 1			LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
1 1			VTTLLCKGLSALAACODCATERROSPSEREDTPIFVTFYQCL
1	1		VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
1 1	i		MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
1		1	LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
<i>i</i> 1	1		YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLGELQALRDF
1		1	AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA
	1		AACAQIVLAVLYYEETKSFLWWTSNMMVIGGSSAVTKRIDGWENY
6579	2		KTPEEPSPKDSEKSAMGV
	-	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
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		1.4	EDIPKEVLMDCAHLVKANSIOGCKMNNVNVVVTDWGNI VVTD DA
	l l	1.	DVGQIGFHRQKDVKIVTVEKKVNEILNRIEKTKVEDEDDLAABE
	i	1	ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
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	i] ;	RPPQEQVGPLMVKVEEKEKGKYLPSLEMFRQRFRQFGYHDTPG
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j	į	7	WVORHCPESAFFAUTI I PDI EDEL CONTROPLITIEDELO
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i		12	KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
_ 1		1,2	DPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE
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amino acid sequence sequence adjunce adjunce adjunce cood, /=possible nucleotide deletion,	1			S=Serine, T=Threonine, V=Valine
Codd, /-possible nucleotide deletion,				W=Tryptophan, Y=Tyrosine, Y=Unknown +-ch
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487 41 RIFSMISGRINGTOPTALMSSISELLETSMIFSPRSISE LSMMLSLPSNIKGLSPTALMSSISELETSMIFSPRSISE LSMMLSLPSNIKGLSPTALMSSISELETSMIFSPRSISE RSPSPLGRLQVLPRSPLHWITHNSGKEVLGLQVGRSRGTGPAC SQAGSGAVGGGMCIP PLEMALGESSGNUTEYVVRVPKNITKKVNIMAFNAADKVNFAT WNQARLERDLSNIKKYQSEEMPESGAGSFRIKLREBARRKKYG IVLKEFRPEOPPHLIGWYGKKGGRYGKGKGVTENTSYYYFTO CPDGAFFAPPVINWYNFTPLARHRTUTAEBAEEMERRIKVIG SDASDASGEGGGRVPKAKKAPLERIKKKGKGVTENTSYYYFTO CPDGAFFAPPVINWYNFTPLARHRTUTAEBAEEMERRIKVIG DDGDFSGGEVDYMSDGSSSSGEPESKARAPQGESGFKGVLDEMS SDASDASGEEGGRVPKAKKAPLERIKKKKGGKKKKKKKGDDEAFPED DDGDFSGGEVDYMSDGSSSSGEPESKARAPQGESGFKGVLDEMS SDASDASGEEGGRVPKAKKAPLERIKKKKKGUKKKKKKGVTENTSYYYFTO DDGDFSGGEVDYMSDGSSSSGEPESKARAPQGESGFKGVLDEMS SDASDASGEEGGRVPKAKKAPLERIKKKKKGUKKKKKKKGDDEAFPED DDGDFSGGEVDYMSDGSSSSGEPESKARAPQGESGFKGVLDEMS ESDIDSEASSAFFMAKKKTPPKRRKFSGGSSRGNSRPGTPSAE GGSTSSTLRAAASKLOGCKRVSEMPAAKRLEIDTGPGSLSGKST RQPPSGKTTPNSGDVQVTEDAVRYLTRKPMTTKDLLKKRFOTKK TGLSSEQTVNVLAGILKRLOPERAMINOKHTSLKKE GFIRMSTDDFVGGDFRAEASCSVLISKFHAMADSRDFASDOM HMKEGRAAQKADVLITTGAGMPVGDKLINVITUPGPGPLLVODVVF TDEMALFDRRITEPEVPLARCAGAGVFFAVKFYTEDGNWDL VINNTPIPFIRDTPIRDTPIPFIRDTPIPGFAVKFYTEDGNWDL VINNTPIPFIRDTPIPFIRDTPIPFIRDTPITKYSKAKVFE HICKTPIAVRFSTVAGESGSADTVRDRRGRAVKFYTEDGNWDL VINNTPIPFIRDTPIPFIRDTPIPFIRDTMALATKKYPSW TYTYQUWIFFNQASTFPPRPFDTMAWGGHTKAUNDMVDFWSLR PSSLRQVSFLESNGTGDAFPRAVANGYGGHGMADNGGAPNTYPBISF GAPEQOPSALEHSIQVSGEVRFNTANDDNVTQVRFYVNVLNE EQRKRLCENIAGILKDAGIT JCKKAVKNFTETVIPDYGSIIQALL DKYNNEKPKNAIHTFVQSGSHLAAREKANL DVFSDSSMDHFGKFLFTVGGGGFSGAGGAACTAGVGG SCSAGQYGSDQCHLGSGSGAGGTGGAGGGAACTAGVGG SCSAGQYGSDQCHLGSGSGAGGTGGAGGAACTAGVGG SCSAGQYGSDQCHLGSGSGAGGTGGAGGGAACTAGVGG TGSGDQAGGGGKHITVFKTYISPREMMODDQCVMEKFITYENHP DVFSDSSMDHFGKFLFTVYGTGPRAMGVDQCVGASGF POGYOPFSMEQLAMLPSVVQHGFKVIVICHMYNSRRDLD LIFPDLVEGLVNNTDPRKGWILVDARAKISGLTSTLPDTVLSH LIFPDLVEGLVNNTDPRKGWILVDARAKISGLTSTLPDTVLSH LIFPDLVVBLVNNLTDPRKGWILVDARAFELOGGRAVALKFA LIFPDLVMCLVNUTDPRKGWILVDARAFELOGGRAVLAKFA LIFPDLVMCLVNUTDPRKGWILVDARAFELOGGRAVLAKFA LIFPDLVMCLVNUTDPRKGWILVDARAFELOGGRAVLAKFA		<u> </u>		QUETSTLVETIRQSIOHNNVLKPINTI.SOOMKPCMKPOPEL VDB
41 RIFSMTSGRIRWSCTURPATALWSSIELGTSSMHFSPRSISIP LSMMLSPLPSNTTGLS PTALFRS PDEARTSCRIPHLWCAPL RSPSPLGRLQVLPRSPLHWHTHNSGKEVLGLQVGRSGGTGPAC SQAGSGAVGGGWCIP PLPMAALGPSSGNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKIYQESEMPESGAGSFNRKLREBARRKKYG IVLKEFRPEDOPPHLIRVNGKSGRKFKGIKKGKGVTENTSYYIFTO CPDGAFFAPPVHNWYNFTPLARHRTLTAEBABEEWERRNKVLSH FSIMQGRILKDQDQDEDESEKSKRGRKKKKGGDEAFPED DDGDFSGGSVDYMSDGSSSSGEPRSKAKAPQGESGPKGUDEMS SDASDASGEGGGRVPKAKKAPLARGKKKKKKKGDDEAFPED DDGDFSGGSVDYMSDGSSSSGEPSSKAKAPQGESGPKGUDEGS DSSESSEERKPPEEKKEKEKEKKKKKKGHKKKKKGDDEAFPED DSSESSEERKPPEEKKEKEPEKKAPTENSKKKKTKT GSSSTLBAAASKLEQGKRVSMMPAAKKLEUTGPGSLSGKST RQPPSGKTTPNSGDVQVTEDAVRYLTKRPMTTKDLLKKRFOTKK TGLSSEQTVNVLAGILKRLMPERRMINDKMIFSLKE GFIRMSTDDFVGGDFRAEASCSVLISKFHAMADSRDFASDOM HWKEQRAAQKADVLITTGAGMPVGDKLINVITUGPRGPLLVQDVVF TDEMAHFDRRIPPERPPBPLFVHAKCAGAPVETVHTHINKYSKAKVFE HIGKTPIAVRFSTVAGESGSADTVRDRRGFAVKFYTEDGNMDL VGNNTPIPPIRDPILPFPIPPDFDLTKWPFWTHTKLUKANGEAVYCK FHYKTDQGIKALSVEDAABLSQEDDPYGIRDINALATGKYPSW TFYIQUWFFKQASTFPPNPPDLWWPHKWPHLYPDFGSHIQALL LGPNLHHPVMCPYRARVANYQBGMCMDNGGAPNYYPBSF GAPEQOPSALEHSIQYSGEVRRFNTANDDNVTQVRFYVNVLNE CQRKRLCENIAGHLKDAGIT ÇKKAVKNFTEVHPDYGSHIQALL DNYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PIPEGPASSTTMPVSGTFAPNKKKRSSKLIMBLTGGGGESSGI NGKRLCENIAGHLKDAGIT ÇKKAVKNFTEVHPDYGSHIQALL DNYNAEKPKNAIHTFVQSGSHLAAREKANL NGKKISVPDWHLEBLSLLTMRGKGFKLRCMRVEKFIYENHP DVFSDSSMDHFGNFLFVUGGGGFSGAGGAACTAGVGE GSGAGQYGSDQCHLLGSGSGAGGTGAGGGAGAACTAGVGE TGSGDQAGGGGKHITVFKTYISPRERMGVDQOKMELGIDLLA VGARGELPKKSFNTTAMPYGGYEKASKMTELITGGGOESSGI NGKGKMEDCHOEGEBEDTETPYGLLEVVGRGFKVRMRITTY HDVGLINKLCFNTFMPSDMQEIKHFVVCHVDAFGQVGASQF POGYOFPSMEQLAAMLPSVVQHFGFKVVICIGGRGAAVVLAKFA LIFPDLVVGLVVNLDPNKGKWILWDAATKLSGLTSTLDGVLGAGAVVLAKFA LIFPDLVVGLVVNLDPNKKKGCHVVUQAAREGOGGAAGAACTVALKFA LIFPDLVVGLVVNLDDPNKKWILVGHFFKVVCHVDAFGQVGASQF POGYOFPSMEQLAAMLPSVVQHVOFGFKVVICHGGRAVVLAKFA LIFPDLVVGLVVNLDDPNKGKWILWGAARAKLSGLTSTLDGVLGAGAVVLAKFA LIFPDLVVNLTULDDPNKGWILWGAARAKLSGLTSTLDGVLGAGAVVLAKFA LIFPDLVVNLTULDDPNKGWILVORANDKINGLDFTUTT				ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLOKIDAR
ATT-SMISSLENNINGCUMPASTERSPERIATSCREIN-HUNCRAPL RSFSPLGRLQVLPRSPLHHTHNSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGGMACTP PLPKAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDISNKKIYQEEEMPESGAGSFPRKLREERRKKYG LVLKEFFRPEDQPWLLEVMGKSGRFKRSSELRIHDTYSYTFTO CPDGAFFAPPVINWYNFTPLARHRTUTAEBABEEMERRNKVINH FSIMQGRIKLDQDODDEDEEMEKRKSGVIENTSYYTFTO CPDGAFFAPPVINWYNFTPLARHRTUTAEBABEEMERRNKVINH FSIMQGRIKLDQDODDEDEEMEKRKSMSSELRIHDLEDDLEMS SDASDASGEEGGRVVAKKKKAPLAKGGKKKKKKGSDEAFEDS SDESSESEBEKPPEEDKEEPEKKAPTOGESKRRKDSGEEDSSSE ESDIDSEASSAFFMAKKKTPKRERRSGGSGSGNSRRGTPSAR GGSTSSTLRAAASKLOGGKRVSSWPAAKRLRDDTGPSLGCKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKPQTKK TGLSSGTVINLAGILKRLNPERRNINDGSLGCKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKPQTKK TGLSSGTVINLAGILKRLNPERRNINDGSLGCKST HICKSTPLAVRFSTVAGESGSADTVEDPERGAVFYTEDGENWDL VUNNTPIPTIPTIPTIPTIPTIPTIPTIPTIPTIPTIPTIPTIP	6583	487	41	PSASVEWCRKCFGAPLI
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189 1750 PLEMALGPSSQNVTEYVRVPKNTTKKYNIMAFNAADKVNFAT WOQARLERDLSNKKI YQEEMPESGAGSEFNRKLREEARRKXYG IVLKEFRPEDQPWLLRVNGKSGRKFKGI KKGGVTENTSYYIFTO CPDGAFEAFPVHNWYNTFTLARRHTLTAEBAEEMBERNKVINH FSIMQORRIKDODDEDEEKEKGRRKASELRIHDLEDDLEMS SDASDAGSEESGERVPKAKKAPLAKGGRKKKKKKGSDDEAFEDS DDGDFSGQEVDYMSDGSSSQEPPESKAKAPQGERGPKGVDEGS DSSESSEEKPPEDKKEEEKKAPTPOEKKRKOSSEESDSSE ESDIDEASSAFFMAKKKTPFKERRKPSGGSGRMSPROFTPSAE GGSTSSTLRAAASKLEGGKRVSEMPAAKKIRLDTGPGSLSGKST PQPPSGKTTPNSGDQVUTEDANRYLITKPMTTKDLLKKFQTKK TGLSSEQTVAVLAQILKRLNPERMINDKWHFSLKE GFINNSRIDDFVGGDPAEASCSVLERSHAMADSSDPASDQMQ HMKEQRAAQKADVLITQAGNPVGDKLNVITVQHFGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGFFEVTEDITKYSKAKVFE HIGKKTPLANFSTVAGEGSDPTVGRDFFAVEYFTEDGNNUL VGNNTPIPFIRDPILPPSFTHSQKRNPQTHLKDPDMVDDFWSLR PSSLIQVSFLFSDRGI FDGHRHMNOYGSHTFKLVKANGEAVVCK FHYKKTDQGIKNLSVEDAARLSDPDTVGRDPDMVDGWLDRIFNALATSKYPSW TFYLQVMTRQAETFFFNFFDLTKWPHKDYPLIPVGKLVLNRN PNYFAEVEGLARLSVEDAARLSGEDPTVGGRDFAVPDTHKHR LGPNYLHIPVNCPYRARVANYQRDGPMCQDNOGGAPNYYPNSF GAPEQOPSALEHSIQYSGEVRFFNTANDNVTQVRAFYVNVLNE EQRKELCENIAGHLKDAQIFTGKASPDLMQGGAPNYYPNSF GAPEQOPSALEHSIQYSGEVRFFNTANDNVTQVRAFYVNVLNE EQRKELCENIAGHLKDAQIFTGKASFKLTMENGYGSHIQAL 6586 32 804 PJEPEGPABSTSTMPVSGTAANEKKASKLIMELTGGGGSSGL NLGKKLSVPRVVMLEEISLLINNGSKMFKLRGMRVEKFIYENHP DVFSDSSMDHPGKRLPTVGGGGFTSKSNGRGGSQAGG GSGAGQYGSDQOHLLGSGGGAGGTGSPAGAAGGAAGTAGVGE TGSGDQAGGGEKHTTVFKTYISPWERAMGVDPQXMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYBRASKRTFGMPKV HDVGLNHKLCFNTFFNFEDMGEITKHFVVCHVDAPGQQVGASQF PQGYGFSMEQLAAMLPSVVQHYGFKYVUGIGVAGAAVLAKFA LIFPDLVEGLVLVNIDPNGKWIDWAATKLSGITSTLPPTVLEH LFSQELVNNIELVQGNARAEDEWNSKRSTURENTSTTTTVLEH LFSQELVNNIELVQGNARAEDEWNSKENSLITHTTTT		1		RSPSDIGDIOULDESDIANTERSPOSEHATSCPRLHLWRCRAPL
PLPMAALGPSSQNVTEYURVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKIYQEEEMPESGASERNKKIKREARRKKYG IVLKEFFPEDQPHLIRVNGKSGRKFKGIKKGGVTENTSYYIFTQ CPDGAFFAFPVHNWYNFTPLARIHTLTABBABEEWERRNKYLNH FSIMQORRLKDODQDEDEEKKKRGGRKKASELRIHHLEDDLEMS SDASDASGEEGGRVFKAKKAGEDDAFFES DDGDFSGQEVDYMSDGSSSSQEPESSKAPQQEEGPKGVDEQS DSSESSEERPPBEDKKEPEBEKKAPTDEKKKKGGDDAFFES DDGDFSGQEVDYMSDGSSSSQEPESSKAPQQEEGPKGVDEQS ESDIDSEASSAFMAKKKTPPKREKKPSGGSSRGRPFOTFSAE GGSTSTLRAASKLEQKKVSEMPAAKKLRUTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKEMTYKDLIKKFQTKK TGLSSSQTUNVLAQILKRLNPERMINDKMHFSLKE GFIRNSTIDPFVGGDPRAERSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGFRGPLLVQDVVF TDEMAHFDRERIPERVHAKGAGAFGVFFVTHDITKYSKAKVFE HIGKKTPIAVRSTVAGEGSGADTVRDPRGFAVKFYTEDGINDL VUNNTPIPPIRPILPFSFIHSQKRNPQHLKDPDMVDFWSLR PESLHQVSELFSDRGIPDGHRPMNYGYSHTFKLVMANGEAVVC PHYKTQQIKINLSVEDARLSGDPDYGIRDLFNAIAGKYPSW TFYIQVMTFNQAETFFNFFDLTKWWPHKDYFLIPVGKIVLNRN PESLHQVSELFSDRGIPDGHPGHRMNYGSHTFKLVMANGEAVVC PHYKTQQIKINLSVEDARLSGDPDYGIRDLFNAIAGKYPSW TFYIQVMTFNQAETFFNFFDLTKWWPHKDYFLIPVGKIVLNRN PENLYSELGSGAFGGAFDFFNNFFDLTKWWPHKDYFLIPVGKIVLNRN PENLYSELGSGAFGTGAFDAGAGAGAGTAGAFVS DKYNNEKKNAIHTFVQSGSHLAAREKANL LGPNYLHIPVNCYPRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQOPSALERS IQYSGVEVRFYTANDDNTQVRAFVNVLINE EQRKRLCENIAGHLKDAQIFIQKKAVKWFTEVHPDYGSHIQALL DKYNNEKKNAIHTFVQSGSHLAAREKANL DKYNNEKKNAIHTFVQSGSHLAAREKANL DKYNNEKKNAIHTFVGGGGFSYSKSNGRGGSQAGG GGSGAGQGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		j		SOAGSGAVOGGNUCTE
WAGARLERDISNKITYGEEMPESGASERPRILIKEBARRKIXYG IVLKERFREDOPWILRVINGKSGRYRKGIKKGUTENTSYYIFTO CPDGAFFAPPVHNWYNFTPLARHRTLTAEEAEEEWERRINVLHH FSIMQORRIKODODEDEEEKEKGRIRKASELKIHDLEDDLEMS SDASDASGEEGERVPKAKKAKAPLAKGRIKKKKKGDDAFFEDS DDGDFEGGEVPYMSDGSSSSGEPESKAKAPQQEEGPKGVDEGS DSSEESEEKPPEDEKKERPTOEKKRIKDSSEESDSSE ESDIDEASSAFFMAKKKTPPKERRKPSGGSSRGNSRPGTPSAE GGSTSSTLRAAASKLEGGKRVSEMPAAKKLRUTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRYITRKPMTTKULKKFQTKK TGLSSEQTVNVLAQILKRINPERRINDKMHFSLKE GFIRNSRIDDFVGGDPRAEASCSVLESKPHAMADSSDPASDQMQ HMKEQRAQKADVITTGAGNPVGDKLNVITVGPRGPLLVQDVVT TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPLAVRFSTVAGEGGSADTVRDPGFPAVRYTEDGNNDL VUNNTPIPFIRDPILPYSSTHLDPDMVDDFWSLR PESLHQVSFLFSDRGIPDGHRHMNDYGSHTFKLVNANGEAVYCK PHYKTDQGIKNLSVEDAARLSGEDDFYGRDFHLENDFMVCK PHYKTDQGIKNLSVEDAARLSGEDDFYGRDFHALATGKYPSW TTYLQVMTFNGAETFFFNFFDTLIKWPHKDYLIPVGKLVLNRN PNWYFAEVBQLAFDFSNMPFGILASFDIKKLQRDAVQDNGGBAPMYYPNS LGPNUHTPURGARTFFNFFDTLIKWPHKDYLIPVGKLVLNRN PNWYFAEVBQLAFDFSNMPFGILASFDIKKLQRDAVGDNGGBAPMYYPNS GAPEQQPSALEHSIQYSGGVAFRFNTANDDNVTQVRAFYVNVLNE EQRKALCENIAGHLKDAQIFIGKAVKNFTEVHPDYGSHIQALL DKYNNAEKPKNAHTHFVQGSSTAAPEKARNL 6586 32 804 PLFEQPAESTSTMPVSGTFAPNKKKKSSKLIMELTGGGQESSGL NLGKKISVFRDVMLEELSLLTNRGSKMFKLROMRVEKFIYRNHP DVFSDSSMDHPGKFLPTVTGGTAGGGFSYSKSNGRGGSQAG GGSAGQYGSDQOHHLGSGSGAGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHTTVFKTYTSPMFRAMGVDPQKMELGIDLLA YGAKARLPKYKSFRRTAMPYGFKYAGKTAGVPKWK HDVSELGKMPECWDGEHDIETFYGLLHVVLRGSFKGNRPAILTY HDVSLIMIKLCFNTFFNFEDMGETTKHFVVCHVDAPGQQVGASOF PGGGFSPSMCLAAMLPSVVGUFKAAKLSGLTSTLPDTVULSH LFSQELVNNTEUQSSVRQJGRVVNAARLSGLTSTLPDTVLSH LFSQELVNNTEUQSSVRQJGRVVNAARLSGLTSTLPDTVLSH LFSQELVNNTEUVGNAPAEDDUVENSKLDETTTT	6584	189	1750	PLPMAALGPSSONUTEVIATRUDENTATIONAL
CPDAFEAPPUNNWINFTPLARHRILABAEEEWERRIKVUNH FSIMQORRLKOQDQDEDEEKEKRGRIKAGUTENTSYYIFTQ CPDAFEAPPUNNWINFTPLARHRILABAEEEWERRIKVUNH FSIMQORRLKOQDQDEDEEKEKRGRIKASELRIHDLEDDLEMS SDASDASGEBGGRUPKAKKAPLAAGGRIKKKKKGBDDEAFEDS DDGDFEQGEUPYMSDGSSSSOBEPSKAKAPQOEEGPKGVDEQS DSSESSEEKPPEDKEEEEKKAPTPQEKKRKDSSEESDGSE ESDIDSEASSAFFHAKKTPPKRERKPSGGSGRGNSRPGTPSAE GGSTSSTLRAAASKLEQCKRUSEMPAAKRLRUDTGPGLSGKST PQPPSGRTTPNSGDVQVTEDAVRRYLTRKPMTTKDLIKKFQTKK TGLSSEQTVNVLAQILKKLNPERKINDKMIFSIKE GFIRNSRIDDFVGGDPREASCSVLISKPHANADSRDPASDQMQ HMKEQRAQKADVLITTGAGNPVGDKLNVITUGPRGPLLVQDVVF TDEMAHFDRER IP PERVVHAKGAGAFGYFEVHADTIKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVNDPRGPAVKFYTEDGNMDL VGNNTPIFFTRDPILFPSFTIHSQKRNPQTHLKQDPMVMDFWSLR PESLHQVSFLFSDRGIPDGBRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARGSEDPDVGIRDLFNA IARGKYPSW TFYIQVMTFNCASTFPNPPDLTKVWPHKDYPLIPVGKLVLINRN PUNYFAEVEQ LAFDPSIMPPG IEAS PDKMLQGLFAYPDTHEHR LGPNYLHIPVNCPYRRVANYQRDGMCMONGOGADNYYPNSF GAPEQOPSALEHSICVSGEVARRINTANDDNYQVRAFYVNVLNE EGRKLCENIAGHLKDAQI FIQKKAVKNFTEVHPVSSHIQALL DKYNAEKENAIHTFVQGSHLAAREKANL 6586 32 804 PLPEQDASSTSMPVSGTPAPNKKKSSKLIMELTGGGGESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFALROMKVEKFIYENHP DVFSDSMDHFCKFLPTVGGQLGTAGGGFSYSKNGRGGSQAG SGSAGQYGSDQOHHLGSGSGAGGTCGPAGAGRGAAGTAGVGE TGSGDQAGGGEKHITVFKTY ISPMERAMGVDCQKMELGTDLLA YGAKAELPKYNSFNRTAMPYGGYEKASKMTPCMPKV 6587 75 1117 RRVFSLGKMPECWGGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFBDMGSITKHFVCCHUPAPQQVCASQP PQGYOFFSMEQLAAMLPSVQHFGFKYVIGIGYGAGAYULAKFA LIFPDLUEGLULVNITDPNGKGWIDMAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSVRQQIGNVVQANLALFHALFFTTT	1			WNOARLERDLSNKKTYOEEEMDESCACCERNRY REGISTRATION
CPUSAFAR PVHNWYNFTP LARHRUTABEABEEMERRINKVLINH FSIMOQRA LENDODODE DEEKE KIGGRAKS ELR IHDLEDDLEMS SDASDASGEEGGRVF KAKKAP LAKGGRKKKKKKGDDEA FEDS DDGDFEGGEVDYMSDGSSSGEPESKAR APQGEESPKOUDEGS DSSESSEER ERPEEDKE EREBEKKAP POEKKRRKOSE BESDESE ESDIDSEASSAF FMAKKTP PKRERKPSGESRGNSR PGT PSAE GGSTSSTLRAAASKLEGGKRVSEMPAKRLILDTOPGSLSGKST PQP PSGKTTENSGDVQVTEDAVRRYLTRKHMTKDLLKKFQTKK TGLSSECTVAVLAGILKRLINDERRIN INDKMHFSLKE 6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSEDPASDOMQ HWKEGRAAGKADULTTOAGNPVGDKINNTUTGPREPILLVODVVF TDEMAHFDRR I PERVVHAKGAGA PG VERVHT YTEDGINDL VGNNTP I PFIRDPILLPSFTHSGKRNPQTHLKDEPMVHDFWSLK PESLHQVSFLFSBRG I PDGRRHMGYGSHTFKLVMANGEAVVCK PHYKTDGG KKILSVEDAAR JEDGDPDVGTDFNATALATGKYFSW TFY1QVMTFNQAETFP FNPFDLITKVMPHKDYPLIPVGKLVLNRN PVNYFAEVEQ I AFDESMMPGI LEAS PDKMLGGRIFAY PDTTRHR LAPPNILHIPVNCPYRRAVANYQRDG PMCMQDNQGGAPNYYPNSF GAPEQQPSALEHS I QYSGEVRFNTANDDNVTQVRAFYVNVLNE EQRKLCENIAGHLKDAQI FI QKKAVNFTEVHEDYGSHIQALL DKYNAKEKPINAHTFVGGSHLAAREKANL 6586 32 804 PLPEGDAESTSTMPVSGTPAPNKKRSSKLIMELTGGGGESSGL NLGKKISVPRDVMLEGGLLTANGGSKMFKLROMRVEKFIVENHP DVFSDSMDHFCKFLPTVGGGLGTAGGGFSYSKSNGRGGOAGG SGSAGQYGSDQOHHLJSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGEKKHITVFKTY I SPWERAMGVDQKWELGIDLLA YGAKAELPKYRSFNRTAMPYGGYEKASKMTFGMPXV GAKAELPKYRSFNRTAMPYGGYEKASKMTFGMPXV HOVGINHKLCENITFFNFEDMGELTKHFVVCHUDAPGQQVGASOP PQGGYFSMEQLAAMLPSVVQHNGFKYLVIGGIGGAGAGYVLAKFA LIFPDLUEGLULVNIDPNGKGWIDMAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSTRQQIGNVVQNALQLFURMNYNSRRDLDD INRPGTYPNAKTLECYMVLVQDNAPABEGVYCKNSKLIPDTTTT		!		IVLKEFRPEDOPWLLRVNGKSGRKEKGTKKGGVTENTGVVJETO
SDADDASGEEGGRVPKAKKAPLAKGGNKKKKKGDDEAFEDS SDADDASGEEGGRVPKAKKAPLAKGGDKAKKKKKGDDEAFEDS DDGDFEQQEVDYMSDGSSSSGEPESKAKKKGDDEAFEDS DSSESSEERKPPEEKKEPETPOEKKRRKDSSEESDSSE ESSIDSERSASFFMAKKKTPPKREKRRKDSSEESDSSE GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST PQFPSGKTTPNSGDVQVTEDAVRYLTRKPMTTKDLLKKFQTKK TGLSSEGTVNVLAQILKRLNPERRMINDKMHFSLKE 6585 3 1678 GPIRNSTIDDFVGGDPRAEASCSVLHSKFHAMADSRDPASDQMQ HWKEQRAAQKADVLTTGAGNPVGDKLNVTTVGPRGPLLVQDVVF TDEMAHSDRRIPPERVMAKGASAPGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVMDPRGFAVKFYTEDGRWDL VGNNTPIPFIRDPILFPSFIHSQKRNPQTHLKDPDMWADFWSLR PESSHQVSFLFSDRGI PORIMMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGTRDLFNA LATGKYPSW TFY1QVMTFNQASTFPRNPFDLTKWPHKDYPLIPVGKLVLNNRN PUNYFAEVEGIAFDFSNHPOGTHAS HYANDLOVTQVRAPYDVNLNRE LGPNYLHIPVNCPYRARVANYCRDGPMCMQDNGGAPNYYPNSF GAPEQOPSALEHSIQYSGEVARFNTANDDNVTQVRAPYDVNLNE ECRKRLCENIAGHLKADAQIFIQKKRKSKSKLIMBLTGGGQESSGL NLGKKISVPRDWHLEELSLLTNRGSKMFKKRKMRVEKFIYENHP DVFSDSSMDHFQKFLFTVGGQLGTAGQGFSYSKSMGRGGSQAGG SGSAGQYGSDQQHLGSGSGAGGTGGPAGQAGRGGAACTAGVGE TGSGDQAGGGGKHITVFFTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASSKMTMPQMKV AGAMAELPKYKSFNRTAMPYGGYEKASSKMTMPQMKV PQGXGFSMBQLAAMLFSVVQHRGFKYVIGGUGGAGGATVLAKFA LIFPDLVEGLVLNILDPNGKGWIDWAATKLSGLTSTLPDTVLSH LIFPDLVEGLVLNILDPNGKGWIDWAATKLSGLTSTLPDTVLSH LIFPGLVENNATURCDVSRQQLGNALQDLFFNMYNSRRDLD INNPGTVPNAKTLRCPWMLVVGNAPLGGLYCHNAYNSRRDLD INNPGTVPNAKTLRCPWMLVVGNAPLGDFFNMYNSRRDLD				CPDGAFEAFPVHNWYNFTPLARHRTI,TAERAEEEWEDDWYNING
SDASDASGEEGGRVFKAKKAPLAKGGRKIKKKKGSDDEAFEDS DDGFFEGGEVDYMSDGSSSGEEPESKARPQGEESPKGVDEQS DSSESEEEKPPEDKEEEEKKAPTTOEKKRRKDSSEESDSSE ESDIDSEASSAFFMAKKYTPKRERKPSGGSRGNRRPGTPSAE GGSTSSTLRAASKLEQGKVSEMPAAKRIRDTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRINPERRMINDKMHFSLKE 6585 3 1678 GPINSRIDDFVGGDFRAEASCSVLHSKPHAMDBSRDFASDGMQ HWKEQRAAQKADVLITTGANPVUGBLINVTUGPRGPLLVQDVVF TDEMAHFDRRIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVADPRGFAVKFYTEDGMVDL VGNNTPIPFTRDPILPPSFHISGKRNPQTHLKDPDMVWDFWSLR PESSLHQVSFLFSDRGIPDGHRMMGYGSHTFKLVNANGBAVYCK PHYKTDQGIKNLSVEDAARLSGEDPDYGIRDLFNA LATGKYPSW TFYLQVMTFCQATTFP MPDLITKVWPHKDYPLIPVGKLVLNRN PWNFAEVEQIAFDPSNMPPGILASPDKNLQGRLFAYPDTHRHR LGFNYLHIPVNCPYRARVANYQRDGPMCMQDNGGABNYYDNSF GAPEQOPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFTGKKAKKFSKLIMELTGGGGESSGL NLGKKLSVPRDVMLEELSLLTNRGSKMFKLRMCWEKFTVENHP DVFSDSSMDHFGKFLPTVGGGLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPMERAMGVDPQXMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTPQMKV FQSYGFSMEQLAMLLPSVYGFTBAHEVYISGSPKGNRFAILTY HDVGINHKLCNTFFNFEUMGEITKHFVVCHVDAFGQVGASGF PQGYGFSMEQLAMLLPSVVQHNGEIKKVIGGGGAGVYLAKFA LIFPDLVEGLVLNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQICHWANGANLGLFINDMYSRRDLD INNPGTVPNAKTLRCEVMLVVGGNAPAEDGVVCNSKLDPTTTT				FSIMQQRRLKDQDQDEDEEEKEKRGRRKASELFTHDLFDDLEMG
DUGPFEGEVNYMSDGSSSGEPBSKARAPQQEEGPKGVDEGS DSSESEBERKPPEDKKEPERKAPTPQEKKRRKDSSESDSSE ESDIDSEASSAFFMAKKKTPPKREKKPSGSSRGNSRPGTPSAE GGSTSSTLRAAASKLEGGKRVSEMPAARKLRLDTGPQSLSGKST PQPPSGKTTPNSGDVYTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLMPERKNINDKMHFSLKE GFIRNSRIDDFYGGPPRAEASCSVLMSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGFPLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTFIAVRFSTVAGEGGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIPFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPPDHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAAALSGEDPDVGIRDLFNAIATGKYPSW TTYLQVMTFNQAETFFPNFPDLITKVWHKDYFLIPVGKLVLNRN PUNYFAEVEGIAFDPSMPPGILKSPHKMCDGLFAYPDTHRHR LGPNYLHIPVNCPYRARVANVQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRNTARDDDNTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL DKYNAEKPKNAIHTFVQSGSHLAAREKANL FLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGGESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHLLGSGGAGGTGGPAGQAGGGAACTAGVGE GGSGGGKKHITVFKTY1SPWERAMGVDPQQXMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKMTFQMFKV HDVGLMHKLCFNTFFPFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQDAAMLPSVVQHFGFKYVIGIGVGAGAVVLAKFA LIFPDLVEGLULVNIDDNGKGWIDWAATKLSGLTSTLPDTVLSH LIFSQEELVNNTELVQSYQGIGVNVONAULQLFWNMYNSRRDLD INNPGTVPNAKTLRCPVMLVVGDNAPAEBGVVENSKIDPTTTT				SDASDASGEEGGRVPKAKKKAPLAKGGPKKKKKKGGDDPADEDG
ESDIDSESSASAFMAKKTPPKERKEKGGSRGNSRPGTPSAG GGSTSSTLRAASKLEGGKRVSEMPAAKRLRLDTGPGSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEGTVNVLAQILKRLNPERKMINDKMHFSLKE 6585 3 1678 GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDFASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVUHAKGAGAFGYFEVTHDITKYSKAKVFE HHGKKTPIAVRFTVAGEGGSADTWAPPRGFAVKFYTEDGNWDL VGNNTPIPFIRDPILFPSFIHSQKRNPQTHLKDPDNVMDFWSLR PSSLHQVSFIFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVVCK PHYKTDGIKNLSVBDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYLQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFREVEGIAFDPSNMPPGIKASPDKMQDNGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRITANDDNVTQVRAFYVNVLNE EQRKRLCENIZAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAREKANL PLPEQPAESTSTMPVSGTPAPNKKRSSKLIMELTGGGGESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMEVEKFTYENHP DVFSDSSMDHFQKFLPTVGGGLGTAGGGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQARGGAAACTAGVGE TGSGDQAGGGGKHITVFKTYISPWERAMGUDPQQKMELGIDLIA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTPQMPKV FQGYGFSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LIFSQEELVNNTELVQSYQGIGVVNVQANLQLFWNMYNSRRDLD INNPGTVPNAKTLRCEVMLVVGDNAPAEDGVVENSKLDPTITT	İ			DDGDFEGQEVDYMSDGSSSSOEEPESKAKAPOOFFGDVGVDFOG
GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRYLTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERMINDKMHFSLKE GSTSNTRAAASKLOVLTGAGNPVGGDPRAEASCSVLHSKFHAMADSEDPASDOMQ HMKEQRAAQKADVLITGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTFIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIPFIRDPILPPSFHISQKRNPQTHLKDEDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGVGSHTFKLVNANGBAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFMAIATGKYPSW TFY1QVMTFRQAETFFFNFPDLITKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQLAFDFSNMPPGIKASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVARFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHEDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL DVSNAEKPKNAIHTFVQSGSHLAAREKANL SGSAQQYGSDQOHHLGSGSGAGGTGSPASGAGTAGVGB TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKMTEQMPKV TGSGDQAGGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKMTEQMPKV HDVGLNHKLCFNTFFFFFDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDDPNGKGWIDWAARKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNNYNSRDLD INRPGTVENNAKTLRCPVMLVVGDNAPAEDGUVCNSKLIRDPTTTT	i l			DSSEESEEEKPPEEDKEEEEEKKAPTPOEKKEPKDSCEESDOOF
TGLSSEQTVNVLAQILKRLNPERRMINDKMHFSLKE GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTFILAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQYHLKDPDMVMDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYLQVMTFNQASTFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSMMPPGILASFDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRINTANDDNVTQVRAFFVNVULNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKILSVPRDVMLESLLTNRGSKMFKLRGMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGB TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTPQMPKV HDVGLNHKLCFNTFNFEDMQEITKHFVVCHVDAFGQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVENNKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT	1 1	1		ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSDGNSDDGTDSAF
1678 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRRIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRPILIPPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFFLVNANGBAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYLQVMTFNQAETFFPNPFDLITKVWPHKDYPLIPVCKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASFDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGBVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQAALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGB TGSGDQAGGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKARLPKYXSFNRTAMPYGGYEKASKRMTFQMPKV GAKARLPKYXSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFFFFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGMIDWAATKLSGLTSTLPDTVLSH LFSQELVNNTELVQSYRQQIGNVVNQANLQLFWNNYNSRRDLD INRPGTVPNAKTHCPVMLVVQDNAPAEDGVVECNSKLDPTTTT	!!			POPPECKTERNAGENEOGKRVSEMPAAKRLRLDTGPQSLSGKST
GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAAQKADVITTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAPGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIPFIRDPILPPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMMGYGSHTFKLVNANGBAVYCK FHYKTDGSIKNLSVEDARRISGEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLIKVWPHKDYPLIPVGKLVLNRN PVNYFABUEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALLBIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL PLPEQPAESTSTMPVSGSTPAPNKKKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQXMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYGFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNILDPNGKGWIDWAATKLSGITSTLPDTVLSH LFSQELVNNIELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNNKTLRCPVMLVVQDNAPAEDGVVENSKLDPTTTT		ļ		TGI-SSECTIONAL ACTI EDI ANDED MATERIALITA DEL KKFQTKK
TDEMAHGRADADVITTGAGNPVGDKINVITTGPRGPILIVQDVVF TDEMAHFDRRS I PERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGRWDL VGNNTPIPFIRDPILPPSFIHSQKRNPQTHLKDPDMVMDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKNLSVEDDARLSQEDPDYGIRDLFNATATGKYPSW TFYLQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSMMPPGIKASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRPNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNABKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKNFKLRCMRVEKFIYRNHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLITSTLPDTVISH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT	6585	. 3	1678	GPIRNSRIDDEVCCODE A RASCOUL VOLUMENT SERVICE
TIDEMAHPORRRIPERVUHAKGAGAFGYEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIIPFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVFDAARLSQEDPDYGIRDLFNAIATGKYPSW TFY1QVMTFNQAETFPRNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRRRVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL PLPEQPAESTSTMPVSGTPAPNKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRCMRVEKFIVENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSQQOQHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDMAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNNKTLRCPVMLVVGDNAPAEDGVVCNSKLDPTTTT				HWKEORAAOKADVI-TTGAGNEVGDELNIZITUGBBGDELIZODE
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	SEQ	Predicted	Predicted end	
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	'A-G-duting, C=CVSCBIDE D-Yenashia yeta =
		location	corresponding	Glucamic Acid, Faphenylalanina C-Glassia
	1	corresponding	to first	namediaine, laisoleucine Katwaine
	1	to first	amino acid	Lateucine, Mamethionine, Nataragaine
	1	amino acid	residue of	Perroline, Q=Glutamine R=Arginine
	į.	residue of		S=Serine, T=Threonine, V=V=line
	1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown + Ct
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	}			A STATISKS KRAQE VEVILLS ENEMLOAKINS OFF DEBLONG TO MA
	6500		<u> </u>) BISKLCSQMEQLEQENQOLKEGAAGAGVAOAGD
	6589	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQIWLLLAICLA
				CRLLWRLGLPSYLKHASTVAGGFFSLYHFFQLHMVWVVLLSLLC
				YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA
		1		QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW
				ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL
i				FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV
				GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV
				TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSFH
- 1	-			LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHQHR
- 1				LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTEEQGYGMAY
L				TVHKWSELSWASHWVTFGCWIFYRLIG
- 1	6590	2177	656	VRAVEHULGLI FARIPTIMEGUSSA
ı	İ			VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR GSLSLDDERNTOKEGREGGER
- 1				GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
- 1	- 1	1		GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
- 1	- 1			VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
- 1				RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
ı	- 1	Ī		FQEYLQKLLQHPELSNSQLLADFLSFNGGETQFLDKILPDWNLG KIIKSVPGKLMKEKGQHLEPPIMNFINSCESPKPKPSRPELTIL
-	ľ	į.		SPTSENNKKI FNDI EKANIANDA DAMESINIAN DA DA DA DA DA DA DA DA DA DA DA DA DA
- 1	i	ł		SPTSENNKKLFNDLFKNNANRAENTERKONONYFMEVMTVEGVY DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLOCKL
		ł		EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
1	1			MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
L				VIQELFPELNKVQKEVTSVTSWM
1	6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
		1		GSLSLDDFRNTQKRGBSFGISRIGSKIKGVFKSTTMEGAMLPNY
1	1			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
Т	ì		1	VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
1	- 1		ľ	RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
	i	1	ł	FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
	J		. [KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
1		i		SPTSENNKKLFNDLFKNNANRARNTERKONONYFMEVMTVEGVY
1	1			DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
	1	1		EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
1	ł			MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
L				VIQELFPELNKVQKEVTSVTSWM
1	6592	3	1861	APEFLGSTISSGSMIDANLKLLQEAEQRLKAIVAEKFAIATKEG
	- 1		Ĩ	DLPQVERFFK1FPLLGLHEEGLRKFSEYLCKQVASKAEBNLLMV
1	ļ	1	j.	LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR
1	1	ļ	i	LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS
	ł	İ		TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS
i	l			MASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEYFMRE
	ľ			TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCL
			1.	CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN
]	1			IMHSSLOQGKPDTKGIESTDEAKMSFLVTLNNVEVCSENISTLK
1		1	l i	KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE
l			17	ELTELNSTAIKPOVOPWINSFFSVSHNIEEEEFNDYEANDPWVQ
		1	17	DELINITEOUNDERRY CLEDATADOS ACTUADA ENTRE EN DATA DE LA COMPLETA DEL COMPLETA DE LA COMPLETA DE LA COMPLETA DEL COMPLETA DE LA COMPLETA DEL COMPLETA DE LA COMPLETA DE LA COMPLETA DE LA COMPLETA DE LA COMPLETA DEL COMPLETA DE LA COMPLETA DEL COMPLETA DE LA COMPLETA DE LA COMPLETA DE LA COMPLETA DE LA COMPLETA DEL COMPLETA DE LA COMPLETA DE LA COMPLETA DE LA COMPLET
		į	13	PFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS
	j	1	[;	PFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN
	.		;	ERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR
-	5593	3		
				AFSAGSRRRGLALQRGVLGGLGGYCPCCCRRGRLLVLLLLVR
		ļ	[⁸	GGEGGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL
-				QYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR

SEQ	Predicted	Predicted end	Draine cold
ID	beginning	nucleotide	Amiro acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- {	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible rucleotide insertion)
ļ		İ	EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLLG
İ]	YLNGEASTSASIDRSAPLEIGLORSTOVKRAADEVLAEAKKPRI
			EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA
İ			IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSRE
	l	}	RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN
{			AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
	İ		GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP
1		ļ	IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENBTL IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQ
1	1		GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKW
	1		DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA
			DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDLL
j			NLSRKKPCGQSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE
ſ	[ARKMEEFREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNYE
ł			QKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK
			AYMLHIGTLDKVREEWQSEHIKACEAFEAQECERINFFRNALWL
			HVNQLSQQCVTSDEMYEQVRKSLEMCSIORDIBYFVNORKTGOI
í			PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP
5500			NYSLVDDYSLI,YQ
6595	57	781	PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH
			RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRKD
1 1			GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVI.SI.S
1			VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
1			GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK
6596	2	1026	QQDPSLPLLHTPIPLVSENPQ
	-	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
1 1	•		FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
1	•		KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
1 1	Ì		AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
			ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6597	2	1026	PRLPVRRYHGRRRLOGRSRGHMAEGDAGSDORONEE I FAMAA TV
F			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLOVMLDNEVPCTAD
1]		PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
[VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACOPESSVKALD
, !	ĺ		FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCPKOV
1			KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLODCEDDGETA
1 1	1	}	AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
6598	1099	410	ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
		419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
j [}	VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
	1	ļ	LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGONNSV
[]	1		FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS
		ļ	DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLOS
6599	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR
	į		MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS
[1	1	DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST
	Ì	ł	DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE
]		l	LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE
			VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN
1		-	EAVAAVTEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILMH
			RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE
		~L	THE THE PROPERTY OF THE PROPER

SEQ	Predicted	Predicted end	Amino agid comment
סנ	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
- 1			VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
	1	ì	AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
			ADDGAHSQNEKLNRYNYIEGTKMLAAYLYBVSQLKD
6600	2	934	PGRLFRVAAMESAGLEQLLRELLLPDTERIRRATEQLQIVLRAP
			AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
1		1	LKSLILTALQRETEHCVSLSLAOLSATIFRKEGLEAWDOLLOLL
1	<u> </u>		QHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
1			LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKI.TMAMO
į			TLIPIDEAKACEALEALDELLESEVPVITPYLSEVITECLEVAR
			NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
			GC .
6601	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
1]		KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPORSMAVSOPNIJM
			NHQHQQQMAPSTLSQQNHPTQNPPAGLMSMPNALTTQQQQQXI.
1	j .		RLQRIQMERERIRMRQEELMRQEAALCROLPMEAETLAPVOADV
1	l i		NPPTMTPDMRSITNNSSDPFLNGGPYHSREOSTDSGLGLGCVSV
			PTTPEDFLSNVDEMDTGENAGQTPMNINPCOTRFPDFLDCLPGT
6602	127		NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
0002	12/	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNF
1	ļ		ERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVD
1			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
6603	79	660	GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
	,,	990	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
1	l i		SGMGATGTLRTSLDPSLEIYKKMFEVKRREQLLALKNLAQLNDI
1			HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
1 1			AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC NQTGVFNQGPHSPILSLM
6604	3	688	TSTAQRQGGERMSFRGGGRGGFNRGGGGGGFNRGGSSNHFRGGG
l	1		GGGGGGNFRGGGFGRGGGRGGFNKGGDDQGPPERVVLLGEFL
			HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDE1FGQLR
			DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
1 1			GPPRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
			GGFRGRGH
6605	7	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
1	!		ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR
1			SVTLKDLDVALPI IENYKDRLLAIGEVGLDFSPRFAGTGEQKEE
	1	ſ	QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL
ļ l	ļ	-	HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
) I	}		LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIEVTT
			QNALKLFPKLRHLLQK
6606	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
1			KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE
1 1			KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
, 1		j	SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGI.
1		ŀ	VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWARD
			VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
		1	YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG
		ļ	MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
		į.	GPYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
	Ì		RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
			LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
}		j	DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIONGAIMNKGTG
			RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLLASPPRLLNTKLOASCRALFSPPIOSROTT
.	ļ	1	GISFQGRGGAGPGVPTRTOVFAAMGAVMGTFSSLOTKORRPSKD
			KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
J	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- }	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion)
į.			SGVVNEDTFKQIYAOFFPHGDASTYAHYLFNAFDTTOTCGUVEE
ł			DEVIAUSILLRGTVHEKLRWTFNLYDINKDGYTNOFFMMDTUVA
J		ľ	I YUMMGKYTYPVLKEDTPRQHVDVFFOKMDKNKDGIVTI.DEFT.E
6608	224	1110	I SCOEDON IMRSEOLFONOM
	-24	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS
1		i	TGTLQLPPQKPFGQEASLPLAGEEELSKGGEODCALEELCKDLV
			CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN
			VVEPAATFVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP
ŀ			AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
i	!		KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTFSGQFYC
6609	1	443	SMCNVGAGEEMEFRQHLESKQHKSKVSEQRYRNEMENLGYV
1			FRLRCRRFRVAGGRLAGAGLRESRVPAPEORLSALTLLSWSAVT
1			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS PATNQAAGQEEKGKAGNVKKAEEBEEIDIDLTAPETEKAALAIQ
·			GKFRRFQKRKKDPSS
6610	319	881	GRKSLCNLHIFIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
			YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
			VSLRQLEKLPSPLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL
i			DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS
			CGWDTESADEF
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSFGVDEBERVRV
			LQGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNLRAPHKEST
1 1	1		LPRSGSSGGQQPSGMKEGVKRYEOEHAAIODKI.FOVAKDEDEDA
1 1			TKHSKASLPTGEGSISHEEOKSVRLARELESPEAFIDDDDTDVV
F .			EQUERIERKNAEMYKLSSEOFHEAASKMESTIKPPPVERVCCCI.
6612	1204		QAQILHCYRDRPHEVLLCSDLVKAYORCVSAAHKG
1 3312 1	1724	992	VSTHASALSRTOGOPOROPRAAASGAGAGTAGGGGGGGGCAEGGVM
1 1			STEAQRVDDSPSTSGGSSDGDORESVOOEPEREOVODKKKEGKT
1 1			SSKIAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIVEWDG
1 1			TILGPPGSVYEGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
} }			SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI
6613	130	748	ATQYMTNRAEHDRMARQWTKRYAT
1		1	ELELSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYI
]			PTVEDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA FILVYSITSRQSLBELKPIYEQICEIKGDV3SIPIMLVGNKCDE
	i		SPSREVQSSEARALARTWKCAFMETSAKLNHNVKELFQELLINLE
			KRRTVSLQIDGKKSKOOKRKEKLKGKCVIM
6614	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPOWRALAPLGWPDCP
[į.		DSRVREKPPWRVLFFGTDQFAREALRALHAARENKEEELTDKLF
]	}		VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF
	1	ļ	GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVL-GDTVT
	}	1	GVTIMQIRPKRFDVGPILKOETVPVPPKSTAKET.RAVI.SDT.GAN
		j	MLISVLKNLPESLSNGROOPMEGATVAPKTSAGTSGTVWFFORG
	1	ļ	EQIFRLYRAIGNIIPLOTLWMANTIKLLDIVEVNSSVIADDVID
	Į		GUALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSI.TATDEV
6615	832		NGYLHPWYQKNSQAQPSQCRFOTLRLPTKKKOKKTVAMOOCTE
		35	GRVGAGASAMSELPGDVRAFLREHPSLRLOTDARKVRCILIGHE
' J	j	1	LPCRLPELQVYTRGKKYQRLVRASPAPDYAEFEPHIVPSTKNDH
		į	QLFCKLTLRHINKCPEHVLRHTQGRRYORALCKYRECOKOGUEY
1		1	VPACLVHRRRRRBDQMDGDGPRPREAFWEPTSSDEGGAASDDSM
		1	TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
	ľ		EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKOS
6616	347		G LLBBCOGARDI GGDDUA CHOM
	- "	E :	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
			VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

SEQ	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
1			PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
1			PPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY
		}	KDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQEA
l l			PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG
1		ļ	EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACF
1		İ	GPCARCSGPEESNCLOCKKGWALHHLKCVDIDECGTEGANCGAD
ļ			QFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGVOOVGEVC
]			DDVDECETEVCPGENKQCENTEGGYRCICAEGYKOMEGICVKEO
l	Ì		IPESAGFFSEMTEDELVVLOOMFFGIIICALATLAAKGDLUFTA
6617	110		1FIGAVAAMTGYWLSERSDRVLEGFIKGR
551,	118	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS
1			LSYHLDTKVRCPMCWOAVDGSSSLPNVSLAWVIEALDI.DCDDED
			KVCVHHRNPLSLFCEKDOELICGLCGLLGSHOHHPVTPTGTVCG
1			RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
6618	548	136	LGPATFTFL
1	1	730	DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR
1	1		NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE
			APLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA WKYGT
6619	246	842	
ſ			PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
ļ			YFQRMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
1			YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG
			ILSDVQEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
1			DEPAPAAPLRGRKDEDAFLGDPDTDPDSFIKSARIOPI.DESSER
1			MGSQDGSPLRETRKDPFSAAAAECSCRODGLTVTVTACLTEATC
1			VTVALVMQIYFGDPQIFOOGAVVTDAARCTSIGIEVISKOGSSV
1 1	,		DAAVAAALCLGIVAPHSSGLGGGGVMIVHDIPPMEQUIIDEBE
			APGALREETLORSWETKPGLLVGVPGMVKGLHFAHOT.VGDT.DWG
)			QVLAFAAAVAQDGFNVTHDLARALAEOLPPNMSEPFPFTFT.bcc
1 1			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ
1 (HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI
1			SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD
1 1			STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT
1 1			AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
1	İ		WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTFWLAFFSREPSCGLDCRCLSYLWLV
			SIPHAANMG
6621	1	662	VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
1 1	j		AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
1 1			SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG
]			KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK
		1	LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL
6622	2	319	GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMCN
1 1			AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
6600			1FDMAGHPFFYEVRKPF
6623	1886	189	KALFEKVKKFRLHVBEGDILYAMYVROTVLKVIKFLTITAVNGA
1			LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHI,FSKI,SFCVI.CR
		i	VSIYGLTCLYTLYWLFYRSLREYSFEYVROETGFDDIPDVKNDF
	İ	ľ	AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKOLNI,NNEWTDDVI.
1	ļ	1	RQKLQTNAHNRLELPLIMLSGLPDTVFEITELOSLKLEITKNUM
1	1	į.	1PATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKEDD
1			MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKT
ļ		I I	LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNI,KKMTN
		<u>-</u>	LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ

SE(Predicted end	Amino acid coment
] ID	beginning	nucleotide	
NO:	nucleotide	location	/ /g-grantue, C=CVSCeine D-long-ria k-13 -
	location		Graduic Acid, F=Phenylalanine G-Glassin-
		corresponding	n=nlStlqine, l=Isoleucine V-tucine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W-Trent V=Valine,
l l	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	sequence	pequence	(Codon, /=possible nucleofide deletion
	bedacise		\=Possible nucleotide insertion)
- 1	1		HLRKLTVLKLWHNSITYIPEHIKKITSLEPLSESUMYISIA BOU
	1		LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
	Į	1	DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
		1	LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
6624	218	1786	GSPRCGCRITANGMINARGE TERSDAKEOMKTE
- 1	<i>\</i>		GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
ı	1		RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
- 1	1	1	REWARVITVLEMARAIPAMVVPNATLIEKTILEKVMDEDGERRIER
ŀ		ŀ	RORGERATTONOMOSILDLHNKI.RSOVVDTASMMEVMONINER
1	ł	1	RSAESWAESCLWEHGPASLLPSIGONIGAHWGDVDDDTDWDGW
1		ļ	YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
1	ľ	1	AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
j		1	ACPPSECCCOPENICAVEROPPHICAVEROPKINGHAPYKHGRPCS
i	{	1	ACPPSFGGGCRENLCYKEGSDRYYPPREEETNEIERQQSQVHDT
1			HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
Ì		i ·	PAGCLOSKAKVIGSVHYEMOSSICRAATHYGITOMDGGGTTDTTTD
1			QGRANTELKSNRNGIQTIGKYOSANSETVSKUTUOMUTODUTO
6625			QUCFFARRASHCPRVYCPRKLYASKSTI.CSCNWMSQLD
5025	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHDGDSSGGTDGGUDTAY
1		I	GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW
1	1	j	SFYGQGRKIAEVCCTSIVYATEKKQTKVEFPEARIFEETLNILI
1	ı	ł	VETERGED DALI ENTEGRA CO.
L	i i	ŀ	YETPRGPDPALLEATGGAAGAGGGGGEDEENREHRVRRIHVRR HITHDERPHGQQIVFKD
6626	3	1498	ATTADERPHGQQIVFKD
ł	i	1430	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
J			LDVPWPRSKIGSDQDSGIELLNVI.HRVII.TPEGDGIOTACT DER.
ł			RQIICAAQEHVKEKRRSAEVDDGAAEKETI.DEEGEGVDWGGIIID
1	i i		GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
1	1 1		GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
i	1		KI DCCOLSCEUN CON MOTE CONTROL OF THE PROPERTY
1	1		KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDLLRSAL
1	1 1		TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ
	1		RECIDER RATEEI KDPVVOIKTYOIJHSTROV DNDAVOV DVIVE
	1		DASCIMEKLOSIDKRKPENTAELEIFOFGIKVI, POLIUMIN 1991111
i	1		RAULVACLUPILISFLIDENSI CSATS IMPNILIDENT ON MOTO
J	1 1		PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
		1	PGKNSSIQLKTSFL
6627	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
1	1		GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
1	1	1	KLOTWOTACOER EDGLETIA TOGIOFRNKVVTVDGVRV
]	1		KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
l	1		WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
l	1	Į	FFLEISAKIGMNVELAFLAIAKELKYRAGHOADEDSEOTEDVID
6628	1 1	1861	SURRESCUSEM
	, - I	1	QCAE FGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	1 1		KEFGDSLSLEILQIIKESOOOHGLRHGDFORVEGVCGBBODD: D
			ATEM FAMGURHAFTGKKVTEELLTDNRYLLLATAMDAED AMOUND
	1	1	QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
	1		LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
	1	[EQAVLYNQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTE
	1	i i	GLIAEKLEAL TTOTTA VON AUMORITE TOTAL CONTRACTOR OF THE STATE OF THE ST
	1	1.	GLIAEKLEALITOTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
]	J.	GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
]	4 '	AVRUITLEGE PGKVSNLOYLHSYT, TV T KT, STA TV DNIENIMA WOL O
	ļ .	1	RALLQQQPEDDSKRSPRPQDLIRLYDIILONLVELLOLDGLEED
	į į	1.	RAFOREIGLKTLVFKAYRCFFIAOSYVLVKKWSEALUT.VDBULK
		1 3	IANEVNSDAGAFKNSLKDLPDVOELITOVRSEKCSLOAAATUDA
	1	1	NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP
	1	1 6	FPQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
		. 18	GFRS
6629	5653		
	1		SATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
			RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	acdacuca	Codon, /=possible nucleotide deletion,
	1 2 2		\=possible nucleotide insertion)
1	[MLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLNAFIDR
	1		KDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWS
j-			SLAVHIAMDNTVVMEBIRRLCRTSVPCAGATAFPADSDRHCNGF
			PAGAEVINRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP
			QSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFI
	1		PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM
6630	2	423	TRKTFGFLRFFFSMLG
	-	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
ļ	1		LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
1	í		NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
6631	2	433	SESMKPKF
]	-	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
i			LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
1			NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMKPKF
6632	1273	568	
1	"-'•	200	WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISAIGR
i .			GICVLLGISLEDTQKELEHMVRKILNLRVFEDESGKHWSKSVMD
			KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQAEGFYNSFLEQL
	•		RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP
Į į	,		KQLSKLEKQQQRKEKTRAKGPSESSKERNTFRKEDRSASSGAEG DVSSEREP
6633	1145	617	ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY
			AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV
	1		GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSCP
1 1			VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSNENATSNS
6634	1	1134	CGGIPRKGSGPRRLPMARLRDCLPRLMLTLRSLLFWSLVYCYC
			GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC
	ł		YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF
1	1		KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY
1	ļ		SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI
1			LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG
1 1			IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH
!!!	ł		HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH
<u> </u>			WLQQDQPDIVNKLIWTFLKEETRKKD
6635	1420	470	EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG
1 1	1		GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK
ļ l		ļ	ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG
			LVPCVVVGHSMGGKTAMLLALORPELVERI.TAVDISDVESTGVG
(l	1	j	HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL
1	i		LTNLVEVDGRFVWRVNLDALTOHLDKILAFPOROESVLGDTI.FI.
		J	LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI
			AAIRGFLV
6636	1514	1801	SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE
ĺ		ĺ	QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD
			DGGDGVF
6637	2	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI
j			KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT
	i i	}	VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
			LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG
	<u> </u>		DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
1			CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW
j	!	1	FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR
ļ	i	1	DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS
		1	TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
1	j	ĺ	RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC
			TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF
			TO TO TO TO TAKE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	L	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
1			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
			PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
	1		EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
	ļ.		RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
ł	I		VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
1			SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
1	ł		PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
1			TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
L			FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPE
			DPEECPEEVYDPRSLYERLQEQKDRKQQEYEEQFKFKNMVRGLD
			EDETNFLDEVSRQQELIEKQRREEELKELKEYRNNLKKVGISQE
			NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
1			KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
			GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
			RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
:			ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
1			KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
			NSKKTSKAEKESQVQELVELIEKMVQCNEGAYFSDDIYKDTEER
			LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK
			YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
6641	1	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
			ASAPPPRGFSAISCTVEGAPASFGKSFAOKSGYFLCLSSLGSLE
1			NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
	i		KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
			APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
			TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
			GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS
6642	22	1296	PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
1 1	1		HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
			NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
			KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
			MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
	l		NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLOEKIPV
	ľ		ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF
			IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL
	j		LDLENIQIPEAPPPIPKEPSSYDFVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
	1		DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLOYIG
	l		HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC
			SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI
i	 		CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEI.
	i		DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	1489	290	FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDOR
	Į	-	LRAONIPGDKARKVLNDIISTMFNRKFMEELFKPOELYSKKALR
			TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL
1	ĺ		LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFO
ĺ			LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
1			EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
1	1		KIGTNMYSVNOPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
ļ			LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEOAALTRPEELSY
			EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM
		ļ	DEL EVINIQATQUQQRSEBLARIMGEFEITEQPRLSTSKGDDLLAMM

D Deginning No: uncleotide location corresponding to first maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid sequence 4646	SEO	Drodd att a 3	T =	
No: Incleation location in location of the corresponding to first in corresponding to first in the corresponding to first in the first in amino acid residue of amino acid sequence seq		Predicted	Predicted end	
Coatagon Coatagon Corresponding Coatagon Coat	,			(A=Alanine, C=Cysteine, D=Aspartic Acid v=
corresponding to first amino acid serious control of the control o				Glutamic Acid, F=Phenylalanine, G=Glycine,
to first a maino acid residue of amino acid and residue of sequence sequenc	l l			H=Histidine, I=Isoleucine, K=Lysine,
### ### ### ### ### ### ### ### ### ##	- 1			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence 8-2 sequence 8-2 sequence 8-2 sequence 8-3 sequence 8-464 sequence 8-464 sequence 8-530 sequence 8-530 sequence 8-530 sequence 8-530 sequence 8-530 sequence 8-530 sequence 9-2 sequence 9-2 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-3 sequence 9-4 sequen	İ			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Con, /-possible miclocide delection, Sequence Con, /-possible miclocide disaction, Construit induction induction induction, Construit induction induction, Construit, Construit, Construi	ł			S=Serine, T=Threonine, V=Valine,
Sequence	ļ			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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ORADPRIAMAGESTALHFARBEAGHIDIVEELIKURASTAVUNGEN MTELKVAABESKADVELLISHADCORSELALELIGASTANI RENYDIIKTYHYLYLAMLERRODODNILEKEVLPPIHAYGRITE CRNFGELESIKORDALHMEGLIVERFILADILOSHIDVSHPIITYR AVVADNMEFECIKUMIALHLQKENRNTHKOLLEFAQVESOK HHINETVARPDIECVLEGSVLEITOSMEVUNSTOADVUNNAMN YECHLYTELILVCISTKTOCSEBOCKINKQIYNLIHLDOGAEVAN GPTLHLAVRSNTPYODPHTNDVCSFRALVTALLIOCGAEVAN VONEGNSALHIIVQYNRPISDPITUMUS FRALVTALLIOCGAEVAN ONETPLEETVOSHLUKTOKMMSLKCLARAVERANDINYQDO IPRTLEEFVOFH 6646 176 890 PSSRNNHLPEDMENALTGSQSSHASLRNIHSINTPOLMRAIESY EGREKKGISUVRRTECHFVFFOLLEVTILHIELAVNNGGIENTL EKEWOXDYYSSYFDITLLAVFREKVLILAYAVCHRIMMAILA THAVTSAFLLAKVILSKLEGQAFGYVLPIISFILAMFITWFLD FKVLDQBAEBENRLLIVQDASERAALIFGGLSGGYSPPESSA GSERABEKQDSKPLLEL 6647 176 890 FSSRNNHLPEDMENALTGSQSSHASLRNIHSINFDOMARIESY CGREKKGISUVRRTECHFVFFOLLEVTILLIIIELAVNNGGIENTL EKEWOXDYYSSYFDITLLAVFREKVLILAYAVCHRIMMAILA THAVTSAFLIAKVILSKLEGQAFGYVLPIISFILAMFITWFLD FKVLDQBAEBENRLLIVQDASERAALIFGGLSDGGYSPPESSA GSERABEKQDSKPLLEL 6649 1367 RSGNNCFTKYFRSPPEDIDHKDSYLITRSIMLERHMAILA THAVTSAFLIAKVILSKLEGQAFGYVLPIISFILAMFITWFLD FKVLDGBAEBENRLLIVQDASERAALIFGGLSDGGYSPPESSA GSERABEKQDSKPLLEL 6648 413 837 RSGNNCFTKYFRSPPEDIDHKDSYLITRSIMLEPDYTEDDNPEL THPOKLINFWISNHNDDJIRRLLIMNQKLPISHFILAPOKEPLAKWON KRKDQVIKOKESERAÇKKASDLEIL 6649 1357 832 WIFRAAGIRHEVKNDLRETGGUNAQAGS GEGENABERYKVKONLRETGGUNAQAGS WIFRAAGIRHEVKNDVEGINSCHUTSGHIYUDALLKEFEOFNRELNEV SKRVALDLEVSILLMERCTRLANTIVEGYANVKKORSGRALM QUPQOFINKLEKLTOIR PIPOKSFUTYIKAYLITENDMENNI KERREYSTRQUTNLVNVCLGSHINKKARQKLLAAIDDIRPRE MCLIPTYGGSPSMCAFARDPRSWMGALTRLIGGAFP QKQGSTGEFFHFQTGGRDSCTMRPSSLGGGAGEWARVDCRNTTO QTYNCEYRGGSPSMCAFARDPRSMTGALTRLIGGAFP LRPSVCREAGPBGAAMGQVTSSLKKSPPENOQPERGTESLRPAT VKLIPLATOLGIUSHBELGIKARATTRTHAVKECKCYPFYVQIR LRPSVCREAGPBGAAMGQVTSSLKKSPPENOGDESGNEAA KAWENCHKPPGALCAFLISFFR GGGDRAESTLIRREGUNARGROCIPSSM TSTWQVADDITONTLDIEVLRFAHKLKGTINGSGHSSANW FPRESSTQISIGAFFTKYKSLKEEBERYTIRGGRDSCHANSSANW FPRESSTQISIGAFFTKYKSLKEEBERYTIRGGRDSCHANSSANW FPRESSTQISIGAFFTKYKSLKEEBERYTIRGGROCIPSORD REGORAPETERVORDSCHARTSGRAFTHVTUSCBOP R				GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
MTPLKVAABSCKADVELLISHADCDRSRIBALELIGASPANI RENYDII KIYHYLYJAMERRODGONIJAHEGI LYRERIIGADSINJUSHII 1786 AVYADNIBFECIKKWIJAHEROKSINTIKOLLEPAQVISON AVYADNIBFECIKKWIJAHEROKSINTIKOLLEPAQVISON HIHINETVKAPDIECVIRCSVLEIEGSMMRVKUNISDADVHNAMIN YECNLYTEIVLUCISTVOGSEDQOKINKQIYNILIDERTER GPILHILAVISNIPVODPHTNIDVCS PRALVITALLIDOGAEVAA VUNEGNSALHIIVQINRRISDEITLHSIIISLUGAEAVAR VUNEGNSALHIIVQINRRISDEITLHSIIISLUGAEAVAR VUNEGNSALHIIVQINRRISDEITLHSIIISLUGAEAVAR VUNEGNSALHIIVQINRRISDEITLHSIIISLUGAEAVAR VUNEGNSALHIIVQINRRISDEITLHSIIISLUGAEAVAR VUNEGNSALHIIVQINRRISDEITLHSIIISLUGAEAVARANDINYQDQ IRRILEPAGH PSSRMMILPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGREKKGISDVRRITCLFVIFOLLFVITLMIIELAVVRGIENTL EKKUMQUYISSYEDIILAVPRIKVALLAVACKLERHWAITAL TTAVTSAFILLAKVILSKLFSQGAFGYVLPIISFILAMIETWIFLD FKVLPQGEEENLLIIVQUDASERAALIPGGLSGQFYSPPESEA GSERAEEKQDSKPLIEL ERREWOONYSSYSPIELLAVPRIKVILIATAVCRIRRIWAATAL TTAVTSAFILLAKVILSKLFSQGAFGYVLPIISFILAMIETWIFLD FKVLPQGEEENLLIIVQDASERAALIPGGLSGGFYSPPESEA GSERAEEKQDSKCPLIEL ERREWOONYSSYSPIELLAVPRIKVILIATAVCRIRRIWAATAL TTAVTSAFILLAKVILSKLFSQGAFGYVLPIISFILAMIETWIFLD FKVLPQBEEENLLIIVQDASERAALIPGGLSGQFYSPPESEA GSERAEEKQDSKCPLIEL TTAVTSAFILLAKVILSKLFSQGAFGYVLPIISFILAMIETWIFLD FKVLPQBEENRLLIVQDASERAALIPGGLSGQFYSPSPESEA GSERAEEKQDSKCPLIEL TRAVILTIKVILSKLFSQGAFGYVLPIISFILAMIETWIFLD FKVLPQBEENRLLIVQDASERAALIPGGLSGGAFGVUNGVSPSPESEA GSERAEEKQDSKCPLIELVILSKLFTGGAFGYVARCKCSNCGRAM KKRKDQVIKOKEEERQKKKSDLEIELLKKQQKLECLELEQKLO ERGENAPERVKKONLRETGGSVQAGEA KKRKGILPVRITSGGSTGGSVGARAALIPGGLSCARCK KKRKGILPVRITSGGSVGAGAFAKKSDLEIELLKKGGGAGEWINGVCGNTIC QLDFOGFLAKLEKLTDIRPIPDKEFVSTYIKAYLITISDMEERH KKRKGTATGGSVGAGAGA VKLITAATQLGSSHMEKKANGSVGATAMICORGAPA VKLITAATQLGSSHMEKARGGSVGARGAALATATATATATATATATATATATATATATATATATAT	1		j	GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
RENYDIIKTYHYLYAMLERRODGONILEKEVLIPPIHAYGNRTH CRNPGELESIRGNDRALIMBEGLIVER ILADAINUSUSPIITSG AVVADNMEFECIKKWIHALHLROKSNRNTHKOLLERFAQVESOM HHINSTYKAPPIECVLKEUSJENGWANISTANUS DADVUNAMIN HUNETVARPIECVLKEUSJENGWANISTANUS DADVUNAMIN YECHLYTELLVCISTETQCSEEDQCKINKQIYNLIHIDEPRTEE GPTLHLAVNSTPUDDFHTINDUS PRALVTKLILLOGASEVJA VDNEGNSALHIVQVNRPISDFITHSIIISLVEAGAHTOMTKK QNKTPLDKSTTGVSEILLKYQMMSLKCLARAVARANDINYQDQ IPRILEEPVOFH 6646 176 890 PSSRNNHIPPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGREKKGISDVRRTCLEVTPDLLEVTLHIIELVNNGG IENTL EKKYWQYDYYSSYFDIFLLAVFREVLILISYLAVCRLHHWATLL TTAVTSAFLLAKVIISKLFSQGAFGVYLHISFILAFICHHWATLL FKVLDORAFERENELLIVQDASERAALIPGGLSDGQFYSPPESSA GSERAEKKOSSKYLLEL EGREKKGISDVRRTCLFVTFDLLEVTLHIIELFWNGG IENTL EKKYWQYDYSSYFDIFLLAVFREVLILATAVCRLHHWATLL TTAVTSAFLLAKVIISKLFSQGAFGVYLPIISFILAHITEWKIGG FKVLDGRAEERNELLIVQDASERAALIPGGLSDGQFYSPPESSA GSERAEKKOSSKYLLEL EGREWGGYVYSSYFDIFLLAVFREVLILATAVCRLHHWATLL TTAVTSAFLLAKVIISKLFSQGAFGVYLPIISFILAHITEWFIGL FRVLDGRAEERNELLIVQDASERAALIPGGLSDGGFYSPESSA GSERAEKODSKYLLEL FRVLDGRAEERNELLIVQDASERAALIPGGLSDGGFYSPESSA GSERAEKODSKYLLEL FRVLDGRAEERNELLIVQDASERAALIPGGLSDGGFYSPESSA GSERAEKODSKYLLEL FRVLDGRAEERNELLIVQDASERAALIPGGLSDGGFYSPESSA GSERAEKODSKYLLEL FRVLDGRAEERNELLIVQDASERAALIPGGLSDGGFYSPESSE GSERAEKODSKYLLEL FRVLDGRAEERNELLIVQDASERAALIPGGLSDGGFYSPESSE GSERAEKODSKYLLEL FRVLDGRAEGNSKYLLEL FRVLDGRAEGNSKYLLEL FRVLDGRAEGNSKYLLEL FRVLDGRAEGNSKYLLEL FRVLDGRAEGNSKYLLEL FRVLDGRAEGNSKYLLEL FRVLDGRAEGNSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEL FRVCKERGOSKYLLEVSTUTTYTIKATHTTWERTEN FRVCKERGOSKYLLEVSTUTTYTIKATHTTWERTEN TYTTAVISTUTTYTSTOTTTSTTTTTTTTTTTTTTTTTTTTTTTTTT				QRADPNAKAHCGATALHFAABAGHIDIVKELIKWRAAIVVNGHG
CRNPGELESTRONDALHMEGLIVERSILGAMISHITIYEE AVVANNINFSCCIKKWILMALHLEKOKRINGLIRFAQVISOM HHINSTVKAPDIECVIRCSVLEIEGSMREVENISDADVENAMD YECNLYTELIVLCISTRYGCSEBOCKINGLYRNISDADVENAMD YECNLYTELIVLCISTRYGCSEBOCKINGLYRNISDADVENAMD VONEGNSALHITUOVINFJISDIFLTHSIIISLAGAEVNA VONEGNSALHITUOVINFJISDIFLTHSIIISLAGAHIDMITIKE ORTFLIBEFVOPH 176 890 PSSRMHILFEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGREKKGISDVRRTECLFVIFDLLFVTLMIILELAVNGGIENTL KEKVWODVYSSYFDIFLAVPRFKULDSRQFYSPPESEA GSERAERKGISDVRRTECLFVIFDLLFVTLMIIELAVNGGIENTL TANVISAFLLAKVILSKLFSQGAFGYVLPIISFILAMIETWFELD FXVLDQDASERALILAVORISKLFSQGAFGYVLPIISFILAMIETWFELD FSRMHILPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGREKKGISDVRRTECLFVIFDLLFVTLMIIELAVORGIENTL TANVISAFLLAKVILSKLFSQGAFGYVLPIISFILAMIETWFELD FSRMHILPEDMENALTGSGSSHASLRNIHSINPTOLMARIESY EGREKKGISDVRRTECLFVIFDLLFVTLMIIELAVGGAFGYVLPIISFILAMIETWFELD FSRMHILPEDMENALTGSGSSHASLRNIHSINPTOLMARIESY EGREKKGISDVRRTECLFVIFDLLFVTLMIIELAVGGAFGYVLPIISFILAMIETWFELD FSRMHILPEDMENALTGSGSSHASLRNIHSINPTOLMARIESY EGREKKGISDVRSTECLFVIFDLLFVTLMIIELAVGGAFDADGAEVALPORKPELDKYME GSERAERKODSKDLLEVTSSHAPPOLGGISDQFYSPPESEA GSERAERKODSKDLLEVTSSHAPPOLGGISDQFYSPPESEA GSERAERKODSKDLLEVTSSHAPPOLGGISDQFYSPPESEA GSERAERKODSKDLLEVTSSHAPPOLGGISDQFSPPESEA FRUNDERSKAPTILDVRSSHAPPOLGGISDQFSPPESEA FRUNDERSKAPTILDVRSSHAPPOLGGISDPRENEW KRKRDQVIKOKSEERAQKKSDLEIELLKRQQKEGLEERQKLO GSERAERVKONDLRRGGGAAPQNKKCSDRGFALM QLDPOQFILMLEKLTDIRPIPDKEFVSTYIKAYVILTINDMEINT GTYNCEYRGQPSMCOAFAADFSVWKCALREGTALATDDIDPRR FRHEYSTSKQINILNVCIGSHINKKARVKCSNEGRALM QLDPOQFILMLEKLTDIRPIPDKEFVSTYIKAYVILTINDMEINT GTYNCEYRGQPSMCOAFAADFSVWGMCLAAFLISFROM VILTEATQLISSHBELKGKARVTTRYTARATOPGOPPREGMEEAK KAWEHCWKPPQALCAFLISFROM VILTEATQLISSHBELKGKARVTTRYTARATOPGOPPREGMEEAK KAWEHCWKPPQALCAFLISFROM GGAGATAERTHANGONGGRAADFSVROMATSKEPLORPSKINFLORMYDCRISTD DLIBLIGGENTALDELBSTTLRGSTYKKOUPTCRYSSILMF HNNOGDMGCSSWPOMTTSLPPOHTTARGSGRADHYDCRNSCHTVSFHIL NKLKINSTVKRSSTVKRSSROMYSTILBFSSAMCULPSSLIN PROSPOLISGAFFYNTARILLKRGGONGNITVYSFHI NKLKINTSTVKRSSROMYSTILLBERNYMINGSORNITVYSFHI NKLKINTSTVKRSSROMYSTILLBERNYMINGSORNITVYSFHI NK	İ			MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
AVVADNMEFECIKLMIHALHEROKGENETHEROVESOW HHADSTVARPDIECVIKESVEHEROKGENETHEROVESOWHAMMON YECNLYTELYLVCISTYTCCEREDOCKINGUY INLIHLDPRITE GFILLHELAVNENTPUDPHTMINCES PENALVYKLILDCGAEVINA VUNEGNSALHI IVOYNEPISDELTHSI I ISLVEGGAHITOMTKK ONETPLEEFVOFH 6646 176 890 PSSRNNHLPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGGEKKGI SDVRRTFCLFYTFDLLFYTLLMI IELNVINGG LENTL EKEVMQYDYYSSYFDIFLLAVFREVULLAVAVCRLHHWATALI TTAVTSAPLLAVILLSKLFSGGAFGVYLEHISFIHAMITEMPLD FKVLPQBAEEENRLLI VODASERAALIPGGLSDGGYSPPESEA GSERAERKODSERPLLEL 6647 176 890 PSSRNNHLPEDMENALTGSGSSHASLRNIHSINPTOLMARIESY EGGEKKGI SDVRRTFCLFYTFDLLFYTLIMI IELNVINGG LENTL EKEVMQYDYYSSYFDIFLLAVFREVULLAVAVCRLHHWATAL TTAVTSAPLLAKVILSKLFSGGAFGVULPHISFILAMIETWFLD FKVLPQBAEEENRLLI VODASERAALIPGGLSDGGYSPPESEA GSERAERKODSERPLLEL EKEVMOYDYSSYFDIFLLAVFREVULLAVAVCRURHWATAL TTAVTSAFLLAKVILSKLFSGGAFGVULPHISFILAMIETWFLD FKVLPGBAEENRLI VODASERAALIPGGLSDGGYSPPESEA GSERAERKODSERPLULEL FKVLROMGARENNELLI VODASERAALIPGGLSDGGYSPPESEA GSERAERKODSERPLURH FKVLROMGARENNELLI VODASERAALIPGGLSDGGYSPPESEA GSERAERKODSERPLURH FKVLROMGARENNELLI VODASERAALIPGGLSDGGYSPPESEA GSERAERKODSERPLURHGENSTARTGGGAFGVULPHISFILAMIETWFLD FKVLLPGBAEENRLI VODASERAALIPGGLSDGGYSPPESEA GSERAERKODSERPLURHGENSTARTGGGAFGVULPHISFILAMIETWFLD FKVLPGVIKKKEERSPETDHRUNGVIKGLAPONKELOKUME EKRENSTRIFTENTENTURDARIERATIFGGLSDGGFGFGENKENLOKUME FKRENGTKKYFROPEDDHRUSFILMSKGGLAPONKELOKUME FKRENGTKKYFROPEDDHRUSFILMSKGGLAPONKELOKUME FKRENGTKKYFROPEDDHRUSFILMSKGGLAPONKELOKUME FKRENGTKKYFROPEDDHRUSFILMSKGGLAPONKELOKUME FKRENGTKKYFROPEDDHRUSFILMSKGGLAPONKELOKUME FKRENGTKKYFROPEDDHRUSFILMSKGGLAPONKELOKUME FKRENGTKKYFROPEDDHRUSFILMSKGGLAPONKELOKUME FKRENGTKKYFROPESIMSTINGSTHEROTHONKELOKUME FKRENGTKKYFROPESIMSTINGSTHEROTHONKELOKUME FKRENGTKKYFROPHTONKERINGSTHEROFT FKRENGTKKYFROPHTONKERINGSTHEROFT FKRENGTKKYFROPHTONKERINGSTHEROFT FKRENGTKHTURCHSTENTENTON FKRENGTKKYFROPHTONKERINGSTHEROFT FKRENGTKHTURCHSTENTENTONCHSTENTONCHSTENTON FKRENGTKHTURCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONCHSTENTONC	1			RENYDIIKTYHYLYLAMLERFQDGDNILEKEVLPPIHAYGNRTE
IHLNETVRAPDIECVLRCSVLBIEGSNNRYKNISDADVHNIAMDN YECNLYTEIVLVUCISTCGEEBDOCKINGUYNLIHDPRTEE GFTLLHLAVNSNTPVDDFTTNDVCSFDNALVYKLLLDCGAEVNA VDNEGNSALHIIVQVSNRPISDETLHSIIISLVEAGAHTDMTKK QNKTPLDKSTTGVSEILKKTMKNSLKCLARARVRANDINYQDG IPRTLEEFVGFH 6646 176 890 PSSRNNHLPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGGEKKGISDVRRTFCLFVTBOLLFVTLLMIIELNVKGGIENTL EKEVMVQDYYSSYFDIFLLAVPREKLUAVAVCRLHHWAITAL TTAVTSABILAKVILSKLFSGGAFGYVLDIISFILAMIETWRUD FKULPOEAEEENNLIIVQDASERAALIPGGLSDGGYSPPESEA GSERAEEKQDSEKPLLEL PSSRNNHLPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGREKKSISDVRRTFCLFVTBOLLFYTLLMIIELNVKGGIENTL EKEVMQVDYYSSYFDIFLLAVFRFKVLILAVAVCRLHHWAITAL TTAVTSABILAKVILSKLFSGGAFGYVLDIISFILAMIETWRUD FKULPOEAEEENNLIIVQDASERAALIPGGLSDGGYSPPESEA GSERAEEKQDSEKPLLEL TTAVTSAFLIAKVILSKLFSGGAFGYVLIISFILAMIETWRUD FKULPOEAEEENNLIIVQDASERAALIPGGLSDGGYSPPESEA GSERAEEKQDSEKPLLEL EKEVMQVDYYSSYFDIFLLAVFRFKVLILAVAVCRLHHWAITAL TTAVTSAFLIAKVILSKLFSGGAFGYVLIISFILAMIETWRUD FKULPOEAEEENNLIIVQDASERAALIPGGLSDGGYSPPESEA GSERAEEKQDSEKPLLEL SERVADEVILSVLAFFERVILITSFILAMIETWRUD FKULPOEAEEENNLIIVQDASERAALIPGGLSDGGYSPPESEA GSERAEEKQDSEKPLLEL REKYMQVDYNSKYFDGARGTVLISFTRAMEDYIEDDNPEL IRPOKLTANPKTTSRNHEDLHREKVLIKAVGKELEPOHRERWIA KEKRDQVIKQKEEERQKKKSDLBIELLKKQQKEEQELDKWEE KEKRDQVIKQKEEERQKKKSDLBIELLKKQQKEEQELDKWEE KEKRDQVIKQKEEERQKKKSDLBIELLKKQQKEEQERDKKWEELGKAK GSERAEERGARAERGVAKKSDLBIELLKKQQKEEQERDKKWEELGKAK KEKRDQVIKQKEEERQKKKSDLBIELLKKQQKEEQERDKEKQKO SKRWILDLEDGARGKWEENGHAIVUTALAVELGSTAGGARGWEENGKOR AUPLYFELLUSSILLEPSDILAGEGTAAKFYPCLLUVTLSCLGTIGGAF KEHREYSTKOLTINLWVUCLGSHINKKARQKKLAAIDDIDRPK KEHREYSTKOLTINLWVUCLGSHINKKARQKKLAAIDDIDRPKE CREKARGGARGAMGVUTSSLKGSPEPROQPERGTPSERPAT VKLITATOTAGRAGATUTSPTMENLSKEEPLASFYSEEFDISA CGATATERVKIDMSGGGLTARASFTISRTOPGPREGREEAK KAWHEHOWATSSLKGSPTISRTOPGPREGRESAK KAWHEHOWATSSLKGSPTISRTOPGRAFGSPTISRTONDERSING FREGGETISTISRTOPSTRICHVYNCHSDHYSSLKG BLÄUGHTIST STATAVANDSTATAKTORGGARGTEIFFGHFCOAPHR NINNQEDMGCSSWYPGMETSLPFGHWTANKKEKCKUESSINF HINNNQEDMGCSSWYPGMETSLPFGHWTANKKEKENDESSING PREGGPTISTISRTOPSTRICHVYNCHSOPGRAFGENSHIN DVSGEATAQENYLPFFGRASSYEDII				CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
YPECNLYTELTLVCISTKTGCEBEDGCKINGGI TNLIHLDPRITE GFILLHLAWNSNIPUDPHTNDVCSPNALVTKLILLOGABVBA UNDKENSALHI IVQYNRPISDFLTHSI IISLVEAGAHTDMTNK QNKTPLDEKSTTGVSEILLKTMKMSLKCLARAVPBANDINYQD IPRTLEEFVGFH 6646 176 890 PSSRNNHLPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGREKKGI SDVRRTFCLFVTFDLLFVTLLMI IELNVNGGI ENYL EKKYMQYDYYSSYFDI FLLAVPRKVLLLAYAVCRLHHWWAITAL TTAVTSAPLLAKVILSKLFSGCAPGVLJI ISFILAMIETWFLD FKVLDQBAEERNELLI VQDASERAALI PGGLSDGOFYSPPESEA GSEBAEKQDSKPLLEL EKEVMQVYYSSYFDI FLLAVPRKVLLAYAVCRLHHWAITAL TTAVTSAPLLAKVILSKLFSGGAFGVVLBIISFILAMIETWFLD FKVLDGBEERNLLI VQDASERAALI PGGLSDGOFYSPPESEA GSERAEKGISDVRRTFCLFVTFDLLFVTLLMI IELNVNGGI ENYL EREVMQVYYSSYFDI FLLAVPRFKVLLAYAVCRLHHWAITAL TTAVTSAPLIAKVILSKLFSGGAFGVVLBIISFILAMIETWFLD FKVLDGBEERNLLI VQDASERAALI PGGLSDGOFYSPPESEA GSERAERKODSKPPLLEL FRUMCHTKYFNSPFEDIDHKDSYLI TRSIMAEPDY IEDNPEL IRPOKLINPVKTSRNHQDLHREILMNQKRGLAPONKPELQKVME KRKRDQVIKQKEERQKKKSDLBIELLKRQQKLEGLEEKQKLO EGGENAEPFVKVGRURKTGGVAAGAU KRKRDQVIKQKEERQKKKSDLBIELLKRQQKLEGLEEKQKLO EGGENAEPFVKVGRURKTGGVAAGAU QLDPQOFLMKLEKLTDIRPI PDKEFVETYI KAYLICHMMEMI KERREYSTRQLTMLVNVCLGSHINKKARQKULLAAIDDIDRPKR KERREYSTRQLTMLVNVCLGSHINKKARQKULLAAIDDIDRPKR OLYMCETSLLVQSKGVVYSTSAMKFYPCLLLVTLSCIGTFIGAGPR QKQSTGEFFPROTGGRDSCTMFPSSLGGAGEWURVDCRNTD URSVCREAGPQAHMQQVTSSLKGSPEPNQOPERGTBSLRPKAT VKLTEATQLIGKDSWEELGKAKTTRPTAKFOTGPRPGGRBEAA KKAWEHCWKPFQALCAFLI SPFRG DSDLDLLGDCRNPRIDLEDSYTLRGSYTRKDVPTDGYESSLNF HNNNGEDWGCSSWYEGHTSLPPGHWTAAVKKEKCVPPYVQIK DLHGILRTYAMFSITKRLKDTMTTAHKJKGTKIENGSGHSASSANV FRESTOTISI GAAPFSKISEAPPHARSPRSPLLVTVYSEDD RPGGQPRRGYTASSLDSSSNERGSINRDLRNSGRNHTVSFHL NKLKYNSTVKSRSNDISLLILNEXAEPRSSPSPLLTVYSSDD RPGGGPRGYTASSLDSSSSNERGSINRDLRNSGRNHTVSFHL NKLKYNSTKSRSNDISLLILNEXAEPRSSPSPLLTVYSSD TSTWQVADDLTQNTLLDEVLTRAKKLKKONGNOFTFODKELL NKLKYNSTKKSRNDISLLILNEXAEPRSSPSPLLTVYSSD TSTWQVADDLTQNTLLDEVLTRAKKLKKENNONGNIFTOSFHU NKLKYNSTKKSRNDISLLILNEXAERPRSSPSPLLTVYSSD TSTWQVADDLTQNTLLBEVTRYKDKSTROBERGSPSTRRSPSPLLTVYVSSD RPGGGPRGYTASSLDSSSNRERGSINRDLRNSGRNHTVSFHL NKLKYNSTVKSRSNDISLLILNEXAEPRSPSPSLOTYVSSD TSTWQVADDLTQNTLLBEVTRYKLKKLKENDERP				AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
GFTLLHLAVISNTPUDDFHTIDVCSFPNALVYELLLOCGASUATION VIDEGNSALHI IVGYNPT SISDELTHISI IISLVERGARITOMTEK QUNTFILDESTIGVSE ILLKTQMKMSLKCLARARVRANDINYQDQ IPRILEFYOGH 6646 176 890 PSSRMHLPEDMENALTGSQSSHASLRNIHSINPTOLMARIESY EGREKKGI SDVRRTFCLFVTFDLLFVTLLMI IELNVRGG IENTL EKEVWCDYNYSSYDTPLTLAVPFRE KULAVAVCRLHWMATAL TTAVTSAB LLAKVILSKLFSGGAFGVVLPII STILAMIETWELD FYKULDGAERENELLI VODASERRALIPGGLSDGOFYS PPESEA GSERAEEKODS EKPLLEL 6647 176 890 PSSRMHNIH, PEDMENALTGGGSSHASLRNIHSINFTOLMARIESY EGREKKGI SDVRRTFCLFVTFDLLFVTLIMI IELNVRGG IENTL TTAVTSAF LLAKVILSKLFSGGAFGVVLPII STILAMIETWELD FKULDGAERENELLI VODASERRALIPGGLSDGOFYS PPESEA GSERAEEKODS EKPLLEL 6648 413 897 RRCWGCTTKYFNSPPEDIDHKDSYLITRSI HARPDYTEDDNEPEL FKVLDGEAREENELLI VODASERRALIPGGLSDGOFYS PPESEA GSERAEKODS EKPLLEL 6649 1357 RRCWGCTTKYFNSPPEDIDHKDSYLITRSI HARPDYTEDDNEPEL HAPPOLITRSI HARPDYTEDDNEPEL KRKRDGVIKGKEEAQKKKSDLBIELLKROQKLEGLEEKQKIO EEGENAPEFYKVKGNLRRTGGVAGAQES 6649 1357 832 WIPRARGIFREVKINDVKEINSGRI IVVOALKKEFEGFNRELNEV SKRVRI ILPEVSI LLEKROQKEGLELEKQKIO EEGENAPEFYKVKGNLRRTGGVAGAQES 6649 1357 832 WIPRARGIFREVKINDVKEINSGRI IVVOALKKEFEGFNRELNEV SKRVRI ILPEVSI LLWENGVER SKRVRI ILPENST			THENETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN	
UNDEGNSALHITUQYNRPISDFITHSIIISLVERGAHTDMTKK QNKTPIDKSTTUSVESILIKTQMKKKCLARARVRANDINYQDQ IPRTLEEFVGFH 890 PSSRMNHLPEDMENALTGSQSSHASLRNIHSINFQIMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLLMIIELNVRGGIENYL EKEVWQYDYYSSYDIFLLAVFRFKVLLLAVAVCRLHHWATAL TTAVTSAPLLAKVILSKLFSQGAFVLPIISFILAHIETWHDD FKVLPQEAEEENRLLIVQDASERAALIPGGLSDQQFYSPPESEA GSEEAEEKQDSEKPLLEL 6647 176 890 PSSRMNHLPEDMENALTGSQSSHASLRNIHSINFTQIMARIESY EGREKKGISDVRRTFCLFVFFDLLFVTLLMIIELNVNGGIENTL EEKVWQYDYYSSYPDIFLLAVFFKVLLLAYAVCRLHHWATAL TTAVTSAPLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD FVLLPGEAEEENRLIVQDASERAFVLIGGLSDQOFYSPPESEA GSEEAEEKQDSEKPLLEL 897 RCMWCPTKYPNBPPBDIDHKDSYLITSIMAEPDYIEDDNPEL RFVLLPGEAEEENRLIVQDASERALIPGGLSDQOFYSPPESEA GSERAEEKQDSEKPLLEL IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKFBLQKVME KRKRDQVIKGREEAQKKKSDLBIIBLLKRQQKLEQLELEKQKLO EEQERAPEFVKVKGNLRRTGGDVALEQCLELEKQKLO EEQERAPEFFVKVKGNLRRTGGDVALEQCLELEKQKLO GERAPEFFVKVKGNLRRTGGDVALEQCLELEKQKLO GERAPEFFVKVKGNLRRTGGDVALEQCLELEKQKLO GERAPEFFVKVKGNLRRTGGDVALEQCLELEKQKLO GERAPEFFYKVKGNLRRTGGDVALEQCLELEKQKLO GERAPEFFYKVKGNLRRTGGDVALEQCLELATHGGRAPK KEHREYSTKQLTNLVNVCLGSHINKKARQKLAAIDDIDTREKR AKHREYSTKQLTNLVNVCLGSHINKKARQKLAAIDDITREKR COTYMCETRGGPSNCOAFAADPKSWPCPLLLVTLSCLGTTGQOAFR QKYGSTGEFFFFTGGGRDSCTMRFSSLGQAGEVMLRVDCRNTD QTYMCETRGGPSNCOAFAADPKSWPCLLLATHGCGGAPV LRPSVCREAGPOAHMQVTSSLKGSPEPNQDPEAGTPSLRPKAT VKLTEAQLCKDSMEELGKAKPTTRPTAKTTGPGPRPGGNEEAK KAWHCWKPFQALCAFLISFFG AKELLKVIDNSGELTAREGSETLSRDGEVGVNSDMTYBLSC DSDLDLLIGDCRSPRLDLEDSTLRGSTTRRTGEVGNSDMTYSESH HNNOKENSTVLSKSTVLSSLSSSSWRERCSHNDLENSGNRTTVSFHL NNIKYNSTVKSRSNDSLSSNRERCSHNDLENSGNRTTVSFHL NNIKYNSTVKSRSNDSLSJLLENSTRADKRWKNSNOPTFOQDKELN DUSGEATAGBWALPFFGRSSPLLVTVVESDD RPGCGPRRGYTASSLDSSSSWRERCSHNDLENSGNRTTVSFHL NKLKYNSTVKSRSNDSLSLLLINERSGLKKHKRSVVKEA CKSTFLFYLVLTETENSFTKISEAPFRIKKROPTHTROGDSPGDV LDHTYGELFRAGGFVISDDKILEKLIKTPSVIFTAGODSPGDV LDHTYGELFRAGGFVISDDKILEKLKTPSVIFTAGODSPGDV LDHTYGELFRAGGFVISDDKILEKLIKTIERGHFCOAFPRO				YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLIHLDPRTRE
GMKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ IPRTLEEFVGFH BSSRMMILPEDMERALTGSQSSHASLENIHSINFTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLLWILLEURLHWARILE EKEVMQYDYYSSYPDIFLLAVFFKVLILAYAVCRLHHWATALL TTAVTSAFLLAKVILSKLESQGAFGYVLPIISFILAWIETWELD FKVLPQEAEEENRILIVQDASERALIPGGLSDQGYYSPPESEA GSERAEEKQDSEKPLLEL 6647 176 890 PSSRMMILPEDMENALTGSQSSHASLRNIHSINFTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLLWIISFILAWIETWELD FKVLPQEAEEENRLILVQDASERALIPGGLSDQGYYSPPESEA GSERAEEKQDSEKPLLEL EKEVWQYDYYSSYPDIFLLAVFRFKVLILAYAVCRLRHWMATAL TTAVTSAFLLAKVILSKLESGGAFGYVLPIISFILAWIETWELD FKVLPQEAEEENROLIVGASERAALIPGGLSDQGFYSPPESEA GSERAEEKQDSEKPLLEL TRYSAFLLAKVILSKLESGGAFGVVLPIISFILAWIETWELD FKVLPQEAEEENROLIVGASERAALIPGGLSDQGFYSPPESEA GSERAEEKQDSEKPLLEL TRYOKLINFWKTSRNIQDLHRELLMNQKRGLAFQNKFBLQKVME KRKRDQVIKQKEEEAQKKKSDLELLKRQQKLEGLELEKQKLO EGGENAPEFVVKGNILRETGGEVAQAGES ANDERAGGIREEVXGDVESTAMGHIIVDALLKEFEQFNRELNEV SKRVRIPLPVSNILWEHCIRLKRQCKLEGLELEKQKLO EGGENAPEFVVKGNILRETGGEVAQAGES ANDERAGGIREVXGWUNGTHSGHIIVDALLKEFEQFNRELNEV SKRVRIPLPVSNILWEHCIRLKRQCKLEGGAEEVMIRVDCRNTD QLDFQQFLMKLEKLTDIRPIDEKEFVETYIKAYYLTENDMERWI KEHREYSTKQLTHLWVCLGSHINKKARQKLLAALDDIDRPKR KEHREYSTKQLTHLWVCLGSHINKKARQKLLAALDDIDRPKR CHERSYSTKQLTHLWVCLGSHINKKARQKLLAALDDIDRPKR CHERSYSTKQLTHLWVCLGGHINKKARQKLLAALDDIDRPKR CHERSYSTKQLTHLWVCLGGHINKKARQKLLAALDDIDRPKR CHERSYSTKQLTHLWVCLGGHINKKARQKLLAALDDIDRPKR CHERSYSTKQLTHLWVCLGGHINKKARQKLLAALDDIDRPKR CHERSYSTKGLTHAVVCLGGHINKARQKLLAKOVENTO CTYMCEYRQPSMCQAFAADFKSWMQALQELRIHHACQGAPV LRPSVCREAGPQAHMQVTSSLKGSPERPMQPEAGTESLRPKAT VKLTEATQLSKDSMEELKAARPTTHAVYLKEEKCVPPYVQIR DLHGILRTYANFSITKELKDTMRTSHCLKRTPSGSPLSSINF HNNQEDBWGCSSWVPGMTSLDFPGHAVAVKEEKCVPPYVQIR DLHGILRTYANFSITKELKDTMRTSHCLRHPSFSANCGLPSSW TSTMQWADLTQNTLDLEYLFRAHKKKCKIKNGDSQHSASSANV FPKESPTQISIGAPPSTKISEAFFLHPARSSSPLLVTVVUESDD RPGGGPRRGYTASSLDSSSSWRERCSHNDELRRHCHRINGSRCHTSFHL NDKLYNSTVKSKRSNIDSLILINEATRANKVKNSNOFTFONKEN DVSGEATAQBWALPFPGRSASSYBDIIIDVCTNIHVKLRSVVKBA CKSTFLFYLVETEDKSFFVRTKNLLKKRGLKHTSFOQDREDGUSCHENDUSCHTUSFHL NDKLYNSTVKSTERSDISSLINGESUKSCHNETUSFHL EKTVALDRAGGEVISDBLILLE	1 1			GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAEVNA
176 890 PSSRMMHLPEMENALTGSGSSHASLRNIHSINFTQLMARTESY EGREKKGISDVRRTFCLFVTFOLLFVTLLWIIELNVNGGIENTL EKEVMOYDYYSSYFDIFLLAVPRFKVLIMAINETWHATAL TTAVTSAFLLAKVILEKLESGGAFGYVLPIISFILAMIETWHAD FKVLPQRAEEENRLLIVQDASERAALIPGGISDQGYSSPPESFA GEREKGISDVRRTFCLFVTFOLLFVTLMIIELNVNGGIENTL FKVLPQRAEEENRLLIVQDASERAALIPGGISDQGYSSPPESFA GEREKGISDVRRTFCLFVTFOLLFVTLMIIELNVNGGIENTL EKEVMOYDYYSSYFDIFLLAVFRKVLLMISIELNVNGGIENTL EKEVMOYDYYSSYFDIFLLAVFRKVLLMISIELNVNGGIENTL EKEVMOYDYYSSYFDIFLLAVFRKVLLMISIELNVNGGIENTL TTAVTSAFLLAKVILEKLFSGGAFGYVLPIISFILAMIETWFLD FKVLPQRAEEENRLLIVQDASERAALIPGGISDQGYSPPESFA GEREKKGISDVRRTFCLFVTFOLLFVTLMIIFIELMVIGGIENTL TTAVTSAFLLAKVILEKLFSGGAFGYVLPIISFILAMIETWFLD FKVLPQREAEENRLLIVQDASERAALIPGGISDQGYSPPESFA GEREKKGISDVRRTFCLFVTFOLLFVTLMINIGDLHRRLLMNDKRGLAPQNKPELQKVME FKVLPQREAEENRLLIVQDASERAALIPGGISDQGYSPPESFA GEREKGISDVRRTFCLFVTRUMAINIGGIENTLMIFTLMITSTMAEPDVIEDDNPEL ITAVTSAFLLAKVILSGPSKGYVLPSTPEDIDHKDSYLITSIMAEPDVIEDDNPEL IRPQKLINPVKTSRNIQDLHRRLLMNDKRGLAPQNKPELQKVME KKRRDQVIKQKEEEAQKKKSDLEIELLKKFFEGNRELQKAR KKRRDQVIKQKEEEAQKKKSDLEIELLKKFFEGNRELQKEL GEGENAPEFYVKVGNLRRTGGGVVAQAGES WIPRAGITHWSCHGSHINKSTVEGAMIYULALKFFEGNRELNEV SKRVWILLFLYSNILMSHCITSHTUTUGANVKKCSNEGRALM QLDFQQFIMKLEKLTDIRPIPDKEFVETYLAXYLTENDMERWI KHRHSYSTKQLTALUWCLGSHINKKARQKLLAAIDDIDRPKR GEGEKKGISDVRRTSUMATHLAVVCLGSHINKKARQKLLAAIDDIDRPKR KHRHSYSTKQLTALUWCLGSHINKKARQKLLAAIDDIDRPKR CHEVETYSTKGLTALUWCLGSHINKKARQKLLAAIDDIDRPKR CHEVETYSTRUMADLAGERSTLANDGUGAVSDHYKLS GERAERQDSCTSARGSTLSRDGEGVVSDMHYSLSG DSDLDLLGDCRSPRIDLEDSTLANDGUGASSANVANDCRSTLSPKAT VKLTEATAOLGKSDMEDELKAAPTTAAPTQFOPGPREGMEEAK KAAMEHCWKDFQALCAFLISFFRQ TKATATATATATATATATATATATATATATATATATATA	1 1	}		VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK
PSSRMMHLPEDMENALTGSQSSHASLRNIHSINFTQIMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTILMIIELNUNGGIENTL EKEVMQYDYYSSYFDIFLLAWGGAEGYVLPIISFILAMIETWHID FKVLPQEABEENRLIIVQDASERAVLPIISFILAMIETWHID FKVLPQEABEENRLIIVQDASGRAGVLPIISFILAMIETWHID FKVLPQEABEENRLIIVQDASGRAGVLPIISFILAMIETWHID FERNMHLPEDMENALTGSQSSHASLRNIHSINFTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLLMIIELNUNGGIENTL EKEVMQYDYYSSYFDIFLLAWFRFKVLILAYAVCRLRHWATAL TTAVTSAFILAKVIISKIFSGGFYVLPIISFILAMIETWHID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETWHID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETHMID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETHMID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETHMID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETHMID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETHMID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETHMID FKVLPQEABEENRLIIVQDASGRAVLPIISFILAMIETHMID FKVLPQEABEENRLIIVQDASGRAVLPIGGLSDEJCQFYSPPESEA GSERABEKQOSEKPLLEI TRPQKLIIHPVETSRNHHQDLHREILMNQKRGLAPQNKPBLQKVMG KRKRDQVIKQKEBEAQKKKSDIELLLKRQQKLEQLELEKQKLO BEQENAPPYKVKONLRRTGGEVAQAQES TAPPACATRIBEVKOVEKSIMSYNDVALIGELGELEKQKLO SEGENAPPYKVKONLRRTGGEVAQAQES SEGENAPPYKVKONLRRTGGEVAQAQES SEGENAPPYKVKONLRRTGGEVAQAQES SERVRIPLEVSNILWHCISTALINGKYGLAFALAVTLTENDMENWI QLDPQQFIMKLEKLTDIRPIPDKEFVETYIKAYVITTENDMENWI QLDPQQFIMKLEKLTDIRPIPDKEFVETYIKAYVITTENDMENWI QLDPQQFIMKLEKLTDIRPIPDKEFVETYIKAYVITTENDMENWI QLDRQGTGEFFFFQTGGRDSCTMRPSSLGQGAGEWUKKUCKNITD OKNOGTGEFFFFFQTGGRDSCTMRPSSLGQGAGEWUKKUCKNITD OKNOGTGEFFFFFQTGGRDSCTMRPSSLGQGAGEWUKKUCKNITD OTYMCETRGGPSMCQAFAADPKSYNNQALQELRRIHHACQGAPV LRPSVCRAAGPQAHMQQVTSSLKGSPENQPEAGTPSLRPKAT KAMELLWUKPPGANCABASERILSHDENGENGNISHTLIKESKCPPPVVOF LRPSVCRAAGPQAHMQDVTSSLKGSPENQPEAGTPSLRPKAT KAMELLWUKPPGANCABASGENTARSPSLLVTVVESSPD RPGCQPRRGYTASSLDSSSWERCSHRDLRNGGNHTVSFHL NKLKYNSTVKESRNISILLILERSFINVMINGNSORPHTOSFHL NKLKYNSTVKESRNISILLILAFFRINGMINGSRASANV DVSGEATAGAMYLPFFGRSASYEDIIIDVCTNIHVKLRSVVKBA CKSTFFFYLVETENKSPISHLHILTRGGHTEIFPGAFCQAFRA DVSGEATAGAMYLPFFGRSASYEDIIIDVCTNIHVKLRSVVKBA CKSTFFFYLVETENKPOSASANIVSPALUKPANINGNSORPHTUSF	1			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ
EGREKKGISDVRRTECHVITDLIFVILLNI IELNUNGGIENYL EKEVMOYDYYSSYFDIFILAVFRYKULLAYAVCRURHWATAL TTAVTSAFLLAKVIISKIFSGAFGYVLPIISFILAVISTWELD FKVLPORABEENRLLIVODASERAALIPGGLSDGOFYSPPESEA GSERAEKQDSEKPLLEI 6647 176 890 PESRNNHDEDMENALTGSGSHASLRNIHSINPTOLMARIESY EGREKKGISDVRRTECHFVTFDLLFVTLLMI IELNUNGGIENYL EKEVMOYDYYSSYFDIFILAVFKVLLIAYAVCRURHWATAL TTAVTSAFLAKVILSKLFSGAFGYVLPIISFILAMIETWFLD FKVLPQEABEENRLLIVODASERAALIPGGLSDGOFYSPPESEA GSERAEKQDSEKPLLEI EKEVMOYDYYSSYFDIFILAVGRUNTURGIENYL FKVLPQEABEENRLLIVODASERAALIPGGLSDGOFYSPPESEA GSERAERQDSEKPLLEI FKVLPQEABEENRLLIVODASERAALIPGGLSDGOFYSPPESEA GSERAERKOSEKPLLEI REPORTINFTENNEDLIKERLIMNOKRGLAPONKPELOKVME KRKRDOVIKOKEEEAQKKKSDLEIELKROOKBELAPONKPELOKVME KRKRDOVIKOKEEEAQKKKSDLEIELKROOKBELAPONKPELOKVME SKRWRIPLPSVNILWEELTRADATIVEGYARVKKCSBEGRALM OLDFOOFIMMLEKKTDIRPT DEVETYIKAYYLTENDMERMI KEHREYSTKQLTNLVNVCLGSHINKKARCKLLAATDDIDREKR KEHREYSTKQLTNLVNVCLGSHINKKARCKLLAATDDIDREKR KEHREYSTKQLTNLVNVCLGSHINKKARCKLLAATDDIDREKR OQQOSTGEFFHFTGGRBSCTMEPSLGGAGGEWARVDCRNTD OTYNCEYRGOPSMCOAFADPKSYMMOALOELRRLHHACQGAPV LRPSVCREAGPOAMQQVTSSLKGSPPNOQPEAGTPSLRKAT VKLTEATQLSKDSMEELGKAKPTTRPTAKPTOPOPFREGEREAK KAWHHUWKPFQALCAFLISFFEG 6651 3425 1353 AKELLKVGDFSLACFGYONTADIMENLSKEPLASFVSESFDISA CGIATEHVKLDNSGEGLTAEAGSETLSRDGEVGVNSDMHTELSG DSDLDLLGDCRNPRLDLEDSYTLRGSYTKKOVPTDOYSESLINF HNNNQEDWGCSSWPOMETSLBPGWTTAKKKEKCVPPTVOIR DLIGITRTYANFSITKELKDTWRTSHGLRRIPSFSANCGLPSSW TSTMOVADDLTONTLDLEVLRRAHLKGTIKNGDHYSSSLNV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPGGQPRRGYTASSLDSSSNRERCSHNRDLMSORGHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPGGPRRGYTASSLDSSSNRERCSHNRDLMSORFHYSFHL NKLKYNSTVKESRNISILLINERSPSFINNVMINSNOFFFOOKEIN DVSGEATAGBMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKBA CKSTFLFYLVETEDKSFFFYRTKNILKKGHTEIEPGAFCAPHR NKLKKNSTVKESRNISILLINERSPSFINNVMINSNOFFFOOKEIN DVSGEATAGBMYLPFPGRSASYEDIIIDVCIKEIIKILEKLINGNG CKSTFLFYLVETEDKSFFFYRTKNILKKEPGROSANITELLH	6646	176	990	
EKEYMYDYYSSYFDIFLLAVPREKULIAYAUCRIRHWAILS TTAVTASALIAKUILSKLESQCAFGYULPI1SFILAMISTMERD FKULPQEAREENELLIUQDASERAALIPGGLSDGGFYSPPESEA GSERAEKQDSEKPLLEL PSERMHHLPEDMENALTGSGSSHASLRNIHSINFTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLEVTLMIIELWYNGGIENTL EKEVMYDYYSSYFDIFLLAVPREVULLAVAUCRIRHWAILAL TTAVTSAFILAVULISKLFSQGAFGYVLPI1SFILAMIETWFLD FKVLPQEAEEENRLIUQDASERAALIPGGLSDGGFYSPPESEA GSERAEKQDSEKPLLEL FKVLPQEAEEENRLIUQDASERAALIPGGLSDGGFYSPPESEA GSERAERQDSEKPLLEL TRPCKLINFVKSSHHQDLHRELLMNQKGELAPQMXPELQKVME KRKRDQVIKQKESEAQKKKSDLEIELLKRQQKLECLELEKCKLO EEGEMAPEFVKVKGNLRRTGGEVAQACES TRPCKLINFVKSSHHQDLHRELLMNQKGLAPQMXPELQKVME KRKRDQVIKQKESEAQKKKSDLEIELLKRQQKLECLELEKCKLO EEGEMAPEFVKVKGNLRRTGGEVAQACES TRPCKVENTILPUSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM QLDFQOFJMKLEKLTDIRPIDDEFVETYIKAYYLTENDMERMI KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDREKR PKEHREYSTKQLTNLVNVCLGSHINKKARQKLAAIDDIDREKR CKGSTGEEFHFQTGGRBSCKTRESSLGGGEWLKRVCRNTD QXQCSTGEEFHFQTGGRBSCKTRESSLGGGEWLKRVCRNTD QTYNCETRGGPSMCQAPAADPKSYMNQALOELRRLHACQGAPV LRPSVCREAGPOAMMQQVTSSLKGSPEPHQGPBRGGEEAK KKAWHCMKPFQALCARLISFFR GGAPSVCREAGPOAMMQQVTSSLKGSPEPHQOPPBRGKEEAK KKAWHCMKPFQALCARLISFFR GGAPSVCREAGPOAMMQQVTSSLKGSPEPHOQPBRGGEEAK KKAWHCMKPFQALCARLISFFR GGAPEKEKKEKCVPPYVQIR DLEGILRTYANFSITKELKDTMRTSHCLRHHSFSSANCLPSSLMF FNKMQADDLTQDYTLDLESTLERSTKRLKDTKDSQRSLNSSANV FPKESPTQISIGAFPSTKISEAPFHPAFRSRSPLLVTVVESDP RPGGPRGYTASSLDSSSWERGCSHNRDLRNSQRNHTVSFHL NKLKXYNSTVERSRNDISLILINEVAEPNKWMKNNONFIFFOKELN DVSGEATAQBMYLPFFGRSASYBDIIIDVCTNLHVYLRSVVKEA CKSTFLFFLUETEDKSFFVTKKULRKGGHTEIEPQHFCQAFM NKLKXYNSTVERSRNDISLILINEVAEPNKWMNNONFIFFOKELN DVSGEATAQBMYLPFFGRSASYBDIIIDVCTNLHVKLRSVVKEA CKSTFLFFLUETEDKSFFVTKKULLEKGGHTEIEPQHFCQAFM ENDTLIIIRNEDISSHLHQIPSLLKLKHPSVIFFAGVSPGDV LDHTYGELFRAGGFVISDDKILEAVTLVQLKEIIKLLEKLINGNG ENDTLIIIRNEDISSHLHKKJKEBGUPTARKNINKLKSFOSANITELHH		-70	830	PSSKMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
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LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK KKAWEHCWKPFQALCAFLISFFRG AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKDVPTDGYESSLNF HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR DLHGILRTYANFSITKELKDTWRTSHGLRRHPSFSANCCLPSSW TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH	1]		QTYWCEYRGQPSMCQAFAADPKSYWNQALOELRRLHHACOGAPV
VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK KKAWEHCWKPFQALCAFLISFFRG AKELLKVGDFSLCAGFYQNTADTMENLSKEPLASFVSESFDISA CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPFYVQIR DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPCGCPRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH]]			LRPSVCREAGPQAHMQQVTSSLKGSPEPNOOPEAGTPSLRPKAT
KKAWEHCWKPFQALCAFLISFRG KKAWEHCWKPFQALCAFLISFRG AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGGSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPQCQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVTKNILLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYGELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH		j		VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYBSSLNF HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR DLHGILRTYANFSITKBLKDTMRTSHGLRRHPSFSANCGLPSSW TSTWQVADDLTQNTLDLBYLRFAHKLKQTIKNGGDQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPCGCPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYGELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH	6651	3425		KKAWEHUWKPFQALCAFLISFFRG
DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCCLPSSW TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVTKNLLRKGGHTEIEPOHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHPPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH		3472	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA
HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR DLHGILRTYANFSITKBLKDTWRTSHGLRRHPSFSANCGLPSSW TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV FPKBSPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH			ľ	CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG
DLHGILRTYANFSITKBLKDTMRTSHGLRRHPSFSANCGLPSSW TSTWQVADDLTQNTLDLBYLKFAHKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPCGQPRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH			1	DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPQGQPRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHPPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH	[[1	HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPGCQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKEGRNDISLILNEYAEFNKYMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH	j 1		i	DEHGILKTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW
RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLDFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHPPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH	1 1	•	j	TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLYLVETEDKSFFVTKNLLRKGGHTEIEFOHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH				FFKESFTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPOHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH		ļ	1	RFUGQFRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELIH	1		1	NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH		i		DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH		ł		CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR
RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANIIELLH	}	1	J	ENDILLILIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
KWAKULUHYRENKKLKEDERUDSTAHKKNIMLKSFQSANIIELLH		Į	1	DELTH LUELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
			1	WHOCDERSON'S DIE HOT TO THE WHOCDERSON THE LEFT
INGCDSKSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV				YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	M-Tweeterham W There is a second
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	pedaeuce	Codon, /=possible nucleotide deletion,
	1		\=possible nucleotide insertion)
6652	2	12.2	FENNGILVTDVNNFIENIEKIAAPFRSSYW
0032	1 2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
1	ł		PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
1			EBVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
1	1	l	TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
			KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
i	1		WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
			YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN
!	1		TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
			ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
i	l		QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
			CNISVGR
6653	170	1910	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
I'	1		RVAAAASRGADDAMESSKPGPVQVVLVQKDOHSFELDEKALASI
			LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
1	i i		NWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
1			VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
1			DLQQLQLFTEYGRLAMDEIFQKPFQTLMPLVRDWSFPYEYSYGL
			QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
]		LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
			SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAAA
			SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
1 1	1		KKMGGKDFSFRYQQELEEEIKELYENFCKHNGSKNVFSTFRTPA
			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
			IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
6654			PSMDKKAQ
0054	1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
{			WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL
i I			PODLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
1 1	i .		VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAQKRELG
			ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
6655	341	16	AISRGPSEYPTKNYV
1	342	10	KDAYMPKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA
1			INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
1	_		DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
i [KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY
] [KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP
1 1			KEKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM
į į		l	EEFVKQYKSEALGVGEVALPGQGGLPKEEGKQQEKPEGAETTAA
[[. (1	TINGSLSDPSKEVEYVCBLCKGAAPPDSPVVYSDRAGYNKQWHP
, l	· ·	1	TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
			IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT
			CSKSKRS
6657	830	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPBYCEP
] [1		LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
	ļ		HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM
	į		IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
] [į		VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
	ļ	ľ	LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
	İ		LEGOWEAOLDDINKI, I AGGGI GITGGGDWGGDWY YGGWTTO
	ļ		LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
	1		AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK
			NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
6658	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM
			THE SET TROUTED SAME CIAFRAMANQS I DEGLI KRMLM

SEQ	Predicted	Predicted end	Amino acid compet
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
1	1]	QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
	1	}	SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
İ			IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSEEMENSSSS
			MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV
			SPPQALLQE
6659	18	523	EPQRGDCETWFQNCslpkfvCffCWGFWLWRAHSMSNLHSLPGL
ł			RGLTSISRNQLQCTNAMRVINNYQRRWKNONTFLLATFANVVNV
			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLOAAAGASARACDSVTSNV
1	Į		LPLLLEQFHKHSQSSQRRTILEMLLGFLKLOOKWSYEDKDORPL
			NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAOPDLLSYED
			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
		1	VPKLAEELRVGESNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV
			KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP
1			ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
1			PG PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
			NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
6662	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
			GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
6663	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
1 1			PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER
			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
1 1			EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
1			PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
1 1			LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM
!			GCYILGNPNGEKLFQNLRTLMTPYRVTFBSPLELSAQGKQMIET YFDFRLYRLWKSRQHSKLLDFDDVL
6564	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMPPFFDIAHYLVSVMA
1			VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
1	1		LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
1			TRIWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIIINFERL
[!		VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL
į l	j		MPLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
L			SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACROVVTQQRSELYPGFQKRQRFLFKAGEEAAAOGGRHL
[PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
[!	ALCPGIPSPCRMTHODLSITAKLINGGVAGLVGVTCVFPTDLAK
] [ł	1	TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
			EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCOVVVTC
1			PMEMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS
1	}	ĺ	ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
			LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
6666	498	2000	KGLGEDMYSGITDCAR
	4.70	2868	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL
		ŀ	WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
į į	1	}	NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
	1	1	CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
	į	ĺ	KGHRSIVNQVRFNPHTYMICSSGVBKIIKIWSPYKQPGCTGDLD
1		į	GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
1	į	į	SASLPRSPPPTVDESADNAFHLGPLRVTTTNTVASTPPTPTCED
			THE TAXABLE TO SERVICE OF THE TAXABLE TO TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO THE TAXABLE TO TAXABLE TO THE TAXABLE TO THE TAXABLE TO TAXABLE TO THE TAXABLE TO TAXABLE TO THE TAXABLE TO THE TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE TO TAXABLE

SEQ	Predicted	Predicted end	Amino o del
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	[n=nistidine, I=Isoleucine, K-typine
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
ł	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	pequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
1	l		AASRQQRLSALRRYQDKRLLALSMESDSEENVCEVELDTDLFPR PRSFSPEDESSSSSSSSSSEDEEELNERRASTWORNAMRRRQKT
ľ			TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST
1		ì	STLEIQPSRASPTSDIESVERKIYKAYKWI,PVSVTSVSINIVDGE
1			TSLVTGEADEGRAGTSHKDNPAPSSSKFACI.NTAMAODNOOL DE
ļ	}	ļ	EGCSKDIFKEETPRTPSNGPGHEHSSHAWAEVDEGTGODTONGO
	İ		SVEHSFETKKLNGKALSSRAEEPPSPPVPKASGSTINSGSGNCD
			RTQSDDSEERSLETICANHNNGRLHPRPPHFHNNGQNLGELEVV AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACETPNAGTREDP
			TDTPATDSSRAVHGHSGLKRORIELEDTDSENSSSEKKLKT
6667	171	1310	ABEVERLAAMRSDSLVPGTHTFPIRRRSKFANLGRIFKPWKWRK
	1		KKSEKFKHTSAALERKISMROSREELIKRGVIKETVDVDGBIGI
1			SNEEDSLENGQSLSSSOLSLPALSEMEDUPMPDDDCCVFVTODC
1			DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLA
}			SYTAQKEGQQGVAQHHHTVLPSOIOHOLOVGSHGOHLDSTTTGST
1 1	j		PMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS
			GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL YTREEEEFFRDRDDSSLYTGGLANGIA
			YTREEEEEERDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR ELEEKNILPRQTDEERLELRQQIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP
1 1			LRGNLVKKDCAESCTPSYTLOGOVSSGTSSTOCCOEDLCMEVLU
6669	450		NAAPTRTALAHSALSLGLALSLLAVILAPSI.
1 0003	459	1207	KDEETRKDYDYMLDHPEEYYSHYYHYYSRRLAPKYDYDYYTTIVS
} [VCAISVFQFFSWWNSYNKAISYLATVPKYRTOATETAKOOGIIW
	ľ		KAKEKGKNKKSKEEIRDEEENIIKNIIKSKIDIKGGYOKPOTCO
1	1		LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK
			KKLANDPRWKRYRRWMKNEGPGRLTFVDD
6670	184	594	VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
1 1	İ		VMQPPPGMPLPPADIGPPPYEPPGHPMPOPGETPDHMGADCTVM
]			PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA
6671	1	763	TIVIV
1	-	/63	LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP
			PEOSRVOPMTASNWTLVMEGEWMLKFYAPWCPSCQQTDSEWEAF
	ł		AKNGEILQISVGKVDVIQEPGLSGRPFVTTLPAFFHAKDGIFRR YRGPGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS
			ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATIVEGI.SMDIVI +v
6672	304		ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHT.RI.
30,2	304	1089	APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGTLGLAVAMAUR
			GVIFFLALLLCIALLSSYSIHLLLTCAGIAGIRAVEOLCODARC
i	İ	1	PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
			DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
			MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD
6673	1116	1963	LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ
1	}	•	SVTCGPSPCVRKQESATKCLHIGACGSDI.WARGUFQG+G+CT NRV
			WLCPCVAFHRGARPQAEEGGARWNSLVSSDWTDDND*HCCTCDE
			NAVPRP*QG*KVNPSGOEROS\WVLPLPVPGEPI.KT.PGI.PG*NV
1		1	SESKV/SGSKGKWILPROLM*AS*R\TPRFVPGTOWVPTTW/DT
1	ĺ	ļ	11WH*SAPTPPLKACPAPRESDPCSSCLSCPCVTOFFRESDTGW
6674	1		FGAGHCHSSCDFTRKGAAGGPG
1	=	110	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
] :	HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY
			KCACLAGYTGORCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ PTPC*IGTRVAFFLT
-			

Destining nucleotide location corresponding continue continue continue continue continue corresponding continue continu	SEQ	Predicted	Predicted end	Desire and American
No: nucleotide	,			Amino acid segment containing signal peptide
Cocresponding	NO:			Glubaria Arid Tarine, D=Aspartic Acid, E=
corresponding to first amino acid residue of residue of amino acid residue of amino acid sequence solvent of the state of amino acid sequence solvent of the state of amino acid sequence solvent of the state of amino acid sequence solvent of the state of the state of amino acid sequence solvent of the state of the st			1	Giutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid sequence 6675 277 1678 6675 277 1678 6675 277 1678 6675 277 1678 6675 277 1678 6675 277 1678 6675 277 1678 6677 277 1678 6677 277 1678 6679 278 6679 279 1678 6679 277 1678	i	i		Hanistidine, laisoleucine, Kalysine,
amino acid yesidue of amino acid amino acid amino acid acquence 6675 277 1678 1678 277 1678 278 278 278 278 278 278 278				Debeucine, M=Methionine, N=Asparagine,
xesidue of amino acid sequence 6675 277 1678 Sequence	1			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence 6675 277 1678 1678 277 1678 277 1678 277 1678 277 1678 277 1678 277 1678 277 1678 277 1678 277 1678 277 1678 277 277 277 277 277 277 277	1			S=Serine, T=Threonine, V=Valine,
Sequence Apposition Inclication Incli				w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1678 1678	ŀ		sequence	Codon, /=possible nucleotide deletion,
LEK.HPPSNPGDSSSIGGSNETGGVYVAGSAGGELKSLFF RRSHTAGRIEBLIKERGNGIKCKNIGWKERNSKGSAGELKSLFF RKSHTAGRIEBLIKERGNGIKCKNIGWKERNSKGSAGELKSLFF KKSLKEKPPISGKGSLISVIELGCP-QLANDIVSKPOKCHKU GTTATKKIDVIPLHSSGRELLDRIVUTMASARVQDLIGLIGW YTSSGREPKLANDVSAYCHLHREDGEVOTDFUKFT GFSTLALVEKYSSPGITSKSSLFVEINAAGGFSLIQVDHTKVTM KEILLKAVKRKSGSKVSSSFAGEVFEEDSGILTVOTOMISSH HYKSFKVSMIRILFITTOVQL/GCALPFGVLKKRAAPVDCLEPS ADTWRQEGIGGCGAGCALARS PSIKK-EGELGYREINAAGGFSLIQVDHTKVTM KEILLKAVKRKSGSKVSSSFAGEVFEEDSGILTVOTOMISSH HYKSFKVSMIRILFITTOVQL/GCALPFGVLKKRAAPVDCLEPS ADTWRQEGIGGCGAGCALARS PSIKK-EGELGKSLFVEINAAGGFSLIGVDFOK KASTKRWIKQRTSISDSLLCAC\DLAEE KRSHKKENDFTIGHTTIAHINGSIVTSDTTGMCEMVLIDGDVG KASTKRWIKQRTSISDSLLCAC\DLAEE RRSHTAGALERLEKKERQNGIKCKNIOWKERASGAGELKSLFP KKSLKKEPPISGKGSILSVRLEGCLQLANPPREYSKPDGKGIN GTTATKKLDVYLPHISSGDRILDWTVVTMASAGAELKSLFP KKSLKKEPPISGKGSILSVRLEGCLQLANPPREYSKPDGKGIN GTTATKKLTOVIC-GCALPFGVLKERAAPVDCLEPS ADTWRQEGIGCCCAACAALSS*DEINGTGGVVAQSVDLTSSWDGGIR GFSTLALVEKYSSPGLTKSKSIPVEINAAMGFSLIQUDTTVVTM KEILLKAVKRRKSGKVSGSRADGVFEEDSGIDTATVQMISSH HYKSFKVSMIRHRIRFTTTOVQL/GCALPFGVLRERAAPVDCLEPS ADTWRQEGIGCCCAACAALSS*DESTGGVVAGSFALKSLFP KKSLKKEVPTISGDSGEGGGOSMETGGVVAGSFALKSLFP KKSLKEVPTISGDSGEGGGOSMETGGVVAGSFALKSLFP KKSLKEVPTISGDSGEGGGOSMETGGVVAGSFALKSLFP KKSLKEVPTISGGSISVELGVLLANDFTGSSDDGGIR GFSTLALVEKYSSPGLTKSSGDFLLAVTUTGSSMDGGIR GFSTLALVEKYSSPGLTKSSGDFLLAVTUTGSSMDGGIR GFSTLALVEKYSSPGLTGKSSIFVEINAAHGPSLIQVDMXVTM KEILLKAVKRRKSGKVSGSRADGVPEDSGIPTYOMMASH HYKSFKVSMIRHLERTTOVQL/GCALPFGVLRKBAPVDCLEPS ADTWRQEGIGCCGAACAALSS*DENGTGGVVAGSFACHAPVGFG GFSTLALVEKYSSPGLTGKSSIFVEINAAHGPSLIQVDMXVTM KEILLKAVKRRKSGKVSGSRADGVPEDSGIPTVGSSMDGGT GFSTLALVEKYSSPGLTGKSSIFVEINAAHGPSLIQVDMXVTM KEILLKAVKRRKSGKVSGSRADGVPEDSGIPTVGSSMDFGT-R FPPCSGLARAGAGERSTENDFTTTISSMDGGT-R FPPCSGLARAGAGERSGENAGERSTENDFTSKFDGGT-R FPPCSGLARAGAGERSGERSGERSTENDFTSKFDGGT-R FFLPLLLGGGCGCCAACAALSS*INDTGGTGTCGTGTTTVGTSGGFF FFLPLLLGGGGCGCAACAALSS*INDTGGGTTCGTGTTTVTGSGGFF FFLTELLGGGGSGGGGGGGGGGGGTTGGTGGTTTTTTGGGGF FRAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6675		1670	\=possible nucleotide insertion)
RESHTADRIEBLERCERQNOINCENTIQUEERNES (GAGGELSELFER KESLEKERPI SEGKSILESVELEGO-FQ-LINDESYERFOCKEN-V GTTATKKIDVIPLHASSORILEMTVUTMASARVODILCICWO TYSSGREPKIANDNASYCHIRABDOGEVOTPOSEPHIKE GPSILALVEKYSSFGITSKESLEVEINAAGGPSILQUENTKUTM KEILIKAVUKRKSGOKVISGSRADVIPERGOINTOYOMLSSH HYKSFKVSMIRIREFTTOVIL/GCAL-PRGVIRKRADVUCLEPS ADTREGGEIGCGGGACALARS PSIKKC*BEIGLEVPINOYOMLSSH HYKSFKVSMIRIREFTTOVIL/GCAL-PRGVIRKRADVUCLEPS ADTREGGEIGCGGGACALARS*BISKC*BEIGLEVEINAAGGPSILQUENTKUTM KEILIKAVUKRKSGOKVISGSRADVIPERGOINTUTMOTHOTHON LEKHIPPSMPODSGSEIGSSNGETGGVVVAGSVDITSSHDFGIR RRSNTADRLERLEKERDQIKCKNIQMKERNSKGSAQELKSIPE KKSLKEKPP ISGGSILSVELEGCLGLANPPSYSKFDGKGHV YTSSGREPKINDNVSANCLHIAEDDGSVDITOSPHISKSFDGKGHV YTSSGREPKINDNVSANCLHIAEDDGSVDITOSPHISKSFDGKGHV YTSSGREPKINDNVSANCLHIAEDDGSVDITOSPHISKSFDGKGHV HYKSFKVSMIHRIRFTTTOVQL/GCAL-PPGVLRRRAAPVOLCRPS ADTWRCGGIGCCAACALARS*DEHKC*BGISGKWEIDFDVN KASTKFNIKKKFISJBBLLCAC\DLAEB 6677 277 1678 GNMPTERMAPLDNFTITIAHRIKSBVTSDDTSMCESWLIDDDV LEKHIPPSMPGDSGEIGSSNGETGGVVVAGSVDITSSWDFGIR RRSNTAGRIEBRIKSRKONGIKKCHIOMKERNSKGSAQELKSILFE KKSLKEKPPISGKGSILSVELBOCHULGHNPFNYSKSPDGKGHV GTTATKKIDVYLEHSSODRILDMTVATMASARVQDLICLERS ADTWRCGGIGCCAACAALAS*BARVQDLICLENSPGKGHV GTTATKKIDVYLEHSSODRILDMTVATMASARVQDLICLERS ADTWRCGGIGCCCAACAALAS*BARVQDLICLICNSV TYSSGREPKINNNVSAVCLHIAEDDGSVDTOPPDLOSNEPIHKR GFSTLALVEKYSSPCLISTSVELBOCHULGHNPFNYSKSPDGKGHV GTTATKKIDVYLEHSSODRILDMTVATMASARVQDLICLICNSV TYSSGREPKINNNVSAVCLHIAEDDGSVDTOPPDLOSNEPIHKR GFSTLALVEKYSSPCLISTSVELBOCHULGHPPPNSYSKSPDGKGHV GFSTLALVEKYSSPCLISTSVELBOCHULGHNPPNSYSKSPDGKGHV KKSLKEKPPISGKGSLSVELBOCHULGHNPPNSYSKSPDGKGHV GFSTLALVEKYSSPCLISTSSTATURVATHAGARVQDLICLICNSV ADTWRCGGIGCCGAACAALRS*DEHGGTGNACHTSPLIDOTNTTURV KEILLAAVARRKGSCKVSGSRADGVPEBBGJDTATVQDMISSH HYKSFKVSMIHRLRFTTTOVQL(CAALFSPVILARDAGFULDOTNTTURV KEILLAGAGCKUCLABARVGSTALAGAFAPTARCHEDGRNV GFSTLALVEKYSSPCLISTSVELBOCHULGGCFNPTHEIDFLICHVVVV GFSTLALVEKYSSPCLISTSVELBOCHULGGFTHEIDFTTARVISSNFGRGVLR ATTWRCTORGARPTGCTTATTURVISSNFGRGVLR GFSTLALVEKYSSPCLISTSVELBOCHULGGTTHURVISSNFGRGVLR GFSTLALVEKYSSPCLISTSVELBOCHULGGTTHURVISSN	""	2''	10/8	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
KKSIKERPISGKGSILSVILEGCP-QLINPPYNKSKFDCKGHV GTTATKKIDVYLPHASSORLINPTVYMASICIJCIGKGY VTSSGREPKINDNVSAYCLHIASDDGEVDTDPPPLDSNEPIHKE GPSTLALVEKYSSPGLTISKESLEVRINAAGFELIQUDNTKYTM KEILLKAVKRKKSGKYSGSRADGVPEEDGOIDIATVQDMLSSH HYKSFKVSHIRREFTTDVQL/GCALFPGUKRAPVUCLERPS ADTKRQEDIGCCGAACAALRS*DSIKK*EGISGDKVEIDPVTNQ KASTKEWIKGKYSISDDLICAC\DLACALDAG ADTKRQEDIGCCGAACAALRS*DSIKK*EGISGDKVEIDPVTNQ KASTKEWIKGKYSISDDLICAC\DLACALDAG RSSTKWIKGKYSISDDLICAC\DLACALDAG RSSTKWIKGKYSISDDLICAC\DLACALDAG RSSTKWIKGKYSISDDLICAC\DLACALDAG RSSTKWIKGKYSISDDLICAC\DLACALDAG RSSTKWIKGKYSISDDLICAC\DLACALDAG RSSTKWIKGKYSISDDLICAC\DLACALDAG RSSTKATKIKGYSICAC GFSTLALVEKTSSPGLTIKSSISTPVENTAAHGFSIJGVDTKVTM KEILLKAVKGRKGSKVSGSRADGVFEESGIDIATVQDMISSH HYKSFKYSHIHRERFTTVQL/GCALFPCVHKRAAPUDCLRPS ADTWRQEGIGCCGAACAALRS*DGRKGSCFVITSSBDFGIR RSSTKATKKIKGYSISTSDDLICAC\DLACALDAG RSSTKWIKGKYSISTSDDLICAC\DLACALDAG RSSTKWIKGKYSISTSDDLICAC\DLACALDAG RSSTKWITKKGYSISTSDDLICAC\DLACALDAG RSSTKWITKKGYSISTSDDLICAC\DLACALDAG RSSTKWITKKGYSISTSDDLICAC\DLACALDAG RSSTKWITKKGYSISTSDDLICAC\DLACALDAG RSSTKWITKKGYSISTSDDLICAC\DLACALDAG RSSTKWITKGSISTSDDTATQMISSH HYKSFKYSHIHRERFTTVQL/GCALFPCHYRRAAPUDCLRPS ADTWRQEGIGCCGAACAALRS*DGRIGGAVPITSSBDFGIR RSSTKATKKGYSISTSDDTATQMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHYRRAAPUDCLRPS ADTWRQEGIGCGCAACAALRS*DETGGVYVAGSVDITSSBDFGIR RSSTKATKKGYSISTSDDTACCYDLACALDAG RSSTKWITKGSISTSDDTATCYDMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILVDJMISSH HYKSFKYSHHALBRETTUQL/GCALFPCHLORDFTILDGGSN HPPLPLUVORMBADAALDFTAKSGSKYSGARAFTARAPTERGOP PPPCSQLPMSQCGCHHLDGCCPWPTITSGGPP PPCSQLPMSQCGGAALGRATGATARTGGP PPCSQLPMSQCGGAALGRA		i	Į	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
GTTATKKIDVIP_HASQORLLENTVARSARVOLIGLICUM YTSSGEREPKINNUNSAYCLHIABDOGEVUDTPPPLOSNEPTHKE GFSTLALVSKYSSPGITSKESLFYRINAAGFSILQUMTKVTM KEILLKAVKRRKGSGVSSGRADVSTEBSGIDTATVQDMISSH HYKSFKVSMIRRLAFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTRRQBGIGCGGACALARS-SDHKK-SIGGKVSIGDVSIDPVTNQ KASTKWHIKQKPISIDSDLCAC\DTLAES GMWFTERMAFLDNFTILLAHIRQSHVTSDDTGMCGMVLIDHDVD LEKIHPPSMPGDSGSIQGSMGTQGVVAQSVDITSSWDFGIR RRSMTAQRLERLRKERQMQIKCHIQMKERNSKQSAGLKSLEF KKSLKKEPPIGSKQSILSVRLEQCPLQLUNDFFMEYSKFPGKGHV GTTATKKIDVILPHASQORLLPMTVVIMASARVQDIGLICUM YTSGGREFKLMDNVSAYCHHABDOGSVDTDFPLDSHEPIHK GFSTLALVEKYSSPGITSKESLEVERINAAHGFSLIQVDNTKVTM KEILLKAVKRRKSGCXVSGSADOVSEEDSGIDLATVQDMISSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEGIGCCGAACALAS-SDHKC-GEISGDKVEIDPVTNQ KASTKRWIKQKPISIDSDLCAC\DLAES RRSNTAQRLERLKKERQNGIKCKNIQNKERNSKQSAGLKSLEF KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEF KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQSILSVRIKCNIQNKERNSKGSAGLKSLEFE KKSLKEKPFIGKQCILJOHANDERSTALIDDRRFHLYND GFSTLALUVEKYSSPGLITSKSLEVRINAAPLOLONFEYNIQN KSILLKAVKRRKGSGKVSGSRADGVFEEDSGILDLATVQDMISSH HYKSFKVSMHRLRFTTDVOL/CCLLFPUNDLASPLICVRIN KSILLKAVKRRKGSGKVSGSRADGVFEEDSGILDLATVQDMISSH HYKSFKVSMHRLRFTTDVOL/CCLLFPUNDLASPLICVRIN KSILLKAVKRRKGSGKVSGSRADGVFEEDSGILDLATVQDMISSH HYKSFKVSMHRLRFTTDVOL/CCLLFPUNDLASPLICVRIN KSILLKAVKRRKGSGKVSGSRADGVFEEDSGILDLATVQDMISSH HYKSFKVSMHRLRFTTDVOL/CCLLFPUNDLASPLICVRIN KSILLKAVKRRKGSGKVSGSRADGVFEEDSGILDLATVQDMISSH HYKSFKVSMHRLRFTTDVOL/CCLLFPUNDLASPLICVRIN KSILLKAVKRRKGSGKVSGSRADGVFEEDSGINDLATVQDMISSH HYKSFKVSMHRLRFTTDVOL/CCLLFPUNDLASPLATT GFSTLALLVRKYSSPGLITSHTOLATATARAPVTOLKRR HYKSFKVSMHRLRFTTD	1	f .		RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
TYSSGREPKINENNSAYCHIAERDGEVDTDPPPLIGNEPHIKY GPSTLALVSKYSSGUTSESLIFVENNAHUTOMISSH HYKSFKVSHIRLSFTDVOL/GCALPGEVLEKRAAPVDCLRPS ADTRRQEOIGCCGAACAALRS*DSHKC*SCISGRVSIDPVTNQ KSSTKPH KOKPISINSDLCACULAE GROPERMAPLONFTILAHTRQSHVTSDTGMCEMVLIDHDVD LEKIHPPSMPGDSSSIQGSNGSTQGVVAGSVDITSSBUTGHIK RRSNTARLERLERKERKRJKICKTIONICKKHIQMKERNSKGSAGLKSLPE KKSLKSKPP ISGKQSILSVRLEQCPLJANPPHEYSKPROKGHV GTTATKKIDVIPLHSSGURLENTPVINASARVQDLIGLICKM YTSSGREPKLNDAVSAYCHHABDGEVUTDFPPLSSHDFGHIK KSLKSKSP ISGKQSILSVRLEQCPLJANPPHEYSKPROKGHV YTSSGREPKLNDAVSAYCHHABDGEVUTDFPPLSSHDFGHIK KSLKSKSSGLIKSKSSBAGDGVSGSRADGVVERDSGIDIATVVINASARVQDLIGLICKM YTSSGREPKLNDAVSAYCHHABDGEVUTDFPPLSSHPHKK GPSTLALVSKYSSGLIKSKSLEVPRINAHOFSLIQVDNTVVIN KEILLKAVKRRKGSQVSGSRADGVVERDSGIDIATVVINASARVQDLIGLICKM YTSSGREPKLNDAVSAYCHHABDGEVUTDFPPLSSHPHKK KSLKKKPPISIGSLICAC\CLACLAL ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGRVEIDPVTNQ KASTKPHKKKPFISIDSLICAC\CLACLAL KRSNTAQLIERLERKENQOLIKCNIQWKERNSKQSAGLKSLEE KKSLKKENPISIGGSULGAC\CLAUMFPHYSKPBCKGHV GTTATKKIDVYLPHSSGORSIGTGGVYVADVUTISSUPGGIR KRSNTAQLIERLERKENQOLIKCHIQWKERNSKQSAGLKSLEE KKSLKKENPISIGGSULLBMTVVTMASARVQDLIGLICKQ YTSSGREPKLNDAVSAYCHHABDGBVDTDFPLDSBPHKF GFSTLALUSVSSSGLIKSLEVENINAHGFSLIQVDNTXVTM KSILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVVMMSH HYKSKYNSWHRIERFTTUVCL/CCALFFGVLRRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KSILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVVMMSH HYKSKYNSWHRIERFTTUVCL/CCALFFGVLRRAAPVDCLRPS ADTWRQEQIGCCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KSILLKAVKRYSISGDSHCLACA\CLABS GFSNQSSSLSILVYGGSSWSSINDTGTTLRULSSNFGROTLR PPPCSQLMSGGGCHULDFANUNSQADJOHNSKRGROTLR PPPCSQLMSGGGGGCHULDFANUNSQADJOHNSKRGROTLR SYCCHEVYNKENLFNILDVSQADJOHNSKRGROTLR SYCCHEVYNKENLFNILDVSQADJOHNSKRGROTLFDVTNQ LLGSDGSVGLBDLCVFWPTLLHVLIGLFP*PHELPFLLPVDLG SYCHEVYNKENLFNILDVSQADJOHNSHDFOTTALDSGRAPDTTLR ELLQTLUTSLCTLVKRVGKSVLVANIHMWVMSTRITLHMQQOLN NQCSQADLPQGAPPGSGGALRTGTGATALP NQVSPDPW*GABENDQDGGGKERGGREILSSSGLIPGS*ALP NQVSPQAPPGTGLPRGGGSSSACG*TTYTHTSPLRPSGIFG PPCSQLMSPARTGUFFRGROTLARGGRAPAVP*LESDPAS TIFKGTRGFGGGGGGGGGGGGGGGGGATGATARAPTP*LESDPAS TIFKGTRGFGGGGGTGGGG	1	1		KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
GFSTLALVEKYSSGLTSKESLFYRINAHGFSLIQUNTKYTM KEILIKAVKRRIGSGWISSRADOVFEDSQLDIATVQDMIJSSH HYKSFKVSMIRRLAFTTDVOL/GCALFPGVLRKRAAPVDCURPS ADTROBOIGCGAACALARS *GDHKK-*SIGKWEIDPVTNQ KASTKRWIKOKPISISDLLCAC\DIABE GRWPTERMAFLONPTILAHTRQSHVTSDDTGMCEMVLIDHDVD LEXIHPPSNPCDSSSIGGSNGGTOGVVAQSVDITSSWDPGIR RRSNTAQRLERLRKERMOIKCKIIOWKERNSKQSAGLKSIFE KKSLKKENP JEGKQSILSVERLEQCPLQLINDPFNEYSKPGKGHV GTATKKIDVYLPHHSQDRILDWTVTMASARVQLIGLICKON YTERGEPEYRLAMDWSAYCLHABDODGEVIDIDIATVQDMISSH KKSLKKENP JEGKQSILSVERLEQCPLQLINDPFNEYSKPGKGHV GTATKKIDVYLPHHSQDRILDWTVTMASARVQLIGLICKON YTERGEPEYRLAMDWSAYCLHABDODGEVIDIDIATVQDMISSH HYKSFKVSMIHRLRFTTDVOL/GCALFPGVLEKRAAPVDCLRPS ADTWRCEGLGCCGAACALASPOBHC-*PGVLEKRAAPVDCLRPS ADTWRCEGLGCCGAACALASPOBHC-*PGVLEKRAAPVDCLRPS ADTWRCEGLGCCGAACALASP-BINC-*PGVLEKRAAPVDCLRPS ADTWRCEGLGCCGAACALASP-BINC-*PGVLEKRAAPVDCLRPS ADTWRCEGLGCCGAACALASP-BINC-*PGVLEKRAAPVDCLRPS RRSNTAQRLEHLRKERGRGIKKIKNIONKERNSKGSGLKSLEF KKSLEKEKPISGKGSILSVERLEQC-PLQLUNDFFNEYSKPDGKGKV GTTATKKIDVYLPLHSSQDRILDWTVTMASARVQLIGLICKO YTESGREPKANDWSAYCLHABDDGEVDLPFPEVSKEPKDKGKV GTTATKKIDVYLPLHSSGDRILDWTVTMASARVQLIGLICKO YTESGREPKANDWSAYCLHABDDGEVDLPFPEVSKEPKDKGKV GTTATKKIDVYLPLHSSGDRILDWTVTMASARVQLIGLICKO YTESGREPKANDWSAYCLHABDDGEVDLPFPEVSKEPKDKGKV GTTATKKIDVYLPLHSSGDRILDWTVTMASARVQLUGLICKO YTESGREPKANDWSAYCLHABDDGEVDLPFPEVSKEPKDKGKV KEILLKAVKRYSSPGLTSKESIJVTUNAAGSFLIDUTTVVTMYATM KEILLKAVKRYSSPGLTSKESIJVTUNAAGSPCJULDVTNYATM KEILLKAVKRYSSPGLTSKESIJVTUNAAGSPCJULDVTNYATM KEILLKAVKRYSSPGLTSKESIJVTUNAAGSPCJULTVTUNTVATM KEILLKAVKRYSSPGLTSKESIJVTUNAAGSPCJULTVTUNTVATM KEILLKAVKRYSSPGLTSKESIJVTUNAAGSPCJULTVTUNTVATM KEILLKAVKRYSSPGLTSKESIJVTUNAAGSPCJULTVTUNTVATM KEILLKAVKRYSSPGLTSKESIJVTUNAAGSPCJULTVTUNTVATM KEILLKAVKRYSSPGLTSKESTORYCHAAPGSPLIDVTUNTVATM KEILLKAVKRYSSPGLTSKESTORYCHAAPGSPLIDVTUNTVATM KEILLKAVKRYSSPGLTSKESTORYCHAAPGSPLIDVTNAAT KERNTAKLDVARVANDAVALLTARDGAPTATUNTVATM KEILLKAVKRYSSPGLTSKARCHORYCHAAPGSPLIDVTNAAT KERNTAKLDVARVANDATARDAPTSTCS SPCCKSTORMANTATARAAPTSLATARAAPTANAARAAPTANAARAAPTAAPATARAAPTAARAAPTAAPATARAAPTAAPATARAAPTAARAAPTAAPATARAAPTAARAAP		[.		GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
KEILLKAVKRRKGSQKYSGSRADGVJEEDSQIDLATVODMISSH HYKSFKUSHIRLBAFTUDVLJGCALFGEVURKRAAPUDCURPS ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGKVEIDPVTNQ KASTKWH KOKPI SIDSDLLCACULABE GEFTON GRAPTERMAFLONDTILLAHTROSHVESDFTGMCERVIJDHDVD LEKKHPSPAPOGSGSIQGSTQGYVYAQSVDITSSWDFGIR RRSHTAQRLERLRKERQMQIKCHNIQWKRNSKQSAQELKSLFE KKSLMKRP FIGSQSILSVRLEQCPLQLINNSPREYSKPOGGHV GTTATKKIDVIPLHSSQDRLIPHTVVTHASARVQDLIGLICMW YTSBGBEPKLMDNVSAYCHHABDDGEVDTDFPLDSBPPHKF GFSTLALVEKYSSBGLISKSLEVRINAAMFSLIQVDNTKVTM KEILLKAVKRRKGSCVSGSRADGVFEEDSQIDIATVOMLSSH HYKSFKVSHMIRLRFTTDVOJ/GCALFPGVJRKRAAPVDCLIRP ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGDKVEIDPVTNQ KASTKPHKKQFFISIDSLICAC\DLACACYLLAE GROPT 277 1678 GNOFFERNAFDDMFT IILAHTROSHVTSDDTGMCENYLJDEDUD LEKHIPPBMPDGGSSIGOSGNGTQVYVATDDDVD GRSTHALVEKYSSPGLTSKSLEVRINAAMFSLIQVDNTKVTM KEILLKAVKRRKGSGVSGSRADGVFEEDSQIDIATVIDDDVD GRSTHALVEKYSSPGLTSKSLEVRINAAMFSLIQVDNTKVTM KRSHKVSHKUBPHSGGSSILGVALDQCPLQLANDPTRYLDDDVD GTTATKKIDVYLDHASQDRLLENTVUTMASARVQDLIGLICMQ YTSBGBEPKLADVSRYCLLEQCPLQLANDPTRYDDGKGFUK GTTATKKIDVYLDHASQDRLLENTVUTMASARVQDLIGLICMQ YTSBGRBEPKLADVSRYCLLEQCPLQLANDPTRYDDKSPETHK GRSTLALVEKYSSPGLTSKSLEVRINAAMFSSLIQVDNTKVTM KEILLKAVKRRKGSGNSGGSRADGVFEEDSQIDIATVIDMISSH HYKSFKVSHMHRURFTTTUVLJ-CACLFFFQLKRRAAVDCLRPS ADTWRGCJGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KEILLKAVKRRKGSGNVSGSRADGVFEEDSQIDIATVIDMISSH HYKSFKVSHKMHRURFTTUVLJCACACALDAE HYKSFKVSHVSHSLEDCPLACQCONFRKGRQRMEN*OS LLGSDGSVGLBCLCVFNVFILLAVLLGLPP*PHELFLLDVDLG FLFPLLLGGGCGCACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFHKKQFTSTDSBLCACCQNHKKGRQRMEN*OS LLGSDGSVGLBCLCVFNVFILLAVLLGLPP*PHELFLLDVDLG FLFPLLLGGGCGCACALLSALRYDGSGASTAGGVFTSDFT CHARAGMPPTJCODWRSTFGROWNTVTVDGWKRTDGROTAR HEILLVARSTKERHGYCTLGRAFNKDDFSTALLDSRRNTVV RLLELLARSGLTSGGGAGCHCLUPANINSOADJORKKTVDGWKGRGTMENTOR SSYCHKEVYNKENLFNSLANTGSADJORGRAFAGTAPPTVPTUESSGGF PPCSGLDMSGAGGAPPASGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ł			YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
HYKSFKVSMIHELRETTDVQL/GCALFFGULRKRAPVDCLRPS ADTHRQEGICGGARCALRS *DISKC* GEISGDKWEIDPVTNQ KASTKWWIKQKPISIDSDLLCAC\DLARE GNWFTERM#FLDNPT! ILAHITGGSWYTDDFTGMCEMVLIDHDVD LEKHPPSMPGDBGSEIQGSNGETQGVYAQSVDLTSSWPFGIR RRSNTAQRLERLRKERQNQIKCKNIQWERNSKQSAQSLKSLER KKSLKEKPPISGKGS ILSVELEQCPLOWPFREYSKPDGKGHV GTTATKKIDVTPLHSSQDRLLPMTVVTMSASRVDDLIGLICNG YTSEGGSPKLNDNYSACHLIAEDDGEDVDTPPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRKRGSQKVGSRADGVFSGGINDILTAVQDMLSH HYKSFKVSMIHRLFFTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWRQEGJGCCGAACALRS* DEBKC-SEIGDKWEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAFE GNWFTERMFLDNFTI LLAHIRGSHVTSDDTGMCEMVLIDHDVD LEKIHPPSMPGDSGSEIQGSNGETGGYVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQNGIKKNIQWKENNSKOSAGELKSLEF KRSLEKKPPISGKGSILSVELGCPCLPUSPPHENSKPDGIRK GTTATKKIDVTLPHSSQDRLLPMTVVTNASARVQDLIGLICNG YTSEGGEFKLDNVSSAYCHLAEDDGEDSDIDATVQDMLSSH HYKSFKVSMIHRLFFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWRQEGIGGCGAACALRS* DEBKC-SEIGGDKWEIDPVTNQ KASTKFWIKQKPISIDSDLCAC\DLAFE GFSTLALVEKYSSFGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRKKSGGVAVGSRADGVFSEIGGNBCTGGVLRS-BATTWAGGIGGGGAACALRS* DEBKC-SEIGGBKWEIDPVTNQ KASTKFWIKQKPISIDSDLCAC\DLAFE GFSNGSSSSLSIIVTG-GCSFVSSIGDLTATVQDMLSSH HYKSFKVSMIHRLFFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWRGEGIGGCGAACALRS* DEBKC-SEIGGBKWEIDPVTNQ KASTKFWIKQKPISIDSDLCAC\DLAFE GFSNGSSSSSLSIIVTG-GCSFVSS-INDTGTTLRVLSSNFGRQ*LR FPFPLLLQGGGCALALARS*D-GSK-KRFLDEKSGSFVSDL SSYCHKEVYNKERLINSLNYD/SCSGERKEGHRS*DGNS\NPTHGTBESGGF FFFPLLLGGGGCALALARVSTORGSSIRDTGGTGFTALDSRRFNYV RILBLIARSQLTSLSGILAGNOFNNILEKVVLKVLEDQQHTTLTR ELLQTLYTSLCTLVRRVGKVULGNINMVVRMKFLDEKGSGFVSDL SSYCHKEVYNKERLINSLNYD/SCSGERKEGHRS*DQNS\NPTHYV RILBLIARSQLTSLSGILAGROPPOSSISER GERM-YSSGORGPTTGGGSSSGGGGFTFTTHSPGGFFVFTDFTSGGG SGPPANSGSSISHRTGGTGTAAVQCAGFTSSGJAR MRSQAGLTUWGSGPFQGGGGAGGGGGGGGGGGGGGGTA*LDP /NQVSPPQPW-GAERNGDRGGGSSGGGGFTSTANDARGPPSTCG SGPPANGSSGGVLQERNERWVGRAGGFTSSRJAADGP PQSQGRGPTQGTVGTERLLSGLGSARARAPVP-LPSDPAS TTPKRGTRGFGSGGVLQERNERWVGRAGGFTSSRJAARTPSTC SGPPANGTGGGGGGGAGGGGGGGGGGGGGGGAGGGGAGGGG				GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
ADTWROEQIGCCGARCALRS*DSKKC*EGISGKVEIDPVTNQ KASTKWN KQKPISIDBLLCAC\LABEB 6676 277 1678 GNWPTERMAFLDNPTILAHTRQSKVTSDDPTGMCERWLIDEDVD LEKHIPPSWPODSGSEIQGSNGSTQGYVYAQSVDLTSSWPFGIR RRSNTAQRLERLRERERNQIKCKNIQWKENSKQSAQSLKSLER KKSLKEKPPISGKGS ILSVALRQCFLQLNNPFPSKPFDGKGHV GTTATKKIDVIPLHASQDRLLPMTVYMASARVQDLIGLKN YTESGREPKLINDNVSAYCHHARDGSVDTDFPPLDSNEPHHKF GFSTLALVEKYSSGCHISKESLFVE INABGFSLQVDUTKVTM KEILLKAVKRKGSCKVSGSRADGVFEEDSOIDIATVQDMLSH HYKSFKVSMIHRLRFTDVOL/GCALPGURKRADVDCLRPS ADTWROEQIGCCGAACAALRS*DSHKC*EGISGKVEIDPVTNQ KASTKWHIQKPISIDDDLCAC\DLABE GRWPTERNAFLDNFTI LIAHTRQSHVTSDDTGMCEMVLIDHDVD LEKHIPPSMPGDGSGIQSNGETQGVVAQSVDITSSWPFGIR RRSNTAQRLERLRERERNQIKKKSAGARLKSLEVE KKSLKEKPPISGKGILSVRLEQCFLQLNNPFNEYSKPDGKGHV GTTATKKIDVVLPHASQDRLLPMTVSTDDTDMCEMVLIDHDVD LEKHIPPSMPGDGSGIQSNABTQGVVAQSVDITSSWPFGIR KKSLKEKPPISGKGSILSVRLEQCFLQLNNPFNEYSKPDGKGHV GTTATKKIDVVLPHASQDRLLPMTVANASAVQDLIGLICXQ YTSBGREPKLNDNVSAYCHITAEDDGRVDTDPPDLDSNEPHHY GFSTLALVEKYSSFGLTFKSELFVCHANSARVGSLAGE KKSLKEKPPISGKGSILSVRLEQCFLQLNNPFNEYSKPDGKGHV KSILLKAVKRKGSQCKVSOSRADGVPEDSQIDLATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/CCALPFQVHKRRAPVDCLRPS ADTWROEQIGCCGAACAALRS*DSHKC*ESISGKVSLIDPVTNQ KASTKFWIKKRPISIDSLLCAC\DLABE GFSTLALVGXYSSSSSSSISIVTGCTGXFRITTCTLRVLSNFGRQ*LR GFSTLALVGXYSSSSSSSISIVTGCTGXFARTTCTLRVLSNFGRQ*LR FFFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HPPLELVVQSRDAVKHLETVQSCLASLGFVCQHTSHGPP FFFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HPPLELVVQSRDAVKHLETVQSCLASLGFVCQHTSHGPP GCKMTYVKKSTKERHGYGTTGLAFFRTNVV RLLELIARSQLTSLGGIAQNFWNLTUERKPLDEKSGFFVSDL SSYCKKEVYNKENLINSLNYD/SCSCEKEGHAB*ONQNS\DFH GEKMTYVKKSTKERHGYGTTGLAFFRTNVV RLLELIARSQLTSLGGIAQNFWNLTUERKPLDEKSGFFVSDL SSYCKERVYNKENLINSLNYD/SCSGEKEGHAB*ONQNS\DFH FFFTULTCTL/KRVGKSTLCHGTGATRFTDATLGSRFPNVV RLLELIARSQLTSLGGIAGAGRAPGAVYPMETTLHMQOLN NIQITRVSGQAPPPGSSSLHRDTGQTRQDFEPTPVTESSGLF FNRNETSCTTLCTLVKRVGKSSLVANTHNFTLEKVGARAPAVP*LEDSGLF FNRNETSCTTLTCTLTRVTGARSSULVANTHPTSGTANLAGRAPSATPC SGPPANSTGGGSGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1		KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
6676 277 1678 CNWPTERMAFLINNFTI ILAHRIGSBYUTSDDTGMCENVILIDEDUD LEKHHPPSMPGIBGSBIQGSNGETGGYVYAQSVDITSSHDFGIR RRSMTAQRIERIRKERGNQTIKCKINJOWKERNSKQSAGELKSIER RRSMTAQRIERIRKERGNQTIKCKINJOWKERNSKQSAGELKSIER RRSMTAQRIERIRKERGNQTIKCKINJOWKERNSKQSAGELKSIER KKSLKEKPPISGKQSILSVRLEQCIQLINNPFREYSKFDGKGHY VTSEGREPKLADVNSACHLIAEDUGEDVDTPPPLSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRKRGSGXACVSGSRADGVFSCBJOINTAVQDMLSH HYKSFKVSMIHRLEFTTDVQL/GCALFFGVLRKRAAPVDCLIRIS ADTWRGGGIGCGAACALRS*BGELKCE GISGDKWEIDPVTNQ KASTKWHIKQKPISIDSDLLCAC\DLAEE GNWPTERMAFLDNFTI LIAHRIGSSTVSTDFTCHCSWALIDEDUG KASTKWHIKQKPISIDSDLLCAC\DLAEE GNWPTERMAFLDNFTI LIAHRIGSSTVSTDFTCHCSWALIDEDUG KASTKWHIKQKPISIDSDLLCAC\DLAEE RRSNTAQLEELRKERGNQIKCKHIQWKERNSKQSAGELKSIEE KKSLKEKPPISGKQSILSVRLEQCIPLQLNNPFNEYSKPOGIR RRSNTAQLEELRKERGNQIKCKHIQWKERNSKQSAGELKSIEE KKSLKEKPPISGKQSILSVRLEQCIPLQLNNPFNEYSKPOGIRGKGHV GTTATKKLIDVILPHSSQDRLLPMTVUTMASARVQDLIGLICKQ YTSEGREPKLADNVSAYCHLAEDOGSESIJOVDNTKVTM KEILLKAVKRKSGGSVATCHLAEDOGSESIJOVDNTKVTM KEILLKAVKRKSGGSVASSARDGVPSEDSQIDIATVQDMLSSH HYKSFRVSMIHRLFFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWRGGGIGGCGAACALRS*BGSHKCSISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLCAC\DLAEE GPSNGSSSSJSLIVTGCSSYNS*INDTGGTLALVENSGRQF\L GFSNGSSSSSSJLIVTGCSSYNS*INDTGGTLALVENSGRQF\L FFFELLIQGGGCHALLDCCPWPFILAVLLSGFRQF\L FFFELLIQGGGCHALLDCCPWFFILAVLLSGFRQF\L FFFELLIQGGGCAACALRS*DSHKKFFILEKSGSFVSDL SSYCKKEVYNKEHLINSLNYD/SCSQEEKEGHRB*NONSN\DFH GEKM-YVYMKSTKERKGVTLGGAFRRKFEDEKGSFVSDL SSYCKKEVYNKEHLINSLNYD/SCSQEEKEGHRB*NONSN\DFH GEKM-YVYMKSTKERKGVTLGGAFRRKFEDEKGSFVSDL SSYCKKEVYNKEHLINSLNYD/SCSGERGGGEGTATLADSPP FVRNLEDTHCKYSTCHTCHARPSGTNATGRAPPSTCC SGPPANSGSSSGGGPGFTGTTALDSRAPPSTCC SGPPANSGSSSGGGPGFTGTSGRANGAGPPFSTCLAAR MRSQAGLICWERGRUVGGGFSSSGGGFTTTHSPSTTCS SGPPANSTCTTCTCTCARGSSSGGGGFTTTHSPSGGAFPSTCLAAR MRSQAGLICWERGRUVGGGFSSGGGFTGTGTLANAGRHPOFOV AQGCPPAGACCWGSQGCGGRGGGGGGGTGTTTHSPLIGHQCADA PQSGGRGPTGGTVGTERLLSGLISAKACGARAPRAVP*LLFSDPAS TIPKKGTRGFGSGGVLQERNERWVGRAGGFTSGARATAPPOFOV *LPAPLSQCPPGAGTGFOCGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
1678 CMPTERMAFLONPTILIANIRQSEVTSDDTGMCERWILDEDUD LEKIHPPSNPOBGSSIZQSINGETGOVAGSVDITSSMDFGIR RRSMTAGRIERIRKERQNQIKCKNIQWKERNSKQSAQELKSLEFE KKSLKEKPPISGKQSILSVELEQCIQLINNFPREYSKPDGKGHV GTTATKKIDVYLPHISSGDRILPMVVYMASARVQDLIGLICNQ YTESGREPFALMDNVSAYCHHAEDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSGALFSKESIFVE INAAGFSLQUVDTKVTM KEILLKAVKRKGSQKVSGSRADGVFEEDSOIDIATVQDMLSSH HYKSFKVSWHIRLFFTDVQL/GCALFGVLARFRAPVDCLRS ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC*\DLAEB GROWPTERMAFLDNPTIILAHTRQSHVTSDDTGMCEMVLIDHDVD LEKHPPSMPGDSSSIQSNBETQGVVAQSVVITSSWPFGIR RRSNTAQKLERLRKERGNQIKCKNIQWKENSKGSAQELKSLEV KKSLKEKPPISGKGSLISVRLDQCPLQIANNFPNSYKFDGKGHV GTTATKKIDVYLDHSSQRFLLPMVVYMASARVQDLIGLCOQ YTSBGREPKLMDNVSAYCHALBDGEVVTAQSVVITSSWPFGIR KKSLKEKPPISGKGSILSVRLDQCPLQIANNFPNSYKFDGKGHV GTTATKKIDVYLDHSSQRFLLPMVVYMASARVQDLIGLICQO YTSBGREPKLMDNVSAYCHALBDGEVVTAQSVVITSSWPFGIR KKSLKEKPPISGKGSILSVRLDQCPLQLANNFPNSYKFDGKGHV GTTATKKIDVYLDHSSQRFLLPMVVTMASARVQDLIGLICQO YTSBGREPKLMDNVSAYCHALBDGEVVTAQSVVITSSWPFGIR KKSLKEKPPISGKGSILGVKSDPVTNQ KSTATKFULVKYSFGLIFSESI-FVULNAGFPSLIQUNDTKVTM KEILLKAVKRRGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHKLRFTTDVQL/GCALFFGVURKRAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGNKVSTDVTVNQ KASTKFWIKQKFISIDSDLLCAC\DLAEB GFSNGSSSSSSILIVTGTCTLTKVLSSNFGRQ*LR PPPCSQLPMSQGCIMHLDCCCPWPYIFQOMRKGRGRMN*QS LLGSDQSSSSSILIVTGTCTLTLVLSSNFGRQ*LR PPPCSQLPMSQGCIMHLDCCCPWPYIFQOMRKGRGRMN*QS LLGSDQSSSSSSSILIVTGTCTLTLGATARTSHAPP PKKYSFVMYKENLINSLNYD/SCSGEKEGHRS*ONQNS\DFH GEKNIYVHKENSTERHERGTCTLGAFARTSHAPULPULG FLFFLLIGTLTVTSLCTLVKRVKSVLVANINVMTSTLHHQOQLN NIGITRVSGQADPPGSSSLHRDTGQTRQDFEFTPVTEESGLF PKRNEPSTTSCCTLVTRVKSVSLVANINTMPSTTLTLGOLDAAC SYCKKEVYNKENLINSLNYD/SCSGEKEGGETGTTSA*LP /NQVSFPOM*GABENGDQRGKERGEELHRSSGITAAPGFF EVHNLLGTFGGFSGSGGHG*GFSSAGHA*SA*LP /NQVSFPOM*GABENGDQRGKERGEELHRSSGITAAPGFF EVHNLLGTFGGFSGSGGGGGGGGTGTTTHSPLSHGRAPCFRCWH* WODFSSFPTGCLGGTARGAYSAPATVPLEFSFTATDSAGARAPFAVP*LPSDPAS TIPKKGTRGFGGGFOULGENRRVVGRAGGFTSAGAGATAPFOV *LAPALSQOPGATEFOURGCMAPSFSGTTGTATVANGRHPGFOV AQGCPPGAGCWGGFGGSGGCGGTTTTHSPLSHGRAPCFRCWH*				ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
LEKIHPPSMPGDSGEIGSNGETQGVVYAQSVDITSSWDPGIR RRSMTAQRIERIRKERQNQIKCKNIQMKERNSKQSAQELKSIER KKSIKKERPISKGSILSVRIEGCPLQLINNPRMEYSKPDKGIR, KKSIKKERPISKGSILSVRIEGCPLQLINNPRMEYSKPDKGIR, GTTATKKIDVYLPHISSQDRILPMTVVTMASARVQDLIGLICWQ YTESGREPKINDNVSAYCLHLAEDDGEVDTDFPPPLISNEPIHKF GFSTLALVEKYSSPGLTSKESLEVRINARAFGSLIQVDNTKVTM KEILLKAVKRRKGSCKVSGSRADGVFEEDSJDLIATVQDMLSSH HYKSFKVSNIHRLRFTTDVQL/CCALFPGVURKRAPVDCLRPS ADTWRCGGIGCGAACAALSS*DSHKC**BGISGDKVSIDPVTNQ KASTKKVMIKQKFISTDSLICAC*\CALFPGVURKRAPVDCLRPS ADTWRCGGIGCGGAACAALSS*DSHKC**BGISGDKVSIDPVTNQ KASTKKVMIKQKFISTDSLICAC*\CALFPGVURKRAPVDCLRPS ADTWRCGGIGCGGAACAALSS*DSHKC**BGISGNKVSIDPVTNQ KASTKKVMIKQKFISTDSLICAC*\CALFPGVURKRAPVLIDHDVD LEKIHPPSMPGDSGSIGGSNGTGVYAQSVDITSSWDFGIR RRSNTAQRLERLRKSRQNQIKCKNIQNKERNSKGSAQELKSLFF KKSLKEKPPISGKQSILSVRLEQCPLQLINNPFNYSKFDKKGHV GTTATKKIIDVLDHASSQDRLICKNIQNTWATASARVQLIGLICWQ YTSEGREFKLNNVSAYCHLOVTVATASARVQLIGLICUCWQ YTSEGREFKLNNVSAYCHLOVTVATASARVQLIGLICUCWQ YTSEGREFKLNNVSAYCHLORDGEVTYADSARVQLIGLICUCWQ YTSEGREFKLNNVSAYCHLORDGEVTYADSARVQLIGLICUCUCHTVXVM KSILLKAVKRRKGSQKVSGSRADGVFEDSGIDTATVQDMLSSH HYKSFKYSMHYRLKFTTDVQL/CALFPGVURKRAAPVCLRPS ADTWRCGGIGCGGAACAALSPSDSKCGGGNKRGVGTVAG KSTKKFWIKQKFISTDSDLICAC*\DLAES GFSNQSSGSISITVTGCSSYWS*INDTCTTRUVLSENFGRQ*LR ADTWRCGGIGCGGAACAALSPSDSKCGGGNKRGVGTN*QS LLGSDQSSVGLEDLVFVSPLIHLVLIGLFP*PHELFLLPVULG FIFPLLLQGGCHCLVLPANLVSQAPQIGKSGCRRRN*QS LLGSDQSSVGLEDLVFVSPLIHLVLIGLFP*PHELFLLPVULG FIFPLLLQGGCHCLVLPANLVSQAPQIGKSCRQRRRN*QS LLGSDQSSVGLEDLVFVSPLIHLVLIGLFF*THLESCHGP 6679 2 786 LEFAGGAMPFIGQDWRSFGQNWKTVDGWKRFLDEKSGSFVSDL SSYCUKEVYNKENLFRUSINTDJSTATLLDSRTATLDSRTSPTVV RLLELIARSQLTSLSCTALSFRSTYCTLCBAFRYVV RLLELIARSQLTSLSCTALSFRSTYCTLCBAFRYTYV RLLELIARSQLTSLSCTALSFRSTYCTLCBAFRYTYV RLLELIARSQLTSLSCTALSFRSTYCTLCBAFRYTYV RLLELIARSQLTSLSCTALSFRSTYCTLCBAFRYTYV RLVKNSTKERRIGYCTLCBAFRYTYNEYRGFTPYTESSGLF P\RKNEPDTHCPRGGRAFCFVHLKVRGSVLVORHVYRNETHTLRQCQLM NQTFRSGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6676			KASTKFWIKQKPISIDSDLLCAC\DLAEE
LEKTHPFSMPGBGSEIGGSNGSTQGYVIAGSVDITSSWDFGIR RRSHTAGRERINKERQNDIKKINIOWKERNSKQSAGLKSLEFE KKSLKEKPPISGKQSILSVILEQCPLQLANPPNEYSKPDGKGNV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICKO YTSEGREPKLINDNYSAYCLHIABDGEVDTDFPLDSNEPIHKF GFSTLALVEKYSSFGLTSKESLEVRINAAHGFSLIQUDNTKVTM KEILLKAVKRRKGSGKVGSGRADVEEPSQDILATVQDMLSSH HYKSFKVSNIHRLRFTTDVQL/GCALFFGVYLKRRAAPVDCLRPS ADTWRGEQIGCGGAACAALS*DSHC**BGISGKVEIDPVTNQ KASTKFWIKQKPISTDSDLCAC\DLAEE GMPHTERMAFLDNPTIILAHTRGSHVTSDDTGMCEWLIDHDVD LEKIHPPSMPGDSGSEIGSNBGTGGYVYAGSVDITSSMDFGIR RRSNTAQRLBEIRKERGNQIKCKNIQWKERNSKGSAGELKSLEFE KKSLKKEKPISKGSLISVELEGCJUNDPFNYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLJPMTVTMASARVQDLIGLICKO YTSEGREPKLINDNYSAYCLHIABDGUTDFPPLOSNBPIHKF GFSTLALVEKYSSPGLFSKSSLISVELEGCJUNDPFNYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLJPMTVTMASARVQDLIGLICKO YTSEGREPKLINDNYSAYCLHIABDGUTDFPPLOSNBPIHKF GFSTLALVEKYSSPGLFSKSSLISVELEGCJUNDFPNYSKPDGKGHV KEILLKAVKRKKGSQKVSGSRADGVFEBSGJIDTATVQDMLSSH HKSFRVSMIHRLRFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWRGEGIGCGGACAALRS*DSIKC**BGISGBKVEIDPVTNQ KASTKFWIKQKPISIDBLLCAC\DLAEE 6678 221 865 GPSNGSSSSLSIVYGGSSYSS*INDTCTTLTVLSSNFGRG*LR HPLELVUQUSDAWKAGCHNYNGKSQRNRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLEVVDLG FLFPLLLQGGCHCLVLPANLUSGAPQIGKESCHQTHDLGSRN HPLELVVGRIDAVKHLETVGGGLASLGFVQGNTSRGPP GESCHYVUKLGSTKRHYDVGCASKFPNVV RLLELIAKSQLTSLSLAFVGCNTSRGPP SYCHKEVYNKELLFNSLAVD/SCSEKSCHAP*ONGN\DPH GEKTYVUKLGSTKRHGYCTLGBAFNRLDFSTAILDSRFRNVV RLLELIAKSQLTSLSLAFLGVGNKFMNILEKVVLKLEDQONITLIR ELLQTLYTSLCTLVKNVGKSVLVONINMWVYNETLIHQQOLN NQTTRVSGGAQPPPGSGSLKRDTGGTROPDFTFTFTESSGIF PLATHFMFALFGMAGERNEKOMPT-GPGGFTGFTFTFTESSGIF PLATHFMFALFGMAGERNEKOMPT-GPGGFTGFTFPTFTESSGIF PLATHFMFALFGMAGERNEKOMPT-GPGGFTGFTFTTCS SGPPLAPPGFTGLRFSGGSSGGGG**PGGTTTARAFGFF EVHNNLQTFFGGSSSGGGG**PGGGARGAGELHRSSSGLTARAFGFF SVHNNLQTFFGGPSGSSGGGG**PGGTTANATGEAFFTTTCS SGPPLAPPGFTGLRFSGGSSSGGGG**PGGTTANATGEAFFTTTCS SGPPLAPPGFTGLRFSGGSSSGGGG**PGGFTTYTTSLGAAAAGFFPGFY *LPAPLSQPPGATERQVARCAGARPFSFTTCCS SGPPLAPPGTGLRFSGGSSSGGGG**PGGFTTANATGEAFFSTTCCS SGPPLAPPGTGLRFSGGSSSGGGG***PGLFVOKV\GAIGAAQD PQSGGRPTGGTVGTFMLSGLGSSKACP	1 00/8	"'	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
RRSHTAQRIERIRKERQNQIKKNI OWRENNSKOSAGELKSLEE KKSLKERPISKOS(SILSVRLECCPLQLINPPNEYSKPOKGHY GTTATKKIDVYLPHHSSQDRILPMTVVTMASARVQDLIGLICWQ YTSEGREPKLINDNVSAYCLHIAEDDGEVDTDPPHESSNEPIHKF GFSTLALVEKYSSPGLTSKESLEVERIPGVURKRADVOLTREIN KEILLKAVKRRGSCKVSGSRADGVEEEDGULATVQDMLSSH HYKSFKVSNIHRLERFTDVQL/GCAPFGVURKRADAVDCLRES ADTWRGEQIGCGGAACAALSS*DSHKC*BGISGDKVEIDPVTNQ KASTKFWINQKPISIDSDLLCAC*DSTGMCEMVLIDHDVD LEKIHPPSMPGDSGSEIQGSNGSTGGYVYARGAVDVITSSMPFGIR RSNITAGRLERLIRKERRONGIKKNIGWKERNSKGSAGELKSLEF KKSLKEKPPISGKGSILSVRLECCPLQLINPPNSYSKPDGKGHV GTTATKKIDVYLPHISSCOPLLIBMTVANSARVQDLIGLICWQ YTSEGREPKLINDNVSAYCLHIAEDDGEVDTDFPPLOSNSPIHKF GFSTLALVEKYSSFGLTSKESLFVZINARAHFSLIQUDINTKVTM KSILKAVKRRKGSGKVSGSRADGVPEEDSQIDLATVQDMLSSH HYKSFKVSMIHRLEFTTDVQL/GCALFFGVLKRRAAPVDCLRFS ADTWRGEQIGCCGAACAALRS*DSIKC*BGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAES GFSNQSSGSLSLIVTGCSSYWS*INDTCTTTLRVLSSNFGRQ*LR FPPCSQLFMSGGCMHLDCCCCWVYIFLLHVLLGLFP*PHELFLLDVVDLG FLFFLLLLGGGCHCLVPANFLLHVLLGLFP*PHELFLLDVVDLG FLFFLLLGGGCHCLVPANFLLHVLLGLFP*PHELFLLDVVDLG FLFFLLLGGGCHCLVPANFLLHVLLGLFP*PHELFLDENGSRN HIPLELVVGRWADAVKHLETVGSLASLGFVCGHTSHGPP 2 786 LEFARGAMPFLGDWRSFGGNNVKTVDGWKRFLDEKSGSFVSDL SSYCKEVYNKENLFNSLNYD/SCSQEKEGHAE*ONNS\DPH QEKNIYVHKGSTKRRHGYCTLGBARNRLDFSTATLDSRRFMVVV RLLELIARSQLTSLSGIAAKNFWINDFSTATLDSRRFMVVV RLLELIARSQLTSLSGIAAKNFWINDFSTATLDSRRFMVVV RLLELIARSQLTSLSGIAAKNFWINDFSTATLDSRRFMVVV RLLELIARSQLTSLSGIAAKNFWINDFSTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLVPRISGSGEBGICTSA*ALP /NOVSPPOPM*GABERGOORGGKEBAGEEHRSSSGLTAAPGFP EVHRNLQTFPGLPSRAGGGP/GGRGTQGSSAGGGP*SCALTGAPGFP EVHRNLQTFPGLPSRAGGRPGGSSSGGGF*POTFTVTEESGLF P\RKNEPDTHCPRGEARREDY-RLLRAPGFTSTCG SGP\PAPPGFTGLFRGGSSSGGGF*POTGSRLVANGRHFGPOV AQGCPPGAGCWGSQFRGSGRCPRTYTHSDLGRAPCPFRCWH* WODPPSSBRTGCLEPGILDRANGSFTSPFGIRTARAFGFP *LPAPLSQPPGAGCWGSQFRGSGRCPRTYTHSDLGRAPCPFRCWH* WODPPSSBRTGCLEPGIRRANGSFTSRPGIRTGRAPCPRICWH*				LEKIHPPSMPGDSGSEIQGSNGETQGYVYAOSVDITSSWDFGIR
GTTATKKIDYIPEHSSORLLPMTVUTMSARVQDLIGLICNQ YTSEGREPKINDNVSAYCHIABDGGUDTDFPPLDSNEPHHKE GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKREKGSQKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFFGVLRKRAPVDCLRSS ADTWRQEQIGCCGAACAALRS*DEHKC*EGISGDKVEIDPVTNQ KASTKWHIKQKFISIDSLLCAC/DLAEE GNWFTERMAFLDNFTIILAHTRQSEVTSDDTGMCEWLIDHDVD LEKIHPPSMPGDSGSIQSMGETQGYVYAQSVDITSSDFGIR RRSNTAQRIERLRKSRQROIKKHIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCFLQLANDFWEYSKFDSKGHV GTTATKKIDVTYLPIHSSQDRLIDWVTMSAAVQDLIGLICNQ YTSEGREPKLNINNVSAYCHTAEDDGEVDTDFPDLOSNSPIHKF GFSTLALVEKYSSPGLTKSESLFVRIAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKVSHHIRLRFTTDVQL/GCALFFGVLRKRAAPVDCLRFS ADTWRQEQIGCGGAACAALRS*DHOTGTFLRVLSSNFGRQ*LR GFSNGSGSSLSIVTGCSSYWS*INDTGTFLRVLSSNFGRQ*LR FPPCSQLPMSQGCLWHLDCCCPWPYIPGQQWKGKQRWRN*QS LUGSDQSSGSLSIVTGCSSYWS*INDTGTFLRVLSSNFGRQ*LR FFFPLLQQGGCCLGVLVPANLVSQGLGSLGFCQHTDELGSRN HHPLFLVVGRWDAVKHLETVQSKGSLGSGVGCTHFDFDVDLGSRN HHPLFLVVGRWDAVKHLETVQSKGASLGFVGORTSGSP 2 786 LEFARGMPFIGQDWRSFGQNWKKTVGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNTD/SCSSPEKEGIAZ*ONNS\DPH QEKN:YVHKGSTKERHGYCTLGBAFRRLDFSTAILDSRFRWYV KLELLIARSQUTISLGTAQNFNLIEKVLKVLUEQQNTLILR ELLQTLYTSLCTLVKRYGKSVLVGNINMAVYRMETILHWQQQLN NQTYVSGQAQPPPGSGSLHRDTGGTPFFTYTESGLF P\RKNEPDTHCPRGRAPBFV*HLPKHBSGEGSABIGTSA*ALP /NOVSPPQPM*GASENODGRGGKAGREELHKSSGITAAPGPP EVHNLQTFPGLPSRGGOP/GGAGTQSWAPGSGPP/SPLDPAS MQRSQALFGWEAGCHESGFNHIPFALRFSGGSSTATAPGPP EVHNLQTFPGLPSRGGSP/GGAGTQSWAPGSGPP/SPLDPAS MQRSQALFGWEAGCHESGFNLINGGLSAKACPARAPAVP*LPSDPAS TIPKKGTRGFGGGSGFQLGENSTNATGAFFTTCG SGPVAPGGGUAGGRUNGAGGFTSADAAGTAPPOV *LPAPLSQPPGATEPQVARCGMAPPSPGTSGRLWAGRHEGOV AQGCPPGAGCWGSQPPGSGRCGRTTTHSFLGRAAQFTR		1		RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
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HYKSFKVSMTHRIRFTTDVQL/GCALFPGVLRRRAAPUDCLRPS ADTWROEDIGCGACACALS-BISHKC**BGISGKVBIDPVTNQ KASTKPHIKQKPISIDSDLLCAC\DLAEE GNMPTERMAFLDNFTIILAHIRGSHTVSDDTMCEMVLDHDVD LEKIHPPSMEGDGSSIGGSNGETGGYVYAQSVDITSSMDFGIR RRSNTAQRLERLKERGNQIKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLKNPFNEYSKFDGKGHV GTTATKKIDVYLDHSSQDRLDMTVVTMSARVQDLIGLIGWQ YTSEGREPKLNDNVSAYCLHTAEDDGBVDTDPPDLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGPSLIQVDNTSVTM KEILLKAVKRRKGSQKVSGSRADGVFEBSQIDIATVQDMLSSH HYKSFKVSHIHRLRFTTDVQL/GCALFGVLKRRAAPUDCLRPS ADTWRQEQIGCCGAACAALRS HYKSFKVSHIHRLRFTTDVQL/GCALFGVLKRRAAPUDCLRPS ADTWRQEQIGCCGAACAALRS GFSNQSSGSLSILVTGCSSYMS**INDTCTILEVLSSNFGRQ**LR FPPCSQLPMSQGCLHHLDCCCFWVPYIPOQWRKGRQRMRN*QS LLGSDQSSVGLEDLCVFWNFLLHVLLGLFP**PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQICHSHGPC HHPLFLVVQRWDAVKHLETVSGLASLGFVGQHTSHGPP HFLFLVVQRWDAVKHLETVSGLASLGFVGQHTSHGPP GEKMIYVIKGSTKERHGYCTLGBAPNRLDFSTAILDSRRFNYVV RLLBLIARSQLTSLSGIAQKWFMILERVULKVLEDQNITLLIR ELQTLYTSLSCILVKRVGKSVLVQNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLMRDTGGTRODFEFTPVTEESGLF P\RKNEPDTHCPTGGARPSVHKQMPLAFGFGTWGTFVGSISBE P\RKNEPDTHCPTGGARPSVHKQMPLAFGFGTWGTFVGSISBE FVHKNLQTFPGLPSRGGGP/GGAGTQGSWAPGBQPFSFTCS SGP\APPQFTGLPFRGGRSSSGGGF**FGLFVKVGALGAAQD PQSQGRGPTQTTVGTEMLSGLGSKACPAARPAVP*LPEDPAS TIPKKGTRGFGGEGFGVLQEKRNWVGRAQFTSADAGTAPPGV *LPAPLSQPPGAGCWGSQPRSGRCFNTYTHSPLGHGRAPCPRCWH* WQDPPSSPRTGCLFGIPARQASSAFTRSAPGITRTGAAPGFF	1			GFSTLALVERYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
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GNMPTERMAFLDNPTITLAHIRGSHVTSDDTGMCENVLIDHDVD LEKIHPPSMPGDSGSEIQGSNGETQGYVYAGVDITSSWDFGIR RRSNTAGRLERLRKERGNGIKCKNIQWKERNSKGSAGELKSLIFE KKSLKEKPPISGKGSILSVRLEQCPLQLNNPFNEYSKPDGKGHV GTTATKKIDVILPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPPIHKF GFSTLALVEKYSSPGLTSKESILFVRINAARGFSLIQVDNTRVTM KEILLKAVKRKRGSGKVSGSRADGVPFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLEFTTDVQL/GCALFFGVULRRRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*ESISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLCAC\DLAEE 6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTTLRVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWPYIPGOWNKGRQRMRN*QS LLGSDQBSVGLEDLCVYPNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLELVVGRWDAVKHLETVQSGLASLGFVGQKTSKGPP GEKNTYVHKGSTKERHGYCTLGEAPNRLDFSTAILDSRFRNYVV RLLEILAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMVVYRMETILHMQQQIN NIQTTRVSGQAQPPPGSGSLHRDTGGTRQDFSFTPVTESGLF P\RKNEPDTHCRRGEARPEV*HLPKPHSPGSEGABIQTTSA*ALP /NQVSPFQPM*GABENGDQRGGKEAGRELHRSSSGLTAAPGF? EVHRNLQTFFGLPSRGGGPGGGGTGGSWAFGEPPFSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPGFFSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPFSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPFSPTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPFSPTTCS SGP\PAPPGPTGLRPGGGSSGGGRARACPARAPAVP*LPSDPAS TIPKKGTRGFGGFGPGVLQERNWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGAGCWGQPPGSARACPARAPAVP*LPSDPAS TIPKKGTRGFGGFGPGVLQERNWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGAGCWGQPPGSQRCPTSTTHSPLGHGRAPCPRRCWH* WQDFPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				WASTYPHILYOYDISTRONA CON CONTROL OF CONTROL
LEKIHPPSMPGDSGSEIGGSNGETGGYVYAQSVDITSSWDFGIR RRSNTAQRLBRLRKERQNQIKCKNIQWKERNSKQSAGELKSLFE KKSLKEKPPIGKQSILSVRLEQCPLQLNNPFNEYSKPDKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLMDNVSAYCLHTABDDGEVTTDFPPLOSNEPIHKF GFSTLALVEKYSSPGLTSKESILFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMHHRLFFTTDVQL/GCALFFGVLRRAAAPVDCLRPS ADTWRQDGIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GFSNQSSGSLSIVTGCSSYMS*INDTCTTLRVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWVPYIPQQWRKGRQRMN*QS LLGSDQBSVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQADQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASIGFVGQHTSIGPP GEKWIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRFRNYVV RELLEILAKSQLTSLGGIAQKNFMILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQIN NQITRVSGQAQPPPSGSSLHDTGQTRQDFEFTPVTESSGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGABIQTSA*ALP /NQVSPPQPM*GABENGDQRGKERAGEELHRSSSCLTAAPGFP EVHRNLQTPFGLPSRGGOP/GGAGTGGSWAPGEQPP/SPLLPAS MQRSQAGLFGWBAGLWSFTHHTPALRPSGTNATCBAFPSTTCS SGP\PAPPGTTGLRPGGSSSGGHG**PGLPVGVJLSAAQD PQSQGRGPTQGTVGTEMLSRGGSSGGHG**PGLPVGVJLSAAQD PQSQGRGPTGGTVGTEMLSRGGSSSGGHAFPSPTTCS SGP\PAPPGTTGLRPGGSSSGGHG**PGLPVKVJLPSDPAS TIPKKGTRGFGGSPGVLQERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATCMCSQCRGRCRAPARPAVP*LPSDPAS TIPKKGTRGFGGSPGVLQERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATCMCSQCRGRCRCPRTYTHSPLGHARAYGFIR *AQCPPGAGCWGQPRSQRCRCPRTYTHSPLGHARAYGFIR *CPPRAGYGGPTGCLPGIPRAQAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAQAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR *CPPRAGYGGPTGCLPGIPRAGAYSAPRTRSRPGIRTGRAAYGFIR	6677	277	1678	GNWDTERMARI, DNDTI II ANTRO GIRITORDEMON CONTROL
RRSNTAGRLERLIKERQNOILKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLIMTVVIMASARVQDLIGLICWQ YTSEGREPKLINDVSAYCLHIAEDDGEVDTDFPPLOSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGPSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQLDIATVQDNIJSH HYKSFKVSMHHRLRFTTDVQL/GCALFFGVURKRAAPVDCLRPS ADTWRQDGIGCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GFSNQSSGSLSIVTGCSSYWS*INDTCTTILRVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWVPYIPQQWRKKGRQRMIN*QS LLGSDQSSVGLEDLCVFVNFLLHVLLGLFP*PHELFILPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLPLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMFFLGQDWRSFGQNWKTVDGWRFKDENSSFVSDL SSYCHKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGEAFRRLDFSTAILDSRFFNYVV RLLBLIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQDLN NIQITRVSGQAQPPPGSGSLHRDTGGTRODFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGABIQTSA*ALP /NQVSPPQPM*GABENGDQRGGKERAGEELHRSSSGLTAAPGGFP EVHRNLQTFFGLPSRGGGP/GGAGTQGSWAPBGPP/SPLLPAS MQRSQAGLPGWEAGUVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGTVGTENGLSSGGMA*PSOPP/SPLLPAS MQRSQAGLPGWEAGUVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGTVGTTGTLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGGP/LGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWVGRAGGFTSADAAGTAPPGV *LPAPLSQPPGATGEDQULGERNRWTGRAPGTRTGRAAVGFIR *UDDPSSPRTGCLPGIPARAAYSAPRTTSSPGITTGRAAVGFIR *WQDPPSSPRTGCLPGIPARAAYSAPRTTSSPGITTGRAAVGFIR	1 1			LEKTHPPSMPGDSGSETOGSNGPTOGSVDTGMCEMVLIDHDVD
RESLRERPFISCKQSILSVRLEQCPLQLNNPFNEYSRPDGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIAEDDGEUDTDFPPLOSNEPIHKF GFSTLALVEKYSSFGLTSKESLFVRINAAHGFSLIQVDNTXVTM KEILLKAVKRKKGSQKVSGSRADGVFEEDSQIDIATVQDNLSSH HYKSFKVSMHRLRFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWROBQIGCGGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GFSNQSSGSLSIVTGCSSYWS*INDTCTILVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWVPYIPGQWRKGRQRMRN*QS LLGSDQSSVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPFLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVCQHTSHGPP 6679 2 786 LEFARGAMPFIGQDWRSFGONWKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYJCSCSGEKBGHAZ*ONOMS\DFH QEKWITVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNITNMWVYRMETILHWQCOLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFFPTVTEESGLP P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSGEGABIQTSA*ALP /NQVSPPQPM*GAEENDQDRGGKEKAGEELHRSSGGLTAAPGGFP EVHRNLQTFPGLPSRGGGP/GGAGTGGSWAPGBQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGTVGTEMLSSCLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGEGPGVLGERNRWVGRAGGFTSADAAGTAPPGV *LPAPLSQPPGATGEDVRACMAPPSPGTSGRLVANGRHPGFPV *LPAPLSQPPGATGEDVRACMAPPSPGTSGRLVANGRHPGFPOV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTTSRPGIRTGRAAYGFIR	[]			RESITABLE PLEKERONO I KOVITOWY PROCESSEL WILLIAM
GTTATKKIDYTPLHSSQDRLIPMTVUTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYDLHIAEDDGEVDTDFPPLDSNEP IHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVPEEDSQIDIATVQDMLSSH HYKKFKVSMHRLRFTTDVDL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSNQSSGSLSIJVTGCSSYWS*INDTCTTLRVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQSSVGLEDLCVFVNFLLHVLLGLPP*PHELFLLDPVDLG FLPPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGMPFIGQDWRSFGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCHKEVYNKENLFNSLNYD/SCSQEEKEGHAE*ONDNS\DFH QEKWIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAKONFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLGTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFFETPVTEESGIF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSSEGAEIQTSA*ALP /NQV3PPQPM*GABENGDQRGKERGEBEHRSSGCITAAPGF? EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHTPALRPSGTNATGBAFPSTTCS SGP\PAPPGFTGLPSRGGGSSSGGHG**PGLFVKV(JALGAAQD PQSGGRGPTQGTVGTEMLLSGLSSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRCWH* WQDPPSSRTGCLPGIPARQAYSAPRTRSRFGIRTGRAAYGFIR	l i			KKSLKEKPPISGKOSTISVPIFOCDI.OLAMIDEMEVOVDDOVOM
YTSEGREPKLNDNVSAVCLHTAEDDGEVDTDFPPLDSNBPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDLATVQDNISSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQRFISIDSDLCAC\DLAEE GPSNQSSGSLSLIVTGCSSYWS*INDTCTTLRVLSSNFGRQ*LR PPPPCSQLPMSQGCLWHLDCCCPWVFYIPGQQWRKGRQRMRN*QS LLGSDQBSVGLEDLCVFVNFLLHVLLGLFP*PHELFPLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGGNWVKTVDGKKFFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHA*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKXVGKSVLVGNINMWVRMETLHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGOTRQDFEFTPVTESGGLP P\RKNEPDTHCPRGFARPEV*HLPKPHSPGSEGABIGTSA*ALP /NQVSPPQPM*GAEENGDQRGKEEAGEELHRSSSGLTAAPGFP EVHRNLQTFFGLDSRGGGP/GGAGTQGSWAPGEQPP/SPLLFAS MQRSQAGLPCWEAGLVESPTHHTPALRPSGTNATGBAFPSTTCS SGP\PAPPGFTGLKFFGGSSSGGHG**PSCHVANGAPGP PQSGGRGPTQGTVGTTMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTARPGV *LPAPLSQPPGATEPQVVACCMAPPSFGTSGRLVANGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRFGIRTGRAAYCFIR	1 1	ł		GTTATKKIDVYLPLHSSODRI LIDMTWYTMASAPWODI TCL TOWO
GFSTLALVEKYSSFGLTSKESLFYRINAAHGFSLIQVDMTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKVSMIHRIFFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFFIKQKFISIDSDLLCAC\DLAEE GFSNQSSGSLSILVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWVPYIPGOQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLEPLLLQGGCHCLVLFANLVSQAPQIGKLSCRLQTHDLEGSRN HPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNONS\DFH QEKWIYVHKGSTKERHGYTLGBAFNRLDFSTAILDSRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVVRMETLHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGABIQTSA*ALP /NQVSPPQPM*GAEENEQQRGGKERAGEELHRSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWAGCLVESPTHHIPALRPSGTNATGEAFPESTTCS SGP\PAPPGFTGLPFGGSSSSGHG**PGLFVGKV\GALGAAQD PQSQGRGPTGGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGGPGGVLQERNRWVVGRQGFTSADAAGTAPPGV *LPAPLSQPPGATCHPARCAMAPPSPGTTSGRLVANGRHEGPQV AQGCPPGGSCWSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAPYGFIR	1 1			YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKE
KBILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKVSMIHRLEFTTDVQL/GCALFFGVURKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSNQSSSSLSLTVTGCSSYWS*INDTCTTLRVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELPLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HPPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH QEKWITVHKGSTKERHGYCTLGBAPNRLDFSTAILDSRRFMYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSGABIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKEEAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGGTQGSWAPGGPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS GGP\PAPPGFTGLRPGGGSSSGGHG**PGLPVGVGALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGFGGULQERNRWVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVACGMAPPSPGTSGRLVANGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLFGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	·			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIOVDNTKVTM
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LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVANGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				TIPKKGTPGFGFGGGU OFFINITION NOOFFCANAL TIPKKGTPGFGFGGGU OFFINITION NOOFFCANAL TIPKKGTPGFGFGGGU OFFINITION NOOFFCANAL TIPKKGTPGFGFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	I			AOGCPPGAGCWGGODDGGODGDDTVTTGDT CUCDA DODDC
FQGGGGG		ł		WODPPSSPRTGCLPGTDAPOAVCADDTDCDDCTDTCDAAACOT-
1			ľ	FOGGGGG

SEQ	Predicted	Predicted end	Amino paid some
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
1	İ		KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
		ļ	LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH*LINARLTRYQ
1		İ	TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS
1]		SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
			S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
		·	VRRRIELIQDFEMPTVCTTIKVSKDGOYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSOSG
	-		FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRINLEOGRYIN
			PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRWRWGT.I.
ĺ			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGOVLT.Y
1	1		DLRSDKPLLVKDHQYGLPIKSVHFODSLDLTLSADSRTVKMWNK
	ł		NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGTYVTPVI.
6683	109	100	GPAPRWCSFLDNLTEELEENPESNE
""	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
1	1		VRRRIELIODFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
ł			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIBFHSQSG
1			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
-			PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
1			D\AP+TVSQQIQR+TSLPTISALKFN\GALTMAVGTTTGQVLLY
			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
f			NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL GPAPRWCSFLDNLTEELEENPESNE
6684	111	527	GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA
			PP\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG
1			ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS
			RNIVQNYR
6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
1			QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT
	,	ļ	ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
1 1			LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRVTOEVICO
			IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCES
	ľ		VLAFENPQVSMTLVNVLVDGELLPOIFVKMLORDKPTEMOLTSA
1 .	1	İ	KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERIJEERVEGA
1	İ		ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSATTDIK
ļ i	1		RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVI,
6686	310	927	TASROGVTST
ļ [<i>'</i>	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
į l		İ	QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV
	1	ſ	LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGYDFITT HYYTSTCFOR SUBGRIDERY
<u> </u>			SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMIND DAKKEED COURSE TANDED TO STATE
			EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
]			SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
			IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
1			PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
			LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF
			SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
i	İ		LPSDGGTGFPSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
į	•	l :	STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE
1	İ	1,	VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC
ľ		[•	TMSELEELFSLFSPAPLLSKLFTSSGSIAICCQDSGPSDTGRLS
			VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL
			The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- (amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SSAVIPGYSSSSDSRLNTVPTVDLLCPFQTKSST
6689	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
1			AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVST*scret.ce
ľ			FFSDSISFCFSSSSFCKR*FVSSKVSONALLSSRISNGBGGGGV
İ			QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAT.*I.SI.NOPE
			GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMIJJJJJJJJJGSGOGP
		ļ	QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMUMTQ
1		1	YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
- 6500			GDGLAIWYTKDRMQP
6691	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
1	1	j	DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYOASKPDALEK
1	İ		LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLOSESIVNRRKPC
İ	1		HEHDAFENIVHCSKSQFLLGONHDIFDLRGKSLKSNLTLANIOSK
İ		1	GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASOKLISTYSOR
ŀ			ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHOVMHTGEKDUD
j			CSLCEKAFSRKFMLTEHORTHTGEKPYECPECGKAFI,KKGBINIT
			HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC
6692	178	939	/GKGFIQKTCLIAHQRFHTER
	-:-	239	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRYAKKCQVE
	1		RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
	,		DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
	1		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
Į.	1		RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
l			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
	j		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVFOGLT
İ	ļ į		DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWOTSU
6694			SCLVFQPVLWPEYTFWNLFEAILOFOMNHSVI.OK
0034	292	813	SLLLHLAPPGAYTPSOPLSSVSTETASSVRROAAESPOHELDUR
			EVHSLGQILPQDGLTAEAGPPEAODPWGSPGTSI.PAAHIGEAAA
]		i	LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIOLGTTHAA
6695	292		NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVVFLD
1 0055	232	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
1	ļ		LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
6696	-	782	NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
	-	702	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRKFQLCAD
1			LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
			DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
1 1			RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
			TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
6697	3	782	LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKQIKSS
1		.02	PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR
		į	IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKLRNE
1		1	LQTDKPF1PLVEKFVDTDIWNQYLEYQQSLLNESDGKSKWFYSP WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES
i			IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
			SL\SGGESSSONTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6698	668	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
6699	325	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
1	Ì	l i	LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK
		1	NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
- 1	sequence	boquence	\=possible nucleotide insertion)
			ESKRIIYNHAFFFQESKWSGGILQ
6700	1098	1392	ESKRITINHAFFFQESKWSGGILQ
*.**	1 2050	1372	TQCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
ļ	ł		FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
6701	2	1485	LLIGLCNLIGK
1 */**	-	1405	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
	1		RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRLGI
ì			IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF
	Į.		FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
j			QTKFGDYNONTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ
1			ASABYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC
j			KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
I			STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
			LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ
			SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM
1			VCCEBEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
6702	397	107-	LLTGSRSQVLAR
""	39,	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
			RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
			NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
}			LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
			ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
i .			YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL
i i			LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
1			VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
1			SPOTELRSDFOCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
1			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
1 1	1		RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
6703	45	1244	YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT GVGPRAAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
			KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
1 1	Į.		YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE
	i		LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
 	1		TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
1 1	1		VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
1 1	j		IGYSGHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
			PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
1			KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
			TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG
	1		LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNEIQRIAEQE
			LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
1			YKQKLKREESVRIKKEAEEAELQKMKAIQREKSNKLEEKKRLOE
			NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
1 1			MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKROOOEOR
1 1		į	RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
			GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
1 F			SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
1	1	1	LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
1 1	1	}	AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
1 1		Į	VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY
		i	PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	PTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDK1FRAHKVVL
į l	[AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
j i		ŀ	LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSOP
			EK EK

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	Talengine M Matting, Kabysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [sequence	sequence	Codon, /=possible nucleotide deletion,
6707	2233		\=possible nucleotide insertion)
1 0,0,	2233	1343	YWSGIGYELQHFHWRKFHFEKKGPPSTCQBRLYESRSRWPCIS*
		1	GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSORASKCHS
1	1	J	FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NU
1	1		SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC
	}	ļ	NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRI.CEH
	1		TD*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARVA
			C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
ł	}		GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL
			ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDIQIYSR
	1		QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES
	i i		GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN
1			A WILD DATA CONTROL OF THE PROPERTY OF THE PRO
1	ľ		AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ
1			NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
1			VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH
1	1		FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKIIAKG
1	<u> </u>		EELLSPINLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV
	1 1		ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI
ĺ			ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI
6709	3	894	LDE\ECLRPGE
		034	PPHEHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
	j		TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP
	1		PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK
1			DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ
			FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKRQLILF
1	i i		GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCQ\
6710	158		IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF
1	135	980	RHKMTNYRVESSSGRAARKMRLALMGPAFIAAIGYIDPGNFATN
1			IQAGASFGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI
1 1			RDHYPRPVVWFYWVQABIIAMATDLAEFIGAAIGFKLILGVSLL
J J			QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI
			FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI
1 1	ı		WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGFVNLAIMATAA
6711	3		SELNFYGHTGVA
1 "' 1	3	347	VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK
			ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMOIIFKELIMI
-			MAMLTWSYHDNMHDADYGPGQQHRPG
6712	118	578	PHGQKRTRYPQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR
	ł		FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENTDDWTAVHV
1 1			VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDBRQYRR
			PAKLSAPRYMALLMDWIESLI
6713	2485	3	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
			PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
	Į.		QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
l I	·		ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
]	ì	ļ	AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
		1	MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL
		ļ	IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
		i	VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
			GROCALITATION A DOLLAR TO THE PARTY OF THE TARKEN LAKETE
		J	GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
' !	1	j	RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
	}	1	GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ
1	Į.		YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL
		ľ	VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ
- 1			GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS
		<u> </u>	EVVGRKRQRSGPNRGAKRRREEARQRDQEFYIPYRPKDFDSERG

SEQ	Predicted	I Described	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	A=Alanine, C=Cvsteine, D=Aenartic Acid n
	location		Giutamic Acid, F=Phenylalanine G-Glygina
1	corresponding	corresponding to first	H=H1Stldine, I=Isoleucine, K=Targine
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	sequence	sequence	Codon, /=possible nucleotide deletion,
	Dequence		\=possible nucleotide insertion)
	1		LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
1			FVGQSGQEDKKKIKTESGRYISSSYKRDIYOKWKOKOKID+C+1
1	Î I		GRRGILTRRRPRTEEVGEARPLAOAGCIPGPHAPPHDIOAEGA
6714	169		LELKTKQQILKQRRRAQKAALSLORWWPOAAT.CPO
0,14	109	1416	NNCQELLPPPPAPMAHIPSGGAPAAGAAPMGPQYCVCKVELSVS
1			GQNLLDRDVTSKSDPFCVLFTENNGRWIEVDRTETAINNIMDAR
ł]		SKKFVLDYHFEEVQKLKFALFDODKSSMRLDEHDFTGOFSCSIG
1	1 1		TIVSSKKITRPLLLLNDKPAGKGLITIAAORI.SDNRVTTI.SI.AG
1	i i		RRLDKKDLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKVTLDDVM
Í	1		KPFTVPLVSLCDGDMEKPIOVMCYDYDNDGGHDFTGFFOTGVGO
1	1		MCEARDSVPLEFECINPKKORKKNYKNSGIIII.RSCKINDDVG
1			FLDYILGGCQLMFTVGIDFTASNGNPLDPSSIHVTNPMGTMFVI
			SAIWAVGQIIQDYDSDKMFPALGFGAOLPPDWKVSHEFAINFND
6715			[TNPFCSGVDGIAQAYSACLP]
1 0,13	32	493	GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP
			GKPKHLGVPNGRMVLAVSDGELSSTTGPOGOGEGRGSSLSTHGT
}	·		PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEPS
6716			AENVTFWKACERFQQIPASDT
0,10	1	176	GAGGPAPRSFGSEEPRAALERDKMSARAAAAKSTAMEETAIWEQ
6717			HTVTLHRVSLCCSK
6/1/	115	896	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
1 1	I		YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN
	I		FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG
1	ļ		PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMT
f			GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
			WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF
6718	290	599	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
	1		VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
			LEKEKKLDIMKTATO
6719	1	691	PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
	1		DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
			QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT
			RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP
1			DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
			RKSSSVTSSG
6720	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
- 1			VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
1			QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
i	1		LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
1	i		IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1			VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
			SVVTLISE
6721	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
1	1	1	VPITEXSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
		İ	QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
1		Ī	LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
1	ļ		IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1	j		VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
	ł		SVVTLISE SVVTLISE
6722	1	390	
1			RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE
I		İ	LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
6723	173	659	PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW
ļ			VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
- 1		1	GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
		<u></u>	AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

SEQ	Predicted	Predicted end	I have a six a
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Ristidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown *-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
6724	1.55		VEVKELQREPLTPREVOSVREHLGHESDNI.
0/24	173	659	VCQYCTARMADFGISAGOFVAVVWDKSSPVRALKGIJDKLODUT
1			GNEGRVSVENIKOLLOSAHKESSFDIILSGLVPGSTTLUGAETT
			AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKICSALTISGI.
6725	356		VEVKELQREPLTPEEVQSVREHLGHESDNI.
0,25	336	722	RRRTPPVILATMDDDLMLALRLQEEWNLQEAERDHAQESLSLVD
1	i		ASWELVDPTPDLQALFVQFNDOFFWGOLEAVEVKWSVPMTLCAG
6726	98		1CSYEGKGGMCSIRLSEPLLKLRPRKDLVEVFFV
0,20	, ,	714	HLQKMERKINRREKEKEYEGKHNSLEDTDQGKNCKSTLMTLNVG
1	{	•	GYLYITQKQTLTKYPDTFLEGIVNGKILCPFDADGHVRIDPDGL
			LFRHVLNFLRNGELLLPEGFRENOLLAGEAFFFOLKGLAFFUKG
			RWEKEQLTPRETTFLEITDNHDRSOGLRIFCNAPDETSKIKSBI
6727	1 .	831	VLVSKSRLDGFPEEFSISSNIIQFKYFIK
	_ '	031	FRGMGDERPHYYGKHGTPQKYDPTFKGPIYNRGCTDIICCVFLL
			LAIVGYVAVGIIAWTHGDPRKVIYPTDSRGEFCGQKGTKNENKP
i l			YLFYFNIVKCASPLVLLEFQCFTPQICVEKCPDRYLTYLNARSS
			RDFEYYKQFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA
1	.		RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRFLAGIMG
			RGMIIMGILVLGY
6728	486	935	FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA
1			VIDVDVMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD
1 1	ļ		LIFNOPDRROLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK
6729			HVPSALKEADSLMRRDT
6/29	259	1191	VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV
1 1			LAGVKKFDVPCGGRDCSGGCOCYPRKGGRGOPGPUGDOGVMGDD
] [GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGT
1	i		PGHPGQGGPRGRPGYDGCNGTOGDSGPOGPPGSFGFTGDDCDOG
1 1	ŀ		PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQM
1 1	ł		GPVGAPGRPGPPGPRGQQGNRGLGFYGVKGEKGDVGQPGPN
]			GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE GIM
6730	784	1015	
l 1			nmvdyyevlgloryaspedikkayhkvalkwhpdknpenkeeae Rkfkevaeayevlsndekrdiydkygteglnef
6731	1	446	GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS
1	1		LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY
()	ł		NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA
			LIKTARVEINRKDEEI
6732	102	1205	GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW
	į	ł	AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN
		İ	LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE
			GRGRLAPQNGGSSDAPAYRTPPSROCPPRUPESPEPPPEUVODER
		ŀ	PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAVVIRSDORDORD
1		ļ	PUBLICEMKTRRTTRLQOOHSEOPPLOPSPVMTRRGIPDSUSSPP
į.		ſ	DEASSQTDLSQTISKKTVRSIOEAPAVSEDLVTRTRRRPDT.RVDD
l	ļ		YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG
6733			DKTTRSSSQYIESFW
6133	613	1311	RSCRQVGMRSRNQGGESASDGHISCPKPSTIGNAGEKSLSEDAK
i	1	1	KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLT
		į.	QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVI.P
1	l	1	VLHRDAILAQEKSIGEDVYEKPISELDRLEEKOKETVRPMLEOL
- 1	1	f	LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEGERERLKK
6734	189		LLEQEKAYQARKE
		551	SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD
			AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, O=Glutamine, P=Arginine
	residue of	residue of	S=Serine, T=Threonine, V=V=line
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine Y-Unknown + a.
İ	sequence	sequence	Codon, /=possible nucleofide deletion
	†		\=possible nucleotide insertion)
6735	280	558	TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA
			QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI
C736			XDGCT
6736	195	808	MNYELNPKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFEN
		i	SSSNPILLRRIEELNKTASGNVEAKVVCFVPPPDTENTT TMT AD
ŀ			AMARETERESETTVEADLTDKOKHOLKHRET.FT.SDOVERT DAME
		ł	TRUKCSVALLNETESVLSYLDKEDTFFVSIAVDDCLVTLL ADVO
6737	150	1209	BIRVGPRYQADIPEMLLEGTFFCVFAVL
			PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLESYRPDTDLS REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
1	1		REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
1			CVALALY YHI KNRDPDGRMLLDI FDENT.HDI.SKSEVDDDVDVID.
i		l	PEQUALIKEVRILESAAOLIAECAIVTI.VVI.EDI.I.TVARIDICO
1			ANWARIVLGAILLASKVWDDOAVWNVDYCOILKDTTVEDMNERE
1			ACT LELLQIN INVPSSVYAKYYFDIRSI ARAMM. CERT PRI CRE
6738	148	653	RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
1			CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL WGAPWTHGRRSNVRVITDENWRBLLEGDWMIEFYAPWCPACQNL
]			QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
6739			KDGEFKKYQGPRTKKDFINFISDKEWKSTEDVSGWP
0/39	3	631	SWPDMAEEEVAKLEKHLMLIROEVVKLOKKLAETEVEGALLANG
1	1		ANALSSESFISRLLAIVADI.VEOFOVEDI.VIVIZODDIVI CALLED
1	i		VLAARSDSWSLANLSSTKELDLSDANDEVIMINI DMILVEDDI DE
	1		REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TABELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
1 1	-		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
1		}	VLAAKSUSWSLANLSSTKELDLSDANDEVTMTMI.DWIVTDELER
1 1			REDUVELTELMKLANRFOLOLLRERCEKGIMGLINNIPNCTDEVO
6741	141	960	THEELNASTLMNYCAEIIASHWVSEVEGVNKAT.
ĺĺĺ		960 ·	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
1	1		HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
1	. [YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
1 1	1		DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
		1	PLAIGILQEGEFESLARRGLLFLACOGNCVVWNI.TGGTGDEVTO
6742	141	960	HIPKIKIP
1			PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
!			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
	ł	1	YDLNSNNPNPIISYDGVNKWIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
	1	1	PHAIGILQEGEFESLARRGLLFLACOGNCYVWNI.TGGTGDFVTO
6743	1		BIPKIKIP
	*	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
İ	ſ	1.	ALIKACSDLEKATATTALIFRNSSDSDGKI,EKATAKDI.I.OTOEDN
			FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
6744	95		DOMIK
			RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT
1		i	DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
- 1	į	[4	SNEEHTQEPUCSLEAOPKYVRGGKRYGRRSI.DEFORSVEEEDE
1		; `	1 VISPLUSEARPSHIPAGDCSEHWKTOPSEEVEARGOLDERNIN
			DLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

SEQ	Predicted	Predicted end	I had a self desired and a self
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
f	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
1			PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCT.
1		}	DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
6745	 		TLALENELLVTKNSIHQACI
0/45	1	588	TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQNNP
-			AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
1	1		ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
			PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
6746	110		RTCQKYIDKYGPLQELEETA
0,10	110	492	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQTTEI
	1		SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
5747	247	484	VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
]/	404	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
6748	201	665	QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
1]	003	MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNL
ł	1		LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC
			QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALDGAM
			SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
1 .			VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQSVSQ
			INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQLQL
			HAKTGQSADSGTIKAKLSGPSVEELERELKAN
6750	3	428	SCESRRPGAKWVWASGALPRDTTGLGSEOPSGDVAOSNRATMGT
1 1	·		TAPGPIHLLELCOOKLMEFLCNMDNKDLVWLEEIOEEAERMFTR
			efskepelmpktpsoknrrkkrrisyvodenrdpirrrlsrrks
6751	152	2425	RSSQLSSRR
3,32	132	1417	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
1 1	,		NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
1 1			QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL
1 1			FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
			SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
J			GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
1 1		ĺ	FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
			YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD
<u></u>			ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMOYSHHCEHLLERLNKOREAGET.
(I	1		CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDOSO
	ļ		VKADGFQKLLEFIYTGTLNLDSWNVKEIHOAADYLKVEEVVTKC
1 1	ł		KIKMEDFAFIANPSSTEISSITGNIELNOOTCLLTLRDYNNREK
1	1	1	SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGONKTVOV
1 1	1	į	PSDILENASVELFLDANKLPTPVVEOVAQINDNSELELTSVVEN
1 1		į	TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAR
			NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
	i	1	CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF
]	ļ	l	HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
		ſ	CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
	İ		KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
1			HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
6753	2	1305	TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
1	- 1	1303	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS
[PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG
	1		SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS

SEQ	Predicted	Drodi-t-3	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	I INTREGULANCE CECVSCOINA DENOMACEIA NASA E
i	location	corresponding	Glutamic Acid, FaPhenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
Í	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion,
			PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
ł		}	GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE
	,		KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
1	1		EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
			EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE
			VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE
i i			LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ
			PLREMIIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
6755			NEATH
6/35	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
			CGNGTGLRNRNGSAIGLPVPPITALTTPGDVPUCOTEDI DVDGG
			LUFER LILLVALFIOYINIYKTVWWVDVNHDACCTOL METER
j			IDIHLAAFITVMLARRLVWALISEATKAGAASMIUVMII TCARI
ļ	i		VLLTLCGWVLCWTLVNLFRSHSVLNLIFI.GVPEGVVVDLCGPUO
i			DSKAHLLLTDYNYVVOHEAVEESASTVGGIAKSKDELSI I POI
			KEQFNNATPIPTHSCPLSPDLIRNEVECT, KADENUD TUBER ENG
6756	180		LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVMVTMMVFT V
	100	754	I IERALGSLPLSIPVSWGSLRTLKYOOOPI.PRVVLLCOMPVOGVE
1	,		LESS OPPOSITE TITE
-1	İ		REAUXRKKKKEKESGMALTOGPITERDVATERGOEDWCZ NOVA
ı			KALYWDVMLENYRNLVPLGKDNFALEVKICPRVFLYFLCCT.SWF
6757	2	459	PEHILTETEALLTHK
	_	423	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
			TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
1			FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ AANQGEFQKPDNKLHQQVLW
6758	1	1008	ASCERI DEBERDE POR DER DE POR
l	1		ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
			RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPS LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCGGGGATK
1	1	1	PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
1	}		TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
			VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT
1		i	QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE
			WFSTLFPRIPVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
1		1	LUHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPTTGT.GT.C.
- 1	,	í	NFEESVLNYRFDPLGIVDGFTAEVGASGAFCDTHI.TI.DVDVC.EV
6760	239		SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTTOM/CV/
- , • •	433	606	VLSKKKGLSAEEKRTRMMEIFSETKDVFOLKDLEKTADVEKGTE
	1		AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFDSKATHADVINTE
6761	29		VLESQLSEGSQKHASLOKSIEKAKTGRCETREDT
1	۶.	1733	ERTLRGLREVAAPSDVADAAVSRRGRCCCCLHCTOTOVACDCDC
1	[1 .	SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALACLUACUD
1		3	NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEDAHAGETGVG
į		į į	MLTGV1AGAVFTSPAVGSILAAIRAVAOAGTVGTLLTVVMVVVD
		[]	RUNFGLAREQARAEGIPVEMVVIGDDSAFTVI.KKAGPPGI.GCTVI
		1 2	LIHKVAGALAEAGVGLEEIAKOVNVVTKAMGTLGVSLSSCSVDC
		į s	SKETFELSADEVELGLGIHGEAGVRRIKMATADETUKTMI.DUMT
1		J [NITNASHVPVQPGSSVVMMVNNLGGLSFLELGI TADATUDGLEG
	ļ	1 1	KGVKIARALVGTFMSALEMPGISLTLLLVDEDI.I.KI.TDARTEDA
1	!	į F	AWPNVAAVSITGRKRSRVAPAEPOEAPDSTAAGGSASKPMAT.UT.
I			
		4	RVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
		Į E	RVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQRL

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
	ľ		QVAFITLAVAAGLYYLAELIEBYTVATSRIIKYMIWFSTAVLIG
-			LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
ļ			LVVVNHYLAFQFFABEYYPFSEVLAYFTFCLWIIPFAFFVSLSA
1	ł	i	GENVLPSTMQPGDDVVSNYFTKGKRGK
6763	2	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
			RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
	1		LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
			SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISK
			ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYLTELEDGF
1	ĺ		YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
6764	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
			KKWQRTDHBLGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
			RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
6765	3	550	ARYSRVDHFCRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL
	_	330	RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
			NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
			VIALGLPFGKVTNILMLKGKNQAFLELATERAAITNGNYYSAVT
		•	PHLENO
6766	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
			AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT
			KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
1			VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL
1			QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ
			ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ
)		•	LQELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF
			RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
1 (IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
			AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
6767	336	919	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV
1 1			GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
1			RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT
1	1		PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
L1			NPDATEILHVKKKKALLL
6768 .	2	363	PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE
1 1	l		LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLOAV
1			ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6769	284	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
6770	1	397	QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMOVPRVEK
1	ł	1	ITLNMGVGEAIADKKLLDNAAADLAAISGOKPLITKARKSVAGF
			KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
		İ	WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEOIQCM
			QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	1	1400	AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA
1 1			CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
1 1	1		P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL
1 1	ľ	ļ	HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY
1 1	1	ļ	LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
1 1	,	į	AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT
		ŀ	IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
1		j	QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
		ļ	FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
1	ľ	ľ	TAPCNAACSCOPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG
	į		QKVYRDCSCIPQNLSSGFGHATAGKCTST

SEQ	Predicted	Predicted end	l minor
ID	beginning	nucleotide	
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ł	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6773	1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
i	1		RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
		į.	CVNMPSGPHCLCPOHLTGNHCOKEKCFRDOLLDEPUVNPTHVPT
			EQAAVARCQCKGPDAHCORLASOACRTNPCLHCCDCL FURGURI
6774	 		CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGTAD
1 0//4	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSESKIICS
6775	704		GLRIGFLTGPKPLIERVILHIOVSTLHPSTFNOLMISO
","	104	614	TCPSQLRVLTARGGRRAPSPOLWTI.VI.ALTEEVWDSUDII.DMVG
	ļ		GRPEIMENLPALYTIFQGEVAMVTDYCAFIKIDGCDKOGLUUDT
}	ŀ		HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVGLGMVIADA
6776	3	1108	QGTGKDLDPNNV\SLSKKRGGGDPSRTTT.cppspt.pt.c
	_	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLH
1			INGITENTSDADMEPCVDGWVYDRISESSTIVTEWDIACDOOST
1	ł i		TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
1			CAALAPTFLIYCSLRFLSGIAAMSLITNTIMLIAEWATHRFQAM
1	1		GITLGMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIFLTS
			SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL
			KSTMXKELEAAQKKKPFLGERLHMPNICKRISLLPFTKFANFMA YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHWGSG
			RVSSRGRVNCLGLFVLQVW
6777	779	63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
]		GRSLGLYAWDDGSPLALLGGHQGGITHLCPHPDGNRFFSGARKD
ł			ABLLCWDLRQSGYPLWSLGREVTTNORIVEDIDDTCORIVECOR
1			SGAVSVWDTDGPGNDGKPEPVLSFLPOKDCTNGVGLUDGLDIIG
1	ĺ	•	HCLPVSVCFLSPTESGGRRRGAGPSLGSPPRHVHI.ECDI.OLIMIC
6778			GGGARLQHP**SPRARKGR
0776	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EETAGDSE/ERSPEEE
1 1		ļ	VQADPKIRSASPKCPTSSPFPKGRSPFGEGET\ npektueubcn
1			KDKSVAEKN\KGP\SPVSSEGIKDFFSMKDFWFNI.NOCNTDDAMI
6779	2		T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENV
	- 1	535	RALRROPRLLAANGIEPESMAISEPIKGSRKPCVNKEBLALKKP
l l	1		MAKCAWKGPREPPODARAEAESPGGASESDODGGUEGDDVVVAI
1 1	1		AW VSAKNPAPMRKKKKVSLGPVSYVI.VDSEDCPKKDIMPVVCDC
1 1		İ	SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
6780	3	403	
1 1			HEVNDNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD
} }		. [SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
			LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
6781	1	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS
			SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT
		ľ	SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
1			TPVFINSSSIIQVMKGSQPSTIPAAPLTINSGLMPPSVAVVGPL
! i			HIPQNIKESSAPVPPNALSSSPAPNIOTGRPIJJLSSPATDVOLD
ĺ		į.	SPPCTSSPVVPSHPPVQQVKELNPDEASPOVNTSADONTLDGGO
İ	1	1 :	STIMVSPLLINSPGSSGNRRSPVSSSKGKGKVDKTGOTTTTVAC
	1	1.	KKVTGSLEKGEEQYGADGETEGOGLDTTAPGIMGTEOLSTELDS
		ļ.,	KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGAI.PTSVPSTVTT
6782		•	EVPSELISAVPTTKSNHGGIASESLAG
0.02	3	1327	RKPTVIRIPAKPGKCLHEDPOSPPPI.PAEKPICNTESTUCCVIC
[1 1	NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTTPTOOPPTV
- 1			VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLOKKOSMLATGE C
ļ		1 1	KAKSQVFKNQDPVLPPRPKPGHPLYSKYMISVPHGTANEDIVSO
}		1 1	PGELSCKRGDVLVMLKOTENNYLRCOKGEDTCDVHLSOMVLTT
		E	PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEQ	Predicted	Predicted end	Amino colid
ΩΣ	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI
1			PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
- [}	LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
			PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
6000			l +
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1	†		TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
		ĺ	GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
1	į.		LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
1	ļ		PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
ļ			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
			PUKLAFMVSLGLVTHDHLEEIOSKROERKRRTTANDUVSGAVER
	1		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVIGEGALTDTGDGG
1			SAPOSPENEKTETTFTFPAPVOPVSLPSPTSTDGDTHEDECSVC
1			RKSGQLLMCDTCSRVYHLDCLDPPLKTTPKGMWTCPPCODOMI V
1			KEEALPWPGTLAIVHSYIAYKAAKEREKOKIJKWSSDLKOPPPO
1	1		LEQKVKQLSNSISKCMEMKNTILAROKEMHSSI.FKVVOT.TDI TIT
l	i l		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSOSCT
6784	3		ANCNOGEETK
	1 1	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
ı			TMPASVVGQRPTIAMVTAINSOKAVI.STDVONTDVMI.OTSCVVM
Ì			GPGALAVQIVAKNTVTLQVOATPPOPIKVPOFTPPDPI.TPPPNE
	1		DPQVRPRPVAQNNIPIAPAPPPMLAAPOLTOPPVMT.TVETTDTTT
1			PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
-			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
1	' [PQKLAFMVSLGLVTHDHLBEIQSKRQERKRRTTANPVYSGAVFE
[PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC RXSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
			KEEAI PWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
1			LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
1 1	1		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSQSCT
			ANCNOGEETK
6785	1	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
	İ		LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
1			KPSPVKKERSPRPQSFCHSSSISPODKIALPGFSTDDDKODLEY
6786			GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPDTTPPP
0,00	1820	1397	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSVOSO
1 1			INHIRNGIDILVGTPGRIKDHLOSGRLDI,SKT,RHTMI,DEVDOMT
1 1			DEGFAEQVEDITHESYKTDSEDNPOTLLFSATCDOWLVTUALVV
1 1		[YMKSKYEQVDLDGKMTQKAATTVEHLAIOCHWSORPAVIGDVI O
1	i		VISGSEGRALIFCETKKNVTEMAMNPHIKONAOCLEGDIAGGO
1 1			ELTLKGFREGSFKVLVATNVAARGI.DTPEVDI.VTOSSBBODVBG
		1	YIHRSGRTGRAGRTGICICFYOPRERGOLRYVEOKAGITEVENG
1			VPSIMULVKSKSMDAIRSLASVSYAAVDFFPPSAODI.TEEVCAT
	,		DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLERTODVCC
1]	1	AWKELNRKLSSNAVSOITRMCLLKGNMGVCFDVDTTPGFDIOAD
		1	WHOSDWILSVPAKLPEIEEYYDGNTSSNSRORSGWSSGPSGPSG
	Į.		KSGGRSGRSGRQSROGSRSGSRODGRPRSGNPNPSPSGGUVDS
		i i	FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
6787	2646		SVMN
		2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
1		f -	FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGTTGTCHHAWT T
6788	16		LVFLVEMGFHHVGQAGLKLLTL\VIHPPWPPKTTGIOT
1		336	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
L			REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ

WO 01/53312

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Grutamic Acid, F=Phenylalanine G-Glyging
	location corresponding	corresponding	n=nistidine, i=Isoleucine K=Tycine
	to first	to first	L=Leucine, M=Methionine, N=Asparagine
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, TaThreonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATOR
			FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEVTAWAMUDGGG
		,	NVKARSSYNEKTPRIVVSRSHSGMVKOVALOTEGNOTTTIDAGG
1			AGYKVLALLDVPDKSQEKADLYIHVTYTKKWDTCAGNATTKATG
			GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT
6789	2	678	GNGINULKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
			GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE
			GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
1			PGVFVLLACGIMSSTCGOLASYPLALVPTPMOAOAGTECADELT
1	į į		MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
6790	2	40.50	TLGVQSR
	-	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
1			EPDVSGDPHVAF5SSSSISGSYSPGYAKTNKRGGAGGWSpenen
1 .			HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
'			KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARVVRIVPLDWNG EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVI
j			ALNPKTSESEGVILHGEGQQGDYITLELKKAKLVLSLNLGSNQL
			GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFR
			TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNEKGCMESTNWAG
1 1	İ		VNITDLARKKLEPSNVGNLSFSCVFPVTVPVFWNATCVI BYDC
			RENODEFSVSFOFRTWNPNGLLVFSHFADNIGNVETDI TERROC
1 1	ſ		VAINTIQIAMSQIDISSGSGLNDGOWHEVRFLAKRNEATITIOG
			DEASAVRINSPLQVKTGEKYFFGGFLNOMNNSSHSVI.OBCBOCC
			MQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCE
			HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTFVVG
			YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL
			NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
			YYCNCDADYKQWRKDAGFLSYKDHLPVSOVVVGDTDBOGGBAVI
			SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFOGRTSADTCDVDV
I I			TLTPWGVFLENMGKEDFIKLELKSATEVSFSFDUGNGDUFTUR
1			SPTPLNDDQWHRVTAERNVKOASLOVDRLPOOTRKAPTECUTEL
- 1	1		ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI
ĺ			SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD VGAFFBEGMWLRYNFQAPATNARDSSSRVDNAPDQQNSHPDLAQ
.	į.		EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG
1	1		GTREPYNIDVDHRNMANGOPHSVNITRHEKTTFLKLDHVDGVGV
		}	HLPSSSDTLFNSPKSLFLGKVIETGKIDOBIHKVNTDGFTGGLC
	f	1	RVQFNQ1APLKAALRQTNASAHVHIOGELVESNCGASPI.TI.SDM
1		j	SSATOPWHLDHLDSASADFPYNPGOGOAIRNGVNRNSATICGUT
		[A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGGPOV
6791	1801	1193	KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
1	1		TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW SAVV*SWLTAASTKVQAILLPQPLE*LGLQIAFMASLATHFSNQ
	[NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV
	1		EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
6702			LRMGNGALHGDHQRFSTFAGFLLFETK
6792	33	1073	VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVIJ
- 1	ļ	ł	PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
]		1	CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLROALYGHTOAV
1		1	TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA
			ITISDVSGTIVSCAGAHLSLWNVNGOPLASITTAWGPRGA LTCC
j			CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
	ŧ	1 4	APGSASKPKRPQVGEEPGLESRAGR*HCFDREAQQNQP\PVTAL
_ 1	i	Ι,	AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Truntophan V-Truncing V V-land
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	Judanie	\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
		""	LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
ŀ			YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
[VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV
	Į.		ACTIFICATING CEVIPOLIDIAENDIATING CEVIPOLITICA ACTIFICATION CONTRACTOR ACTIFICATION CONTRACTOR ACTIVITIES ACTIVITIES ACTIVITIES ACTIVITIES ACTIVITIES ACTIVITIES ACTIVITIES ACTIVITIES ACTIVITIES ACTI
1	i i		ASILEGCAFLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
1			SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
1	}		YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
1			CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
i			ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
			HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	169	1349	DDVKRKPEASAH*EXPGPPSRPGVRGGRERAGGRGSHGARSCR\
ļ	[EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
1			NLPTDITEEDPKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
			IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
1			FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
			AFLITTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
			RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
	!		MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR
L			HEEEHRREEEMIRHREQEELRRQQEGFKDNYMENYVCHFLR
6795	1740	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
			TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
			EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
1 1			VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNROLLEEMPR
1			FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
			DEQRERENEAKLSELRALSIVADD
6796	48	683	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
			LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET
1			SVQEGRDCWQR*LPRLFSALVGQPGCWPQGAPPERCV*PGRCKW
i I	.		HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST
6797	1620		SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
0,3,	1020	211	TERMTPSQPTRGSSCTRFSSMLWTSTWRCLTCHWAGMRMSVVGV
1 1	<u> </u>		TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
1			ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP
1 1	1	İ	LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
[1	1	ļ	VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
			TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS* RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
, ,	1		PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
	}		CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
1	1		ASSSTWCSASSSRSSPAPTTPSSIPAQAQRRASCRPTSHSART
	į		APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
1	į		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
j . I			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
1 1	}	1	VFDDEEKSKLLAKLKSKNPDDLQEANKLIKSMVREDEARIQKV
]			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
]		j	ENKRRILFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1		į	QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
		f	PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
		l l	PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
			APSAGSSLFSTGVAPALAPKVBPAVPGHHGLALGNSALHHLDAL
			DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- }	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ļ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- (amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	seducuce	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
ı	1		PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
j	į.		RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSTVLOAAVDVC
ĺ	ſ	1	MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
6799	3894		LTFALGEQLSTEVGEVDQFPPVEOWGNL
0,55	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
		1	ALWGQLRGSGLGRGTTMAKEGOPGSPRLSALECVIJVPO\ POTA
- 1	1		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLVSWTM
	· ·	1	ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKND
1	i	1	VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARTOKV
	i		TKRLHTLEEVNNNVRLLSEMLLHYSOEDSSDGDRELMKELFDOC
J	1		ENKRRILFKLASETEDNDNSLGDILOASDNLSRVINSYKTITEG
	ſ		QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVI.A
			PAPTPPSSGIPILPPPPOASGPPRSRSSSOAEATIGPSSTSNAT.
l	1	1	SWLDEELLCLGLADPAPNVPPKESAGNSOWHLLOREOSDLDERS
ł	1		PRPGTAACGASDAPLLQPSAPSSSSSOAPLPPPFPAPVVPASVP
į	1		APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAT.
1			DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPI.RO
1			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAVDKNGP
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLODAVPKC
}	1	i	MKVKLQPPSGTELSPFSPIQPPAAITOVMLLANPLKEKUPLPVV
6800	<u> </u>		DTFALGEQLSTEVGEVDOFPPVEOWGNL
0800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AC
ŀ	ſ		*PQAW*LGLAPAIAFI/GLTRGRKONKEKMAEGGSGDVDDAGDC
1	1 .		SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA
1			RATRARRAVQKRASPNSDDTVLSPOELOKVLCLVEMSEKDVILE
1	1		AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPTVKEKAI.
i	1		I VLNNLSVNAENQRRLKVYMNOVCDDTITSRLNSSVOLAGI.DI.I.
	1		TNMTVINEYQHMLANSISDFFRLFSAGNEETKLOVI.KI.I.I.NI.AP
1			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
1	1		FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
			VKVGKFMAKLAEHMFPKSQE
6801	2	1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVEDT
	, l		YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKI.
i i	l I		RSQAQSYIAQNFKQLSHMGSIREETLADLTLAOLLAVI.RI.DSL.D
I	[İ	VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDOD
1		İ	YLEGLLTKPIVKKYCLDVIEGALOMRYGDLLYKSLVPVPNSSSS
i		ĺ	/R*QQQLSCICSRKSTPETGYVCOGDGDLLWTPORST.S\RVDBv
		ļ	SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAOPRKDIW
			VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDDITTGIV
			LKEVECYSVQRNQWALVAPVPHSFYSFELIVVONYLYAVNSKDM
			LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
]	}		PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
1			VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
j	ļ	1	QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
			VAPORNAQDQQGSL
6802	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
j !		ļ	PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQWDQQFRSMKELYE
į i	1	İ	RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
			RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
l i		ľ	EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
	1		QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
	ļ		IKACOMEKEKLEKOI KOMKODDONGGI INDITATIONALINSQ
[1		IKACQMEKEKLEKQLKQMYCPPCNCGLVFHLQDPWVPTGPGAVQ
<u> </u>			KOREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR
	!	1	TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
6803			KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN
	1	2203	KLSGR DYRUMGUT CTCVT VDTDVTT TTTTTTTTTTTTTTTTTTTTTTTT

Deginning mucleotide location corresponding continue corresponding cofirst smino acid smino acid smino acid smino acid smino acid smino acid smino acid sequence smino acid sequence smino acid smino aci	SEO	Predicted	Predicted end	Amino acid coment contains at a large
No: nucleotide corresponding to first amino acid residue of amino acid residue of amino acid sequence acid sequence acid seque	1 -			Amino acid segment containing signal peptide
Cocation Corresponding Cofirst Contrasponding Cofirst				
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence should be acid sequence should be acid se	I NO:	L	1	Glucamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid amino acid amino acid sequence ### Sequence ###				
amino acid residue of amino acid sequence ### Security				
residue of amino acid sequence WHITYPODAINA, N-TYPOSAINA, N-TUNKNOWN, "-Stop codon, /-possible nucleotide deletotide d		•		P=Proline, Q=Glutamine, R=Arginine,
amino acid amino acid sequence WHYPYDOPHAIN, Y=TYDOSINE, X=TUNKNOWN, *=SLOP Codon, /=possible nucleotide deletidency Codon, /=possible nucleotide insertion RIVEMIRTIDIS/LGSRMRNTGOPTIFFISHSNLDERGYSINS SILAALER/MOGOFFGRANVOTCKLSERLITISCCTHLS/SMDGEDGE GKLVSREVDINDIVISLSSRNMRD/DETSIRACCEPURAYLDHILL ARTAPHEKLAPTSOKGOLDFFQRAVOTCKLSERLITISCCTHLS/SMDGEDGE GKLVSREVDINDIVISLSSRNMRD/DETSIRACCEPURAYLDHILL ARTAPHEKLAPTSOKGOLDFFQRAVOTCLIMSLVYKAKELHVO WINHYLPTKLDASRPSHILLDFDETSIRACCEPURAYLDHILL ARTAPHEKLAPTSOKGOLDFFQRAVOTCLIMSLVYKAKELHVO GGEVUPKALVLQLKETSSIQEQADILYMLITIMGEDENTELIDERGE TOLLSHOKHLTVGLPEPERKYISAPPRQEDIVISTAMEPHANDLINGERSENGERGOVERLINGER GSILTOELMVILVAKVRETORIALIHITIMGEDENTELIDERGE TOLLSHOKHLTVGLPEPERKYISAPPLYRALIHITIMGERGEFGVERK/SYR PTDSNVSPAISTHEGAVGATTERGTINGKRETORIALIHITIMGERTERGETK SISLAGSREATEGLANISSPANKALLHHILGGKEFGVERK/SYR PTDSNVSPAISTHEGAVGATTERGTINGKRETORIALIHITIMGERTORIAL SISLAGSREATEGLANISSPANKALLHHILGGKEFGVERK/SYR PTDSNVSPAISTHEGAVGATTERGTINGHANGERGVERKISTORIALIHITIMGERGOVERFRUGHT AVEKTIVHANDLEGEKTUGP JOHTMLANDPASTUGHTER AVEKTIVHANDLEGEKTUGP JOHTMLANDPASTUGHTER AVEKTIVHANDLEGEKTUGP JOHTMLANDPASTUGHTER AVEKTIVHANDLEGEKTUGP JOHTMLANDPASTUGHTER AVEKTIVHANDLEGEKTUGP JOHTMLANDPASTUGHTER AVEKTIVHANDLEGEKTUGP JOHTMLANDPASTUGHTER AVEKTIVHANDLEGEKTUGP JOHTMLANDPASTUGHTER AVEKTIVHANDRIALIHIMAR AVEK		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /-possible nucleotide deletion, -possible nucleotide insertion -possible nucleotide insertion	1	residue of	amino acid	
Apossible nucleotide insertion		amino acid	seguence	Codon. /=nossible nucleotide deletion
### WIVEMERTOLSYLCS REWYTGOPT TF PISHENIL DEDGTS: SILAADERMOOD PROGRAMYTCH SEPTITS COTHES PRODUCED GRUSSENDDMYDTLESCAMMODDYSTSHARCDEVARYLDHIL APTAPHENLADTO KOOLDEPOANUTT TOLMSLYT KARGELEY WIVEMPLETTLE OKOOLDEPOANUTT TOLMSLYT KARGELEY WIVEMPLETTLE OKOOLDEPOANUTT TOLMSLYT KARGELEY WIVEMPLETTLE OKOOLDEPOANUTT TOLMSLYT KARGELEY WIVEMPLETTLE OKOOLDEPOANUTT TOLMSLYT KARGELEY ERSATYRELITE IN CKYGE IR WELL IR YI SCHLIKK VERALDEAC TOLLSROCKHIT VOLDEPOPRAKTI SAPLEY FALTOLID OKATATI BERSATYRELITE IN CKYGE IR WELL IR YI SCHLIKK VERALDEAC TOLLSROCKHIT VOLDEPOPRAKTI SAPLEY FALTOLID OKATATI HISLACSABEATEGLAMIS PSAKKHLIGHHI LEGGEK OKATEK / SYR PIDSINS PALS HIELD GLAVERY LEGGER OKATEK / SYR PIDSINS PALS HIELD GLAVERY LEGGER OKATEK / SYR PIDSINS PALS HIELD GLAVERY LEGGER OKATEK / SYR PIDSINS PALS HIELD GLAVERY LEGGER OKATEK / SYR PIDSINS PALS HIELD GLAVERY LEGGER OKATEK / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR PIDSINS PALS HIELD GLAVER / SYR SAR GERFON	1	sequence	1	\-noggihla nucleotide incortion\
SILAALRHOODYFGGARVOTGLISEFLTTSCCTHLS SPINDGER GKLYSBYDDYNYLESGNMINDYDISTSHARCDBVARYLDHLI, ARTAPHRILAFTSGKGGLDRFQANOTTCOLMSLYTKAKELHOO NVINYLDFLICAGSRESHLILDSFHARCDBVOYSVAVEBILLEDD QSGBVDFKALVLOLKSTSLLGGADILYMLYTHKGPDWNTELYN RESATVRELLEYLGASRESHLIDSFHARCHTSKVEALDBEAC TPLLSHORLLIVGLPPEPREKTISAPLBYRALFOLLDEARGDM SISILTOGEUWYLDAWWRTGGGLPARMPRILALUQMATELA HSLCCSAERATGLMNILSFRAMKNILHHILSGKEFGVERK/SVR PTDSNVSPALSHLISHGANAVATKRTGINGLKSBIKQVPERRLS ISAESQSPGTSMTPSSGSFPSATDQSSKDSRGQWGRRRELDG ALARNYVGFYGKWKKVLJKCHGISVEGFVLPSSTTRENTFGSIK FSVHZSAVINVLIRFERRGLUPSATLUTHLISHTBGIK FSVHZSAVINVLIRFERRGLUPSATLUTHLISHTBGIK FSVHZSAVINVLIRFERRGLUPSATLUTHLISHTBGIK FSVHZSAVINVLIRFERRGLUPSATLUTHLISHTBGIK FSVHZSAVINVLIRFERRGLUPSATLUTHLISHTBGIK FSVHZSAVINVLIRFERRGLUPSATKIKLLISHDEHSIGSII AVEKTVHIANDLELGGKTLGF DDTUMANDPASCA LCTLRYD GSFGKREEKAKESICGENSSSSSSDDDEETEKKAKMFPTKKYN KDWWSSIGGOMPKKTIKSLESDDTEAAASPPHPAPEBGVARES LQTVAREBSGSPSVLEEEPPFAVSFKIKLLISHDELNSRAKOR KDWWSSIGGOMPKKTIKSLESDDTEAAASPPHPAPEBGVARES LQTVAREBSGSPSVLEEEPPFAVNSKYLEISHVDRAKAFF OERVARISHSTOTTIVPSGSSEVANKRILLISHSKAFF*COCL- KQ**SARTHTS*KSIYRSKSBKCSGRKFIKKAEKKFF*SNSGK OCKEKRIKL CQ**SARTHTS*KSIYRSKSBKCSGRKFIKKAEKKFF*SNSGK OCKEKRIKL CQ**SARTHTS*KSIYRSKSBKCSGRKFIKKAEKKFF*SNSGK OCKEKRIKL CQ**SARTHTS*KSIYRSKSBKCSGRKFIKKAEKKFF*SNSGK OCKEKRIKL LHCHISTOROVLYCOCCHSTNOPEDLHANVONEHACKLIELSD LKCHMILKHKRIDSNVCRVCKSSFSTIMLLIEHALMEDFYI CKYCDYKTVIFENISGHLADITSSHLYWCGDOVOPSSSSELY LHTGBISCDEQVLCOPCCHSTNOPEDLHANVONEHACKLIELSD KYNNGEHGOYSLLSKITTDEKGKFFFVCVOVG FSSSELY LHTGBISCDEQVLCOPCCHSTNOPEDLHANVONEHACKLIELSD VHETT CKYCDYKTVIFENISGHLADITSSHLYWCGOVOPSSSSELY LHTGBISCDEQVLCOPCCHSTNOPEDLHANVONEHACKLIELSD THATCHTON HAND HAND HAND HAND HAND HAND HAND HAN			 	
GRLYSBOYDDNYDYLSSGMWNDYDSTBHARGGDEVARUBLIC AHTAPHRILAPSGNAGLOFFGANOUTCHBLUTKAKELHVO NVNHYLDTKLFQASRFSINLLDSPHRGENQVESVRUETILEDD QGGRUPKALVLGLKETSSLEQGADILMSLYTKKFEDHUNDEN GRSATVRELLFELYGKGETERHSLIKYISGLKKKVEALDEAC TDLLSHORLTUKLDEARSTEN BERSATVRELLFELYGKVEETERHSLIKYISGLKKKVEALDEAC TDLLSHORLTUKLDEAPSGROME SISILTOEINVYLDAVMRTQGGLPABMPRIRGICLIQVMATELA HSLEGSAEBATBGLMBLSPSAMKNLHHILISGKEFGURKFSVR PTDSNNSPALSIBETGANVLASBEKKGKGVGWGRRRRLDG ALNRYVEGFYGKVMKVLKGKGISVEGFURKSET KYPER PTDSNNSPALSIBETGANVGATKTERTGTMIGLKSETKGVERFALS ISABSGROTSMTPSSGSFPSADQGSKDSRQGWGRRRRLDG ALNRYVEGFYGKVMKVLKGKGISVEGFURDSGAICTRINTYGE STANDAS ALNRYVEGFYGKVMKVLKGKGISVEGFURDSGAICTRINTYGE STANDAS ALNRYVEGFYGKVMKVLKGKGISVEGFURDSGAICTRINTYG SAPSGRRFTMTYLSJRAAATTVQEFLJKISTIAMTGESIT AVEKTIVITAMLDIELDGANTLTSPADTTAMTTENTTGESIK FSVIRVSSAVITAMTUKLERGSTITAMTGESIK FSVIRVSSAVITAMTUKLEGANTITAMTOSTATAMTOKATAMTUKLEGANTITAMTOKATAMTUKLEGANTAMTUKLANDIELDGANTAGAICH DOTTAMADAS (TCTIR, YY) SAPSGRRFTMTYLSJRAAAATVQGFLJKISTAMTOKATAMT GLEEKRASLRTTGFYSGFSEVASKRIKLLANDSBELDGASADR KOWSSIGGGOMPKKTIKELPSDATEKARMTPTKKYN GLEEKRASLRTTGFYSGFSEVASKRIKLLANDSBELDGARADR KOWSSIGGGOMPKKTIKELPSDATEKARMTPTKKYN GLEEKRASLRTTGFYSGFSEVASKRIKLLANDSBELDGARADR KOWSSIGGGOMPKKTIKELPSDATEKARMTPTKKYN GEBURSIKSETDSTTEVDSVAGSLODLOSERS*LASKFY COCKL KQ**SARRTS*SKLSTERSERSSRKFIKKAKMFYNSKAKE OOKKATAMTOKATA	1	1		ANT VEHICK TODS I DESKWANT GOPTITFPISH SMLDEDGTSLNS
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BRSATVRELITELYGKVGETRIMGLIRYISGILRKKVEALDERG TIDLISHORLITTGIP PEPREKTI SAPLPYBATIGLIDEASEGDM SIS LITGE IMVYLAMYMRTQDGLFAEMFRIEDGILIQVMATELA HSLECSAEEATGIMMISPAMKNILHHILSGKEFGVERK/SVF PTDSNVSPAISHEIGAVGATKTERTGIMGKESIKQVEFRLS ISABSGSFOTSMTPSSGSFPSAYDQGSKOSRQGOMRKRILDG ALNEVFUGYVGKWKKVLGKGHGLVSEFFUPSSTTREMTFGEIK FVHNUSS\VLAVULREFXRQLLVEATLVLTMLADIELHSIGSII AVEKIVHIANDLFLQSKKUGHGVGHDVASSGYLCTRKYD SAPSGRFOTMYILS\RAA\ATYVQEFLP\HSITAMTPFKKYN GLEKKRSLRTTGPYSGFSEVAERRIKLLMNSDERLONSRAKDR KOWSSIGQOMPKKTLUELFSDSDTERANFPKKYN GLEKKRSLRTTGPYSGFSEVAERRIKLLMNSDERLONSRAKDR VOWSSIGQOMPKKTLUELFSDSDTERANFPKKYN GLEKKRSLRTTGPYSGFSEVAERRIKLLMNSDERLONSRAKDR VOWSSIGQOMPKKTLUELFSDSDTERANFPKKYN GLEKKRSLRTTGPYSGFSEVAERRIKLLMNSDERLONSRAKDR VOWSSIGQOMPKKTLUELFSDSDTERANFPKKYN GLEKKRSLRTTGPYSGFSEVAERRIKLLMNSDERLONSRAKDR GSEVRSIKSETDSTIENSVAGELQOLLGSERR*LASRFFCQCEL KQ**SARTTS*KSITRSSKSERCSGRRKFIKKAEKKP*SNSGK GOKEKGRH* QCKEKGRH** QCKEKGRH** GREWASIKSETDSTIENSVAGELQOLLGSERR*LASRFFCQCEL KQ**SARTTS*KSITRSSKSLLNDLPKFADGIKARNRNONYL CKYCDKYTIYFENJSGHIADTHFSDHLWSDJCKCCELFFSKYFS DLKOHMILKHRRTDSVCRVCKESFSTNMLLIEHAKHEEDPYJ CKYCDKYTIYFENJSGHIADTHFSDHLWSDJCKVCCLEFFSKYFS DLKOHMILKHRRTDSVCRVCKESFSTNMLLIEHAKHEEDPYJ CKYCDKYTIYFENJSGHIADTHFSDHLWSDCDVOPSSSSSLLV LHFQBISCDEGYLCOPCREETINDEDLHSHWINBHACKLIELSD KYNNGEHGGYSLLSKITPDKCKNPFVCQVCGPSRSCLITHVNKRHV AIEHTKIPPHVCDDCOKGFSSMLE\TAMGINSGLIKCCLLEFISKYFS DLKOHMILKHRRTDSVCRVCKESFSTNMLLYTARKDAGSGOV VALCFINSBODWIFMDAFYGCLLAELGPVFIEVPLTRKDAGSGOV VALCFINSBODWIFMDAFYGCLLAELGPVFIEVPLTRKDAGSGOV TERKLSVLTYQDVGGWMFGNAVCVVKLEGTFYLCKTVGTWHA SLLACCRALITOACCYSEAFATTINVLDFRUGUTSVGTWSTWN MHVVSPYALMKANPLSHIQKVCFYKARAALVKSRDMHWSLLAQ RQQDSUSISSESLEMLIVADGAMPWSISSCDAFINYOFGGRIRPEV TERKLSVLTYQDVGGWMFGNAVCVVKLEGTFYLLCKTVGTHA SLLACCRALITOACCYSEAFATTINVLDFRUGUTSVGTWGTWHA MHVSVYCLALVPANTLPKADGOVARLERSTFYLUKYGFMFYV RGRIAVFSUTVLIDDRIVLVALVSROMGSNSCVTRUV TERKLSVLTYQDVGGWMFGANVCVVKLEGTFYLLAKDTVT STATCVOLHKRAERVAAALMEKGRLSVGDHVALVSPRAFYY STATCVOLHKRAERVAAALMEKGRLSVGDHVALVSPRAFYP DULANLDSVSTTGLLGAVVGRSHATTSOLGVCFYEXRACVLTT QAVTALLESSETGALGCLSVYSGG				QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
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SISILTGETMYLLMYMRTQDGLPARPRIERGLILQUMATELLA HSLCCASEATGIMMILSPAMKALLHHILGSEIKQVEPRLG 15ASSQ PETSMTSSGS PERMYDQSKORSGTGVERRIGG ALNRYPVGPYQKVMKVLQKCHGLSVEBTVLSSTTREMTPGBIK FSYNUSS\VIAVLIBPETRQLLVERILVSTTREMTPGBIK AVEKIYHIANDLEJGOKCHGP\DDTHARASG\1CTRQ\YD SAPSGRFGTMYTLS\RAA\RTYVGEFLP\HSITREMTPGBIK FSYNUSS\VIAVLIBPETRQLLVERILVTMIADIEHGISII AVEKIYHIANDLEJGOKCHGP\DDTHARASG\1CTRQ\YD SAPSGRFGTMYTLS\RAA\RTYVGEFLP\HSICAM\ GSPGKKEBEKAKRSSICMENSSNSSSDEETKARMTPTKKYN GLEKKRSLRTTGPYSGFSEVAERGIKLLIMNDBERLONGRAKDR KOWSGIGGOMPKKTLKELFDSDTERARFORSTAKNTPTKKYN GLEKKRSLRTTGPYSGFSEVAERGIKLLIMNDBERLONGRAKDR KOWSGIGGOMPKKTLKELFDSDTERARFORSTAKNTPTKKYN GLEKKRSLRTTGPYSGFSEVAERGIKLLIMNDBERLONGRAKDR KOWSGIGGOMPKKTLKELFDSDTERARFORSTAKEP SSGSNFSA\IPLPYLLINLHGHGSI*\OKGOSVTVSBEPLAPR OEBVESIKSETDSTIEVDSVAGELQDLQSERE*LARFFYCQCLL KQ**SARTRTS*KSITRSEKSERCSGRRKFIKRAEKKPF\SNGGK GOKEGKRH\ KQ**SARTRTS*KSITRSEKSERCSGRRKFIKRAEKKPF\SNGGK VGPSVLRILDHTAPSTEKSESULDLEFFADGIKARNENONYL VGPSVLRILDHTAPSTEKSESULVCDEGOSVTVSBEPLAPR KLCKILDKSQALNVTAQOKEPLLARMSSESLIKCELEFFSKYFS DLKOHMILKHRRIDSNYCRVCKESFSTNNLLIEHAKHEDPYI CKYCDYKTYTERLSGHIADTHFSDHLWOFSERLHTVNLSDY ALEHTIPPHVCDDCCKGFSSMLE\IAHHINSHLSEGIYLCQYW BYSTGQIEDLKIHLDPRIGADFFHCKOSDCLMPGNGRELISHLED LHFGEHSCDEGYLCOPCHERTMD EDLHSHVVNSHACKLIELSD LHFGEHSCDEGYLCOPCHERTMD EDLHSHVVNSHACKLIELSD LHFGEHSCDEGYLCOPCHERTMD EDLHSHVVNSHACKLIELSD VHETT 6806 272 3794 VALCFFROSDVMFMDAPYGCLLAELGPVFIEVPLTRKDAGSQOO' VALCFFROSDVMFMDAPYGCSLLAELGPVFIEVPLTRKDAGSQOO' FELLSCCOVPLAILTTDACQKGLFRAGTGEVAAFKGRPPISKUVT DGKHLAKPPKDMIPLAQDTGGTAYIEYKTKSGSTVGTVSHN MIVVSPYALMKANPLSHIQKCCYKARARALVKSRDMHYSLLAQ RQQDVSLSSLEMLIVADAAPWSILSGANTYGSRCHREV ICCASSPEALTVAIRRPPDLGGPPPRAVLSRMGHLSYGVIRVD TEEKLSVLITVODUGGWMFGANVCVVLREGTFTLLCUGGLCV VLMCPHTCVTHILDFRIULVLAGRPPAFSGESSFOWNSKULQAID SHQVVXCLALVPANTLPKARJGGHTSETKCRFPLECTLIPC VLMCPHTCVTHILBFRIULVLAGRPTAGAEBESSFOWNSKULQAID SHQVVXCLALVPANTLPKARJGGSHTSETKGRPLSVSGACUTT QAVTELBESSTGLALVLAGRGSAGGSUVUPPLELESNUSLILL ANGEVKARVYTCCSSVTGGIGSULVPPELEESNUSLILL ANGEVKARVYTCCSSVTGGIGSULVPPELEESNUSLILL ANGEVKARVYTCCSSVTGGIGSULV	1	}		
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ISASGGFOTSNTPSGGFPSATDQQGSKDGRQGQRRRRIDG AINNEVPGYPQKVMKUQKCHGISVEDPSSTTREMPTGEIK FSVHVES\VI.NULLRPEXGLLVEATLVLTMLADIEIHSIGSII AVEKIVHI.NDLFLQGCKTLGP\DDTMLAKDPSGYICTLR\YD SAPGGRGTMTYLS\RAA\ATVQEFLY\HIGAGGYICTLR\YD SAPGGRGTMTYLS\RAA\ATVQEFLY\HIGAGGYICTLR\YD SAPGGRGTMTYLS\RAA\ATVQEFLY\HIGAGGYICTLR\YD SAPGGRGTMTYLS\RAA\ATVQEFLY\HIGAGGYICTLR\YD SAPGGRGTMTYLS\RAA\ATVQEFLY\HIGAGGYICR\XT GEFKRSILTGTGYSGFSVLRKIKLINGDERLQNGRARDR KDVWGSIQQWFKKTLKELFBDDTEARASPPHPAPEGVARES LQTVABEESGSPSVELBERPPWNVDSIEKKIVENVDRAEFP SGGNFSA-IPLPYHHINRIHQSL*QKGGOGSVTVSEPLAPN QEEVESIKSSETDSTIEVDSVAGELQDLQSER*LASRF*CQCEL KQ**SARTRTS*KSLYSSEKSEKSGRKYIKKAEKKP*SNSGK QORGGKRHK RYPSKYFKKSFDVSVSESSSLISNDLFKFADGIKARNENONYL VPSSVLRILDHTAFSTEKGADIVICDESCOPPSVAQGTQESSP LCVHTAEDVP1AVEVHALSSDYDIETENNSSELVQCTOEBSPA KLCKILDKSQAINVTAQQKMPLIRANSGLYKCELCEFNSKYFS DLKGHMILHHRITDSNCVCKKESFSTEINNSSELVACHLEEDPYI CKYCDVKTVIFFNLSQMIADTHSDHLJWCKGCOVOPSSSSELY LHFQEHSCDGYYGLOFCCHETDSPDACHMINGHLYNGHRACKLIELSD KYNNGBHQYSLISKITFDKCKNFFVCQVGGFRSRHITNVRHV AIEHTRIFPHVCDDCKGFSSNLE\IACHLNSHLSEGITLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCGURFGNERGLIEHLE VHETT VHETT 4ALCFINSDFWFMDAFYGCLLAELGPVPIEVPLTRKDAGSGOV GFLLGSGGVFLALTDACQKGPLRAQTGEVAAPKKMPPLSWLIVL DGKHLAKPPKDMHPLAQDTGTGTAYIEYKKBGSTVGVTVSHA SLLAQCRALTQACGYSERETLTNVLDFKRDAGSINGWILTSWMR MIVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMWSLLAQ RQQDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSLSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSSLRMLIVADGANPWGISCOAPHINFOKSRUAPEV GRGRDVSLSLAMCHURANTERAPPHLEGHHISTKGACHTHEOTHPC VIMCPHTCVTURLEPRROKGPSUGPANIVONLVACKRACAGAGG ELAHLEBDSDQARKFLFLADVLQWRAHTTPDHFLFLLIAMKGTVT STATCOULKRAERVAAALMEKGRISVARDFALVANVFAKFAGAGG ELAHLEBDSDQARKFLFLADVLQWRAHTTPDHFLFLLIAMKGTVT STATCOULKRAERVAAALMEKGRISVARDFALAVFAKFAGAGG ELAHLE				
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SEQ	Predicted	Predicted end	Amino acid cogmont
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
			LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL
			PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
			HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
- 1	[VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
	1		VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
L			INSRGEKQRMHLRDGFLADQLDPIYVAYNM
6807	1444	606	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
			SVFQAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAQSGEPR
	ļ		RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE
			SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE
1			KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTEGCLRSLSGDLN
J			RFPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLRDRSR
L	Į į		FLFRLPMGLSCPLQVQ
6808	2063	737	GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMQRLAMDLRML
			SRELSLYLEHQVRVGFFGSGVGLSLILGFSVAYAFYYLSSIAKK
1			PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\
			ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRFTI
1	1		LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
1 .	i 1		PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL
1			GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
1			LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI
[·			DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKON
1			PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH
			BLS
6809	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
			TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
1 1	1	ļ	GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
1 1	1		EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
1	1		VIGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPDPDTDTVG
) !	i		AVVYQDGFYGAEI\LEATQPTDTLSPLORROPTATVTAFSTOLD
6810			TRTITPSGPRRPTALEPCETFHRFLLGP
0070	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEOPGSEASTOPTAGTOTVPO
		Í	TDEAAQTDSQPLHPSDPTEKOOPKRLHVSNIPFRFRDDDLBOME
1 1	ľ		GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKINGTIV
1 1			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVVGPREVA
1 1	ŀ	ł	VIGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPDDDDTDTDTVG
1 1	1		AVVYQDGFYGAEI\LEATQPTDTLSPLORROPTATVTAESTOLD
6811	1522		TRITIPSGPRRPTALEPCETFHRFLLGP
		658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
1 !	1	ļ	FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
1			SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
1	ŀ	f	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
1	1		SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
			TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI
6812	4001	1682	VTACQEGFICTWGRPGKVVSFNP
			EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ
[KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL
j [ł	1:	SPODKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL
i i	,	1.	VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV
	1	1:	HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE
1] ;	ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI
	}	Į į	TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
		•	evvespalllokedtvrrlvlpavoledsgeylceiddesasft
			VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
		! !	DGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA
			FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV

SEQ	Predicted	Predicted end	Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			VWSHNGRPVQEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSG
		1	AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
1	1		LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA
i			GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
ł		1	CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART
1		1	CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
			MVSYWPTRAPTAARATTIAPWPGSA
6813	9	836	SSTQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
1		,	LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
1		}	QRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGKGQVYNNLHLLS
		i	QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
			TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
ŀ			TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
			LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
			LRLAKNYIWALSEILRIGKRPDLLTFVONLCKGLSOPTTNLVAG
i			CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
1	1	1	TLDNSKSMKPYNYCSAYESFYESTSPECASPOFEGPLSPPPINY
1	İ	į	NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGOGAMFRLPTD
6815			SHFPYDLHLRSQSLTMQDELNAVFHN
0013	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE
	. 🛘	[DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLQGGT
6816	1 1	803	PQEPPNPRMKRASSLNFLNKSVEEPTQPGG
1	1	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID
1			PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
1			SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
1	1		LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
İ			TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
1			VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK
6817	1.72	3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
ļ	į į		DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
]		NNLISPOLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA
]			IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI
ł	}		LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
į	j i		TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE
			ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSRIFARIET
1		i	CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKI.
1		‡	FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHDINAAHR
		}	GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPONDLOHYAFHF
	1	1	EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH
		ļ	KKFEVPASEIHIVIWERKISOVTDKEAACLPLKKTNDOHALSNR
{		j	KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSODTAVTHGD
	İ	}	HLLSGPKGLVDNILPLTLEETIQKTASVSOLNSEAFL\LENKDV
l i		ľ	AENTGILKTNTLLSQESLMASSVSAPCNEKLIODOFVDISFPSO
	ĺ	. 1	VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIOGVKSVEIEKDAO
		ŀ	LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
			SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
		ļ	VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
			SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
1			EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE
j			QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
[j		QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS
	1	1.	EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL
6818	2	240	ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY
			RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTYTL

SEQ	Predicted	Predicted end	Amino and assessment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	bequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
6819		961	DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
1 1025	_	301	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
ſ	Í	İ	GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK
	į.		YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
	i		TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
			EAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
1	1		DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLELTVW
	1		DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
6820	1014	316	PNLWTDMTLVLH
1 0020	1074	340	GDMVYIVGHVPPGFFEKTQNKAWFREGFNEKYLKVVRKHHRVIA
}			GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
1	Í		GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY
			QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
]] .		VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
6821			LGLCT
1 0021	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
1	}		FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
1			GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLQRRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
i i			GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
6823			GSVIEVLQRRQEGLAS
6623	654	221	PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC
1			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE
			YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL
6824	858		ILRKGVLALNPLL
0024	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG
] [ł		ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV
1			NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
	1		LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV
, ,	}		WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
6825	3		AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
****	,	1173	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
į l			PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
j 1			NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
			KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
			GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
		ļ	IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF
			VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
1	1	1	TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
6826	2204		PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
0029	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP
	1	ļ	LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
f †	i	ŀ	NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
	ľ	1	DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
			AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
	ì	}	PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID
]	RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEEDKS
			VLKNHDLSVRAKMAIKLRLGEKEILEKAVKSAAVNREYYROOME
[ĺ	EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI
			REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK
			GSSSDSTAGVKE
			

No.	SEO	Predicted	Predicted end	
MO: bocatide corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first acid to the first amino acid corresponding to the first acid to the first amino acid corresponding to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid corresponding to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the first acid to the firs		beginning		
corresponding correspondin	NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
corresponding to first anino acid anino acid residue of residue of anino acid residue of anino acid sequence sequence company to the sequence company	l	location		Glucamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid sequence 6827 1 779 6827 1 779 6828 3 1684 6828 6828 3 1684 6828 6828 3 1684 6828 6828 3 1684 6828 6828 3 1684 6828 6828 3 1684 6828 6828 3 1684 6828 6828 6828 3 1684 6828 6828 6828 3 1684 6828 6828 6828 6830 6840 6854 6856 6857 6858 6	1			Manistidine, I=Isoleucine, Kabysine,
amino acid residue of anino acid amino acid amino acid amino acid sequence 6827 1 779 SEVERIDE, TSTRICO, NEW YVSILINE, WSTYDEOSIBLE, XSURROW, *Stop POSSIBLE NUCLectide insertion) 779 SEVERIDE NUCLectide insertion) 779 SEVERIDE NUCLectide insertion) 6828 3 1684 SEGRING CHARLES FLILLES SEVERE S		to first		D-D-dine, M-Methionine, N-Asparagine,
residue of amino acid sequence 8-Tryptoghan, Y-Tyrosine, X-Unknown, *-Stop Codp, (-possible nucleotide deletion, 'possible nucleotide deletion, 'possible nucleotide insertion) 8-SVPETGUSVIGGETGUSVIGGETGUSVESMIGHTENERGERPRECERRENL 'possible nucleotide insertion) 8-SVPETGUSVIGGETGUSVESMIGHTENERGERPRECERRENL 'possible nucleotide insertion) 8-SVPETGUSVIGGETGUSVESMIGHTENERGERPRECERRENL 'possible nucleotide insertion) 8-SVPETGUSVIGGETGUSVESMIGHTENERGERPRECERRENL 'possible nucleotide insertion) 8-SVPETGUSVIGGETGUSVESMIGHTENERGERPRECERRENL 'possible nucleotide insertion) 8-SVPETGUSVESMIGHTENERGERPRECAGGRESSORSHEPALAPPE REGISTRATE CONTINUE CONTI	1	amino acid		r=Froline, Q=Glucamine, R=Arginine,
amino acid sequence CCdon, /-possible nuclectide deletion, \possible nuclectide cinsertion) 1 779 SVYPFGENTAGENERMGLERREGERREGERRENE FYRALDERSSGMALOPLQAAPERGAGGERNSCHPPALAPPG RGGSHENGGOFD TYMWILDGGINLIUGHAAPS RGGSHENGGOFD TYMWILDGGINLIUGHAAPS RGGSHENGGOFD TYMWILDGGINLIUGHAAPS RGGSHENGGOFD TYMWILDGGINLIUGHAAPS RGGSHENGGOFD TYMWILDGGINLIUGHAAPS RGGSHENGGOFD TYMWILDGGINLIUGHAAPS RGGANLGVGLSLEPPLTPEWGVATVAGULFYNDHALPSS GAPAYAHVILDGIGLLINGCHMAITTLEERLLEVTTOS SGRAVANHULDGIGLLINGCHMAITTLEERLLEVTTOS LGHISGTASLKROSS POGRODDWR YKTPHRVAFVELLYKLUS OLPHWRIUM SYVNGSLESSERAKSGOTES RUKKORONDPKKM IOEVWHSINVALTRGALLEIS TROGSROYGGWEKKCELSGGMLA HAIGTVALTHSSTAALFINDLOTTOLLLIUGHTYPDALDI THESTYDSSPDLFGS SHEDPSLTSEGRILIUSSNCCHERT FINASHIPSKINTEGTEKT (VORMASLKELDGISTYPDADT) DITHLSYDVSSPDLFGS SHEDPSLTSEGRILIUSSNCCHERT FINASHIPSKINTEGTEKT (VORMASLKELDGISTYPDADT) DITHLSYDVSSPDLFGS SHEDPSLTSEGRILIUSSNCCHERT FINASHIPSKINTEGTEKT (VORMASLKELDGISTYPDADT) DITHLSYDVSSPDLFGS SHEDPSLTSEGRILIUSSNCCHERT FINASHIPSKINTEGTEKT (VORMASLKELDGISTYPDADT) DITHLSYDVSSPDLFGS SHEDPSLTSEGRILIUSSNCCHERT FINASHIPSKINTEGTEKT (VORMASLKELDGISTYPDADT) PRIVASHIC (CECEPASVYOOPARS) PRIVASHIC (CECEPASVYOOPARSAKKELDGISTYPOSTICE ROSSPESILIUCTOROASSTHMY REMERSERGILIUCTOROASSTHMY REMERSERGILIUCTOROASSTHMY REMERSERGILIUCTOROASSTHMY REMERSERGILIUCTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTANDOMPROHYTYTOROGSTHUSEN REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTHMY REMERSERGILIUTOROASSTANDOMPROHYTYTOROGREPHITUTORO REMERSERGILIUTOROASSTANDOMPROHYTYTOROGREPHITUTORO REMERSERGILIUTOROASSTANDOMPROHYTYTOROGREPHITUTORO REMERSERGILIUTOROASSTANDOMPROHYTYTOROPPENTERRENTITUTOROASSTANDOMPROHYTYTOROPPENTERRENTITUTOROASSTANDOMPROHYTYTUTOROASSTANDOMPROHYTYTUTOROASSTANDOMPROHYTYTUTOROASSTANDOMPROHYTYTUTOROASST	ļ	residue of		S=Serine, T=Threonine, V=Valine,
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HAIQIVELIHESITALEIINDILQTIQDLIDLRURCCMARTION TAEEIKKIARKEMUVDNEGIISDLCOFEGCIVGLSIKWDADI TAEEIKKIARKEMUVDNEGIISDLCOFEGCIVGLSIKWDADI CKPGEASYGOPKTQEVOQLSINIMQVTIYCLEQLSTKPDADI DTHLSUVDSSPDIFGSIHEDPSLTSEQRILIVLSNCCYLERHT PLNIAEHFEKHNPQGIEKTQVSMSSLKELDQRIFENYIELKAD PIVOSLEBGIYAGYPDWKOCLPFTGVENYLKRALVNIIAVHENY FTISKELVPRULSKVIEAVSESISANCOVSSFSKAGLQARLM ICALRDIVAVYLTPESKSSFKOALEALPQLSSGADKKLLEELIN KKSSMHIGUTCCAASSTMMKT. ICALRDIVAVYLTPESKSSFKOALEALPQLSSGADKKLLEELIN KKSSMHIGUTCCAASSTMMKT. KKSSMHIGUTCAASSTMMKT. ICALRDIVAVYLTPESKSSFKOALEALPQLSSGADKKLLEELIN KKSSMHIGUTCAASSTMMKT. KKSSMHIGUTCAASSTMMKT. KKSSMHIGUTCAASSTMMKT. KULJAKDMAEGGULEBAFYNIGPIIRIIKDRMEEKNYTTOVP PKHYYRVLQCQEELITQMVSTMSDGWRFFOLUNIGSSYNYGSED QAEFLCVUSKELHSTYPALSSESSKIKTSIBGUEBOQQOSEEV EBVEVEQVQVURADAGGK/CCKVERAPGCEAPDHLQGLGVPI PKHYYRVLQCQEELITQMVSTMSDGWRFFOLUNIGSSYNYGSED QAEFLCVUSKELHSTYPALSSESSKIKTSTBGLBEOQQOSEEV EBVEVEQVQVURADAGGK/CCKVERAPGCEAPDHLQGLGVPI RYRPPBLADPDTCVSFRFCHGLDFSTSGALCVALNKAAGSAXR CFKERRVTKAYLALLRGHIQGSEVTISHAIGRNTEGRAHTMGI BSGGGCENKPBJLTDVUSHGHGVSKANKTUSTERAHTMGI BSGGGCENKPBJLTDVUSHGHGVSKANKTUSTERTHTMGI BCSGGCENKPBJLTDVUSHGHGVSKANKTUTGTHGL RV\HCSALGHPVVGDLTYGEVSGCEDRFRMMLHAFYLRIPTDT ECVEVCTOPPPLPSILACKGEDGONVKEKSMILSN VELQQYSLIGEKLWREAKTIVPPHTDSKRVQAARAPDFPPP LEPDS DRGPRGSPSALLBGGGRPPPPTFTBRGRGFCHOLISEST LEPDS SIFKEEPRSDQKKSLLSFDVVDKVPQOPPSASSNFASKNITKE SEPPESILTPVESKSKALDFFSGRYLKKEMONTISKISEETK LKSVSPTEKKNILENRISTILVAEKKVLAEKONSVAPLELRDS NGIKTOTILGSRSTELKESKADAMPQHFYQNEDVNERPKILIV SEKEKDBKKKK SEKERBEKKSKADAMPQHFYQNEDVNERPKILIVG SEKERDBKKKK SEKERBEKLKSKRADAMPQHFYQNEDVNERPKILIVG SEKERDBKKKK SEKERDBKKKK RSSSFTENLINGERSTELKESKADAMPQHFYQREPVLEVV SKKKKRSEDDYSFIITYGFPRENLINGGGEEERLLKATPPBG PLIFKVCIITSCIGCELFSKILLBYGGEEERLLKATPPBGL PRIFKVCIITSCIGCELFSKILLBYGGEEERLLKATPPBGG PRIFKVCIITSGGGCEFFSTICKSKRIPTSGGIHAAALLLY PFSMAHTYIPVVPESILATVCCOPPFVIVIOHASVIKREANGGOMPFPGENFCK ALTSKTMRRFVKKFVKTOLFSLFIIDGAEKSKNPAGYFQCKLLE ALGUSFPGOMSPHE				QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM
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6830 1 939 MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALMKAAGSAYR CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI EGSQGCENPKPSLTDLVVLEHGLYAGDDVSKVLLKPLTGRTHQL RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTFDPFLPSLDACWSPHTLLQSLQLVQALRATPDPDPED DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTIVKSGDGQNVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVYTSADGENL SIFKESPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESILIPVESKGSLIDFSEDRIKKEMONFTSLKISEETTK LESVSTEKKDNLERR\SYTL\AEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKITVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRLLPAGPG PRLPKVYCIISCIGCFGLFSKLLDEVERKHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTFFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPSSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLGSTFLANGVGDEKDILPPKLQDDILDSLGGGINELKT AEQINEHVSGPFVQFFKKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFJQEAEKSKNPPAGYFQQKILE	1	ĺ		OAEFLCVVSKELHSTPNGLSGESGEVTVCTERGI BEGGGGE
MEPGSVENLSIVYRSRDFLVVNKHMDVRIDSKAWRETLTLQKQL RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR CFKERRVTKAYLALLRGHTQESRVTISHAIGRNSTEGRAHTMCI EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVQDLTYGEVSGREDRFFRMMLHAFYLRIPTDT ECVEVCTPDPFLDALDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPPTKPPETEAQRGPCLQWLSEWT LEPDS 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNP VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVYTSADGERL ETQSYSLIGBKLVMEEARTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEPPSDQKQKSLLSFDVDTKVPQOPKSASSNFASKNITKE SEKPESTILPVEESKGSLIDFSEDRLKKEMQNFTSLKISEETK LRSVSPTEKKDNLENR\SYTL\AEKKULAEKQNSV\APLEIRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK CSEKEKDEKKKK VGSGLISGPPQDNSGEALKEPERAGEHSLPNFAGGQHFPEYLLV VSLKKRSEDDYEPIITYQFPKRENLLRQQCEEEERLLKAIPLF CFPDGNEWSLTEYPREFTSFVLTTVDGSRRIGYCRRLLPRAGGE PRIPKYVCIISCIGCFGLFSKILDEVEKRHQISMAVIYPPMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDGSHLEHVDFSSL LHCLSFEQILQIFASAVLERXIIFLÆGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRPQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGGGHFQERSFCK ALTSKTNRRFVKKFYKTQLFSLFTQEAEKSKNPPAGYFQQKILE				EBVEVEOVOVEADAGEK/CCVKPEAPGCEAPDULGGLGVDI
CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI EGSGCCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVGDLTYGEVGGREDRFFRMMLHAFTIRIPTDT ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEENNINSVYTSADGENL ETQSYSLIGEKLVWEEAKTIVPPHVTDSKRVQKPALAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQOPKSASSMFASKNITKE SEKPESTILPVEESKGSLDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK GSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFPEYLLV VSLKKKRSEDDYSPIITTQFPKRENILRGQOEEEERLLKAIPLF CFPDGMEWASLTSYPRETFSFVLTNVDGSRKIGYCRRLLFPAGPG PRLPKVYCIISCIGCFGLFSKTLDEVERRHQISMAVIYPFMQGL REAAFFAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVYPESILLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTGLFSLFIGGAEKSKNPPAGYFQQKILE	6830	1	939	MEPGSVENLSIVYRSRDFLVVNKHWDVPIDGVAVDETT TV OVC
CFKERRVTKÄYLALLEGHIOESRVTISHAIGRNSTEGRAHTMCI EGSQCCENPKPSLTDLVVLEHIGLYAGDPVSKVLLKPLITGRTHQL RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSFSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSCDGQNVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL EIQSYSLIGBKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKMNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPXSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEETTK LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITTQFPKEENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVERHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPUVPESILATVCCPTPFMVGVOMRFQQEVMDSPME EVLLVNLCECTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGGGHFOERSFCK ALTSKTNRRFVKKFVKTGLFSLFIGGAEKSKNPPAGYFQQKILE	1 1			RYRFPELADPDTCYGFRFCHOLDFSTSGALCYALNYARAGGAND
EGSQCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPPTKPPETEAQRGPCLQWLSEWT LEPDS SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKONLENR\SYTL\AEKKVLAEKQNSV\APPLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDBKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFPEYLLV VSLKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLKAIPLFAGFG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFFAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCHAAAALLY PFSWAHTYIEVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGGGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFTQEAEKSKNPPAGYFQQKILE	1 1	i		CFKERRVTKAYLALLEGHTOESPYTTSUATGPNGTGDAYT
RV (RESALGHPV/GDLTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFIPSLDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTILVKSGDGONVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL EIQSYSLIGEKLVMEEAKTIVPPRVTDSKRVQKPAIAPPS KWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK LERSVSPTEKKENLDENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQTTLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNPAGGQHFFEYLLV VSLKKKRSEDDYEPJITYQFPKRENLLRGQGEEERLLKAIPLF PROFERSEL CFPDGREWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAATTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGGGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	1	Į		EGSQGCENPKPSLTDLVVI.EHGI.VAGDDVSVVI.I.VBI TODTVICE
ECUSUCTIPDEFLIPSLIDACMSPHTLLQSLDQLUQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEEDS 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGONVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESILIPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQTTLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKKEBEKKDK VSLKKKRSEDDYSPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL HCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKPVKTQLFSLFIQGAEKSKNPPAGYFQQKILE	1	Ī		KV \HCSALGHPVVGDLTYGEVSGREDRPFPMMI.HAEVI.DIDDD
DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS 3 1087 SIFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGONVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL EIQSYSLIGEKLVMEEAKTIVPPRVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQTTLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGGGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	1			ECVEVCTPDPFLPSLDACWSPHTLLOSLDOLUOALPATROPPDP
SLFFGSSTPDNKVAEQEDLETQFSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKPISEVSRETYGKKEISGDSEEMMINSVVTSADGENL EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQGEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCHAAAAALLY PFFSWAATYIPVVPSSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	1 1	1		DRGPRPGSPSALLPGPGRPPPPPTKPDFTFACPGPGLCWLCOUT
SIFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTILVKSGDGONVKEKSMILSN VEDLQOPKISEVSREDYGKKEISGDSEEMNINVYTSADGENL EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGGRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGMEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE				LEPDS
NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKPISEVSREDYGKKEISGDSEEMMINSVVTSADGENL EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK 6832 1809 412 MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISITRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESILATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKPVKTQLFSLFIQAEKSKNPPAGYFQQKILE	6831	3	1087	SLFFGSSTPDNKVAEOEDLETOPSPSVEKAVTVIDDECTIDENE
VEDLQOPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL EIQSYSLIGKLVMEEAKTIVPPHVTDSKRVQKPAIAPPS KWNI SIFKEEPRSDQKQKSLLSFDVVDKVVQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQTTLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKKEBEKKKE KOMPON SEKKEDEKKEN VSLKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	1 1	1		NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGONVKEKSMILEN
ELGSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAAALLY PFFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	<u> </u>	1		VEDLQQPKFISEVSREDYGKKEISGDSERMITNSUUTGADGENT
SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQTTLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERXIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVOMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKYKTQLFSLFIQGAEKSKNPPAGYFQQKILE	1 1			ELQSYSLIGEKLVMEEAKTIVPPHVTDSKRVOKPATADDSVUNTT
SEKPESILDPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQTTLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERXIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKYKTQLFSLFIQBAEKSKNPPAGYFQQKILE	1 1		1	SIFKEEPRSDQKQKSLLSFDVVDKVPOOPKSASSNFASKNTTKE
ARSVSPTEKKONLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGMEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	1 [i	1	SERVESTILPVEESKGSLIDFSEDRIKKEMONDTSLKTSPERRY
MEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKBEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKYLDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISITRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESILATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	1			DRSVSPTEKKDNLENR\SYTL\AEKKVLAEKONSV\ADT.ELDDG
SEKENDEKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEFIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAAALLY PFSWARTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE	1 1]		NEIGKTQITLGSRSTELKESKADAMPOHFYONEDYNER PKT TVG
MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVMLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKYKTQLFSLFIQEAEKSKNPPAGYFQQKILE	6832	1900		SEKEKDEKKKK
VSLKKRSEDDYEPITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERXIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVALCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKYKTQLFSLFIQBAEKSKNPPAGYFQQKILE		1003	412	MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGOHFFEYLLV
PREPKYYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFAPAGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERXIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVMLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKYKTQLFSLFIQEAEKSKNPPAGYFQQKILE	[]			VSLKKKRSEDDYEPIITYOFPKRENLLRGOOFFFFFFI.KAIDLE
PRIBYYCIISCIGCFGLFSXILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESILATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKPVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQIKO/TETTGANGELBANNONG				CFFDGNEWASLIEYPRETFSFVLTNVDGSRKTGVCPDI.T.DAGDG
REAAFPARGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWARTYIPVVPSSLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQIMEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKPVKTQLFSLFIQBAEKSKNPPAGYFQQKILE YEEQIKO YETTGANGELBANNOTA	i i	1		PRLPKVYCIISCIGCFGLFSKILDEVEKRHOISMAVIVDEMOGT.
LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESILATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKYQTQFSBAWAYAY]	1	Į.	REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHUDFGGI
PFSWARTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKTQLFLFIQEAEKSKNPPAGYFQQKILE VEEOKO/TETYGRNGETERANDOOD		i	ł	LHCLSFEQILQIFASAVLERKIIFLAEGLSTT.SOCTWAAAALTU
EVLLVALCEGTFIMSVGDEKDILÞPKLQDDILDSLGQGINELKT AEQINEHVSGPFVKIVGFYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKTQLFSLFIQEAEKSKNPPAGYFQQKILE VREQKKO-TETTGANGETER-MANGET	}	1		PFSWAHTYIPVVPESLLATVCCPTPFMVGVOMRFOORVMDGDMD
AEQINEHVSGPFVQFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKTQLFSLFIQEAEKSKNPPAGYFQQKILE VREOKO-TETYGRNGETER MAYOTE		l	1	EVLLVNLCEGTFLMSVGDEKDILPPKLODDILDSIGOGINELET
ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YREOKKO/TETYGYNCETERAHAYATA			1 -	AEQINEHVSGPFVQFFVKIVGHYASYIKREANGOGHFOERSECK
YKKUKKO/TETYGIOTONIO	ŀ		1.	ALTSKTNRRFVKKFVKTQLFSLFIOEAEKSKNPPAGVFQQKTLE
6833 1 1139 DIMINISCOCCOTAGNICE TRAVVINID	6833			YEEQKKQ/TETKGKNCEIRAVVNKND
PLMTLSQCGGIPGHGHSHGGHGHGLPKGPRVKSTPDGGGTTY		-		PLMTLSQCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
VAPGEQGPDQEETNTLVANTSNSNGLKLDDADDRNDDSCDTURV	1		1.3	VAPGEQGPDQEETNTLVANTSNSNGI,KI,DDADDRNDDCCDTURY
QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV				QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

Г	SEQ	Predicted	Predicted end	Amino poid
- 1	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glucamic Acid, F=Phenvialanine G-Glucino
		location	corresponding	H=H1Stldine, I=Isoleucine K-Lycine
		corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
- 1		amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
J		residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine
- 1		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		sequence	Doqueste	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA
- 1				GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALIILQTVPKQID
ı				IRNLIKELRNVEGVEEVHELHVWOLAGSRIIATAHIKCEDDTEV
- 1	1			MEVAKTIKDVFHNHGIHATTIOPEFASVGSKSSVVDCELACDTO
-	- 1		•	CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSNNLEKKDPDTK
-	6834	78	1151	AENIPA\VVIEIKN\IPNK\OPESSL
		,,,	1151	AGOERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP
	į			LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP
				CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGEE SRAL+LIBEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
	ŀ			AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVEEAGCVEFGQ
-	}	į		AHGRPGLALAKGRGGTNEVEEOVOVDGVOKLVLSAHRCHELVAG
1	1	J		QQDGEDQAARTRLLOAGAHSVAHGRROGOAPCRPHOFACUSCUS
				LUQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
\vdash	6835	1	834	QLLRQL
-		_ [034	GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG
1	ł	ļ		AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ
-	- 1			MAFFRVDHGLMLTYFAAFEVFFEENLPKLFAHFKKNNLTPDIYL IDWIFTLYSKSLPLDLACRIWDVFCRDGEBFLFRTALGILKLFE
	ŀ	ļ		DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKKWA
		ĺ		QVLTALQKDSREMREGKSVPPTLRLOREFALGTNOSPMPRPI.CC
-	6836			FRLTPGQPRRTDAL
		1	850	MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
1	ľ			YIPREPHTKAPRGFAFVRFHDRRDAQDAEAAMDGAELDGRELRV
ł	- 1			OVARYGRRDLPRSROGRRHAAGPEAA/RYGRRSRSYGRRSRSPR RRHRSRSRGPSCSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSRS
	- 1	,		PYSRSRYRESRYGGSHYSSGYSNSRYSRYHSSRSHSKSGSSTS
1		1	i	SRSASTSKSSSARRSKSSSVSRSRSRSRSSSMTRSPPRVSKRKS
\vdash	6837			KSKSKKPPKSPEEEGOMSS
1	000,	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP
1		1		PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGGGGGGGDCPVPDG
1	- 1			GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
ĺ	l	i		RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSP
1			1	KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH
ŀ	1		}	PGTPGLEQVRTPTSSSGAPPPDEIHPLETLOAOIOLOBOORSTS
1				EUQPLGLKGGKKGECAVGASGAONGDSELGSCCSEAVKSAMSTI
1		1)	DLDSLMAEHSAAWYMPADKALVDSADDDKTI.A PWEKAKDONDMC
	1		1	KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR
-	838	16	499	SLHSDISNRFGTFVAALT
		1		LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDEE DQTRDMELVETRPAGDGTFQKWAAVVVPSGEB/Q/RYMCHVQHE
				GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC
<u> </u>	070			RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
l ٩	839	1	1195	AAPAGGGPDPEALSAFPGRHLSGLSWPOVKRLDALLSEDIDIUG
ŀ	1	1		RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSbashyr.
			1.	HPESGLGYKDLDLVFRMDLRSEASFOLTKAVVLACLLDF1.PAGV
	ł		T I	SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK
				FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG
	İ			ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
			13	PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLBRYLEAHFGGAD AARRYACLVTLHRVVNESTVCLMNHERRQTLDLIAALALQALAE
	1	1	13	QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
	940			CN
6	840	4254	2061 I	ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
			!	FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW
				

SEQ	Predicted	Predicted end	1 mino and 3
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
· I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	-	\=possible nucleotide insertion)
			TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
ı			TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
			EMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD
ŀ		ļ	PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
1			LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT
			LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
			LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
l			HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGELTEN
			FKGLAIPYLEHIIHVWEETGSRFHNCLIOLYCEKVOGIMKEVII.
1			SFPAGKTPVPAGEEEGELGEYROKIJMFLEISSVVDDGBLIGDE
			PFDGLLEERALLLGRMGKHEOALFIVVHILKDTPMARRVCHVHV
1			DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEDVANLOAR
	i		LOVLELHHSKLDTTKALNLLPANTOINDIRIFIRKITERNAOKY
			RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
6841	1	3206	IGNSAFARYPNGVVVHYFCS\KEVNPADT
	_	1200	TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA
			REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD
ľ			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA
	1		KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
1			IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFTRVEMARVLMB
1			RNQYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
1			LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSORRNHAMCDISAG
İ	İ		SRPLEFFPDDDCTSSARREOKREOYROVREHVRNDDCPLOACCW
1.	ł I		SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKI.WCa
			AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
[i	PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANODGTUD
			QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
i i			LAGITLYGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
1	}		NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT
	[PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
1 1			AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
1 1			GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR
1 1			LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
].			LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
1 1		ļ	TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
		į	GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVFGO
1 1			KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
6842			ERSHIIVWQVSYTPE
0042	3	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
ļ [ļ		RRLFQSVKLHCPKCHLLOEVPHEGDLDIIFODGATKTPDVKLON
į l		ľ	TSLYDSKIWTTKNOKGRKVAVHFVKNNGILPLSNECLLLTEGGT
}		1	LSEICKLSNKFNSVIPVRSGHEDLELLDISAPFTJOGTVUVCC
		!	KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLOVVEVMTET
]]			LDDGTGVLEAYLMDSDKFFOIPASEVLMDDDLOKSVDMTMDMFC
6843	2		PPGIKIDAYPWLECFIKSYNVTNGTDNOICYOIFDTTVAEDVI
	~		NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
		1.	CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR
		F	VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
		[;	SRKSSLIIHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
Į	[į ;	RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
		! :	LLLQGORVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE CNECEKAFSPLSLVTTIFT
6844	244	642	EHOLAGERI DETOTEMET COMPORTATION OF THE PROPERTY OF THE PROPER
		17	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE
			TTOTOT VENETATONIPPQGCNSEKIKKLVAVKRQQE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
f	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
\	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	- Sagnones	\=possible nucleotide insertion)
	1 1		PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
1	İ		I I I I I I I I I I I I I I I I I I I
6845	3	1519	VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLD
1	_		GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV
l l			GLAFELYYHTTQDLQLFREAGGWDVVRAVAEFWCSRVEWSPREE
1	1		KYHLRGVMSPDEYHSGVNNSVYTNVLVQNSLRFAAALAQDLGLP
1	i		IPSQWLAVADKIKVPFDVEQNFHPEFDGYEPGEVVKQADVVLLG
			YPVPFSLSPDVRRKNLEIYEAVTSPQGPAMTWSMFAVGWMELKD
]		AVPARCIA DROESNIMA EDEKAMBENA OGGANISHI MONGOLI AD
			AVRARGLLDRSFANMAEPFKVWTENADGSGAVNFLTGMGGFLQA
1	}	l	VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF
			SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLLPGHKVSFPRS
ŀ			AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
J			TESLTVDPASE*SGTGASETSLGPSLWPRLHPPLLGTLLACHPS
6846	212		PAARLSGKVHAAWPEFKAFCL
00.20	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
			IIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP
1			MTQNEQKBVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
1	1		VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
1			MYKAIHCVQNMKPEEYAHKILBLQMQSIMEKKMKTKRNIAKHYK
			NNPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV
1 1		•	RENKTLOKKCADYQINGEIICKCGQAWGTMMVHKGLDLPCLKIR
			NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
6847	1450	348	SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
			WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
			PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
1	ļ		PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
			YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG
1			IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
			RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR
	İ		ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
6848			GRLFSVIFKYEVPAE
1040	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
1 1	1		LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH
	}		IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN
] [1		VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK
] [Í	[VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA
6849	70		YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH
""	,,,	821	SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC
			VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK
1 1	į		PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
1 1			VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ
1	ļ	ľ	YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
6850	 _	1335	VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
	-	1235	ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD
1 1			LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL
			RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI
1	i		GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
1	J	j	KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
1 }			NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL
[1	}	YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ
1 1		1	HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ
1	i		LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK
- COF			EALNQDINIPFANGI
6851	1765	660	VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD
	J		LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA
			CYCVYKLTIGRDDSEKLEEEGEEEWDDDQELDEEEPDIWFDFET

SEQ	Predicted	Predicted end	Amino agid coment control
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Sodanion	\=possible nucleotide insertion)
		 	MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE
			HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSQD
ļ	ļ		INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM
1	}		YINEVCRETVSRCCNSFLQQAGLNLLISMTVINNMLAKSASDLK
			FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL
			FIRNGNREILLETPAP
6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT
			GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
1			IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
			KTD
6853	3	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
			KCDILKALGIEVDVEDGSVSLQVPVSNEIPNSASSHEEDNRSET
			ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
			VDNPTFEEDETPNQETAVREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYEFSTQAK
ı	i l		PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
	i i		IICVEGFKEHCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR
}	}		LFHSFEELLLEAHGDYGLRNDYHMNLGQFLEFLKKHKSEHVFQI
6855	1040		LFGIESKSSDS
0055	1913	1148	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK
			EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF
1			YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
1			QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL
			GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL
6856	1617	. 997	LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
]	331	VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
			SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
1			RKFKIGGEWATWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP
			HWALFGASERGFDPKDTRHQRKNKSKAISGC
6857	1	617	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
1 1			KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF
			DLQQRLSDEDGTMMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT
1 1	j		TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF
L			RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858	-2	669	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA
1	ŀ		LRCVQTAKLILEELKLEKKIKIRVBPGIFEWTKWEAGKTTPTLM
1 1	1		SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
			IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAOLVR
	1		KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
J- 60.55	<u> </u>		GN
6859	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG
			KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
1			AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPOPIPSNRIDTT
1 1			SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT
1 1	. 1		VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN
]]			AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
; l		İ	SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
Į		l	VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF
6860	1889	1510	YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
	2003	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
ļ i	1		DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
6861	1889	1515	MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
		*272	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
			DTGLT1LQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862	2	471	EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
1			DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNAET
1			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
1			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKOVCSTVGGS
	}		AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRROFCVNTLGSF
1			YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
Į.	1		GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCOPGFLCONT
ŀ	1		KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
1	}		NTVGSYTCQRNFLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHT
		}	CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY
			GSYQCYCRQGYQLAEDGHTCTDIDECAOGAGILCTFRCLNVPGS
			YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIOGS
])		FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYOLN
	ŀ		FQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
1			FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
1			FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
1			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
1			ERBEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP
i		•	WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
1			EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
}			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
1			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYOMVRDENLKF
1			MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
			FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
1			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
			HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
			LRHSALRHMISFLLGASRONNQIRRWSSAQAREFGNLHNTVALL
			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
]			SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
	[FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN
			GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
1	!		wswavqwlqkkmsehywtlqsnvsnetstgktfqrtisaqdtla
[YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL
			RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
1			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
1			LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
1 1			DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
			PFGQSSVQTIQPKRDS
6866	1571	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
		-	IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
<u> </u>	J		SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR
[[VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
			IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL
			GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF
			QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL
	ì		EMAQLH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
6867	2833	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
			LQSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
			YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
	i		KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL
			LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE,
1			VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
			HSAMDPRSTSCLLKDPPVEAADOP
6868	1.	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
1			KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
			GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
1			KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
1 .			FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT
1			NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
			LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
1			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQLNKFLQNLLSDER
1			LCQSEALYAFLSPSPDYLKVIDVQGKKNSFSLSSFLERLPRDFF
			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM
			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF
			RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL
			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
			HLDQLKAGQV
6870	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
[]			DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
			GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
1 1			YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP
	i		NIPVYRDWEMVGRYYEBFPINLKTGEANLTQIYLQEALDFIKRQ
1			ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
1 1	i		IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
1 - 1		Ì	GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
1]		AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
1	ľ		QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
1 1		ļ	IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQP
6871	209	1126	QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
		4440	RMSLNPPIFLKRSEENSSKFVETKQSQTTSTASEDPLQNLCLAS
1 1	1		QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
	(EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
] [FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE
] [j	RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
1	ŀ		DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
6872	880	459	FGLLMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGNT
į į	-		KKLITEYFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
į į		İ	LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
j (1	PTSRPPPR
6873	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
	-	,,,,	IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSOKEK
		1	DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
1	1	}	
[i	DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
			CLKCYGKKYVDEGEVYFELDADKICRAARMLLQNAVKFNLAEF
[ļ	QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
1		İ	DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH SSMQNGVKVYNSRRPIS
			OUNDAIN - WALLANDER - WALLAND

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	
6874	1	307	\=possible nucleotide insertion)
1 00/4	1 -	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
			GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
6875	1600		SCPDLPSQTDKKCS
00/3	1688	349	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
1	1		TLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
}		*	LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
İ			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
	[VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
]			PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
j			CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
1			IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
			QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
1			KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI
L	}.		KVNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
	! 1		LHTKPRMPPCDFMPERYQVIFLVNSGSEANELAMLMARAHSNNI
ļ.			DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
			RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
			VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
1 1			EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
4			PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSO
1			EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
1			PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
İ			AVEVFRSALTOHMERRAK
6877	1	778	GTSPSPARAYAPPTERKRFYONVSITOGEGGFEINLDHRKLKTP
J j			QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
			PTQRNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
1			EWAEKRYGVEISSSTSIMGPSIPAKTREVLVSHLASYNTWALOG
1			IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN
			IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	931	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
1 1	į		LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAP
1	i i		EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD
	i		TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
1	1		VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
Li			II
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
	†	i	KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
]	1	į	FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF
	•	l	FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY
	}	İ	NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA
j i	!	İ	FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE
		l	CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
1			MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS
, ,	J		NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
1 1			VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
			KPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESD
			EDTF
6881	2638	2244	NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
			QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYOS
			IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	1	850	GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN
, ,		.]	QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
	!	[TNAVHKCRVHGLEIEGRDCGEATAOWITSFLKSOPYRLVHFEPH
		i	MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK
·	L		YANNONDON TO TOTAL TOTAL BEING THE BEING THE BEING

SEQ	Predicted	Predicted end	Lamino and comment combatation of the state
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location		Giucamic Acid, Fernenylaianine, Geglycine,
J	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
1			LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
			VLENPGTIKVGDPVYLLGQ
6883	2794	2256	NSKLKLNQNLKLFITLTYQVLSLHGWGPGIHLQKEGAFPVTQNR
ł			ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
			DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
I			NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
			ANC
6884	2	99	EFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
Ī			LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
			TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
1			YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN
1			LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
]			GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
]		MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR
1			DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
İ			LYGLAKQFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA
			IMNLDNISYADCLKQLYIKHNY
6885	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
ı	1		QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
1	1		LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
1			GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
{			LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY
			QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA
Í I	(VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
			DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
			LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
	į l		GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
6000			KVVLWQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
1			GQQRAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG
1 1			TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
!			NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
1			FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
			DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
]			LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
6888		000	SL
0000	1	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
1 1	ł		NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
1 1	ĺ		IFEMYEEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
; !	1		LSASMORTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL
[1		EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
[' i		LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
			AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
6889		353.	LILSDDIRVAISKKVPSFLGHH
2003	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
1 1	1	i	AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
	ł		ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
j	İ		ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL
			WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
			KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
			EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
j 1	1		EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
			DSSEIPGALWHIYAGKDVDKIREFLQKISKEQGLEVLPEHDPIR
			DQSWYVNKKLRQRLLBEYGVRTWTLIQFLGDAIVLPAGALHQVQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid Fulbranial anima Collection
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	F=Florine, Q=Glucamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
-	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	seddence	Codon, /=possible nucleotide deletion,
	Dadacuec		\=possible nucleotide insertion)
}]	İ	NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
6890	3	667	NILYHAVKEMVRALKIHEDEVDDMEEN
1 0050	1	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
Í]		TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
ı	İ		AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
1			ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
			LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
6891	1000		V
6891	1980	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
			LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
	•		AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKPKPNCVNVD
			EVLPHWLSWLPLHEDKERAIQTLSFLCDLIESNHPVVIGPNNSN
			LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
			VSQLDDEQQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
j 1			FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
			QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELB
			NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
1 1			TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
			IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG
1 3			RTVTIKLKNVNFEVKTRASTVSSVVSTABEIFAIAKELLKTEID
1			ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS
1 1	ŀ		ATECTLEKTOKOKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC
1 1			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
1 1	ľ		AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
			NVPASSLCEKODYEAH
6894	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
[[ſ		DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS
			VFNPW
6895	2379	478	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
1 1	4		TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFODLLAL
ł	l		VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
1	ł		EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
1	ļ	ļ	AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
	į	}	EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKOLL
1			QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKOMLES
1		1	SGDPLPLSDQDVEPVLSAPESLQNLFMNRTAYVLADVMDDOLKS
1 1		į	MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL
			SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
1			PPPRGRGGGGGGGGRPHDIFRQRKQNTSRPPSMHVDDFVAAES
			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
] [FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
] [J		PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
			KFVSGGSGRGRHVRSFTR
6896	1	. 555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
j	j	}	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
] [1	·	SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSBKRFLLPSO
		,	SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
]		1	DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
, ,]		AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
]	Ì	1	STANCETADUDITECT DEDUCARDESPINALS LATASCERÉFSVE
			SLAWGFIADVDLESEKYRRIGEMRFTIGTFLRLAALRTYRGRLA
	1		YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
			DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

Deginning location	SEQ	Predicted	Predicted end	Amino poid
location corresponding corresponding corresponding corresponding corresponding corresponding to first a mino acid amino acid amino acid amino acid sequence corresponding corresponding corresponding corresponding to first and acid corresponding correspond				
to first amino acid residue of residue of amino acid sequence 8equence 898 919 346 6898 919 346 6899 120 827 6899 120 827 MANAGARIAN THE STAN SERVICE ERVICE THE SERVI	NO:		location	Glutamic Acid, F=Phenylalaning C classic
Leucine, MeMethionine, Ne-Asparagine, amino acid amino acid acid acquence			corresponding	H=Histidine, I=Isoleucine, K=Tysine
amino acid residue of amino acid sequence seq	1			L=Leucine, M=Methionine, N=Asparagine
residue of amino acid sequence	İ			P=Proline, Q=Glutamine, R=Arginine
amino acid sequence codon, /-possible nucleotide delatein-ston) LELPIAMERGEMENTSCHIVOLYVAFRISPENDGRGVFAVDGE AND STATE CODON, /-possible nucleotide insertion) LELPIAMERGEMENTSCHIVOLYVAFRISPENDGRGVFAVDGE LEVERANGE CONTRANSLIKERGESTTENTERGRAVITETEFERTHIVOLTICAL LANGERGEMENT STATE PRINCE COMPETENCY LEVERANGE CONTRANSLIKERGEST TENTERGRAVITETEFERTHIVOLTICAL LANGERGE CONTRANSLIVER COMPETENCY LENGESTYPHOLD LANGER COMPETENCY CONTRANSLIVER CONTRANSLI				S=Serine, T=Threonine, V=Valine
Sequence Codon, /-possible nucleotide deletion, /-possible nucleotide dispertion				W=Tryptophan, Y=Tyrosine, Y=Unknown +=G+==
Appendix Appendix			sequence	Codon, /=possible nucleotide deletion
September Sept	 	sequence		\=possible nucleotide insertion)
OKTYTAVASLIKGROGI TIENEREMSAJ KIEFFEKIMULTION LEIN I INSILLEPLEMOTION ROSILKEVETAKTIFFEKIMULTION OGFILISLAPYGWTOCSLIGFGSPEKSI (MESLITSAABGAHPSPL MPHENPASCKVSQVGGGTDSBEASMLSEGDASTISHTHASSES NENEROPALPTHOLD 827 MKUKKENDAYLIDENNINNDETISCFFKORLITIMFSHESILISL LEHGESTTSLPCAYARSILITVEWELLGKVSVNCAKTGYSASI TEHKSPFKORLINTIAVERUPLEKODPSERELMKEVTDSLIGES EIDKATEHKHILLERGRITERTTOTPIKKTIVIKEDGWVY NOSTKYVDLITLIAVTKKEVRPLEKODPSERELMKAVTDSLIGES EIDKATEHKHILLERGRITERTTOTPIKKTIVIKEDGWVY HEPLIMITIPTOPAS 6900 3 451 TEVIGRKENTERLESSTSLLHALESSASLLITHVERALPSTHIP VLPKKVORSSTERELLERTKVSOCGOLLESTTEHLKKARQCKES MEDSTVSGLITRITUVIKKARTHLEVRRILINGSEAPSLSGTHHHE LADLIVGBWAPALRPOEK 6901 1 201 DDINVORLETTPFORTLOGOSTLEGWAAMLDNVMQALKPYEGRE FFRAARGILKKRSYTXVHLOFS GAPPFPSGPFROFPGAAFSSEPSDITTFNSSALEGOAGAGGA GAPPFPSGPFROFPGAAFSSEPSDITTFNSSALEGOAGAGGA SDMEPSILDLIKKRSYTXVHLOFS 6903 1 149 RINGVYRGFTGHLIVTDGWONFOPSSCFLFSTVKAESSBGI HILL 6904 464 2092 MEASLBVSLSCVLACGDVECKFDLIFRIVOATQKKSGNFDLLC VGRYFGSTGDABEWSYKNIKKAPIGYPVLAAMORSTVKYPODA DGCELAEMITYLGRKGIFTGSSGLQVVJLSGTRSINEPVDGYSF SPRUNSLRMUCTTSGFKSVDTLITSPPBAYCRSSSGEVD VTRNYFRSGGRASIGKOLLAPVESACOFFPLLIKKORKRSS TGRDSKSSPIPMORDKUCTSGFKSVDTLITSPPBAYCRSSSGEVD VTRNYFRSGGRASIGKOLLAPVESACOFFPLLIRKGRKRSS TGRDSKSSPIPMORPKOPPOPPOGEWCLASPSTENDLIVORHY RKGGSALVSSLATGLRFYHFALEKTYTYRLPYNHILIQEN ADHATFITLANVONPEKKYLVAFSIVWELLUVNIOTH TKKGSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRKCSSALVSSLATGLRFYHFALEKTYTYRLPYNHILIVEN TRYCHTKINGTSTTUDGTCHTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1			LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGE
SATE SATE	6898	919	346	LMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL
GSPLESLAPYGKOTCSLIGFOSPRETQMESITTEMAEGAHEPSIL MPHENDASCKYQUUGGTEDELAMLSEGGDATIBIHTASESC NNEGDPALPTHGOL NERGENTESLPCAYARSILTYPWYBLGCKUSVNCAKTGYSASI LEHGESTTSLPCAYARSILTYPWYBLGCKUSVNCAKTGYSASI THYKPY GGKHRUTTABEVCHITTMTVVCRVQGEMBULEFTYS NERYKYDLIKLAUTKKRVRPLEKQDFYSERLIKKWYTDSIRES ELDKATEHKHTLEERGRTEERHRTETGTPMKTKTYLKEDGWVY HKPLIKLIPTYDAR 451 TEVLGSKGIHBLRSSTSALHHALESSASLLTMFWRAALPSTHIP VENGKVGSTSTERELLBERKVSOCGCLIGSTEHLKNANTQKES MEGFIVSGLTRHHUVLKKARTNLEVKKJOCGCLIGSTEHLKNANTQKES MEGFIVSGLTRHHUVLKKARTNLEVKKJOCGCLIGSTEHLKNANTQKES MEGFIVSGLTRHHUVLKKARTNLEVKKLLHGSEAPSLGFTHHE LADLVGGSPAPALRFORK MEGFIVSGLTRHHUVLKKARTNLEVKKLLHGSEAPSLGFTHHE LADLVGGSPAPALRFORK MEGFIVSGLTRHHUVLKKARTNLEVKKLLHGSEAPSLGFTHHE LADLVGGSPAPALRFORK MEGFIVSGLTRHHUVLKKARTNLEVKKLLHGSEAPSLGFTHHE LADLVGGSPAPALRFORK MEGFIVSGLTRHHUVLKKARTNLEVKKLLHGSEAPSLGFTHHE LADLVGGSPAPALRFORK MEGFIVSGLTRHHUVLKKARTNLEVKKLLHGSEAPSLGFTHHE BADLVGGSPAPALRFORK MEGFIVSGLTRHHUVLKKARTNLEVKKJCHGFTSSALESGARAGGA SPFKARAGFLIKKMFYRTVLLGFS GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGA GAPPPFSGTGPARASSHEHBSDLFFNSSALESGARAGGARAGA HILL LIKL GAPPFGSTGPARASSHEHBSDLFFNSSALESGARAGGARAGA AGATTATATATATAGGARAGAARAGAAR			240	QKTVTAVASLLKGRQGIYTENERRMGAVIKIRFFKIMLVLIICW
6899 120 627 MINNERGIPALPHIGU MINNERGIPALPHIGUI MEYRKINDAYLLDENKINNDCFISCFFKKUNTTIMFSGILST EHGGEVTSPLCAYARSILTYPWELGKYSVANCAKTCYSASI TEHTKOPYGGKLHRUTAEVGINITUTVUCUCGENGULDETS NGETKYVDLIKLAUTKKUPGLEKODPFSRRLWKUVTDSIRBS EIDKATEHRHTLERGRTEERRTETGTPWKTKYFKEGDGWY HOPLWKI DITTOPAB 6900 3 451 TEVIGGRGTHELRESGTSALHHALESASLLTMFWRAALPSTHIP VLPGKVGESTERELLELRTKVSOGGLLGSTTEHLKANNQCKES MEGPINSCHTHULKKARTNLEVKKLHGSEAPSLEPTHHU LADLVOLSWPALRROCK 6901 1 201 DDNNVQRETEDFFRATUOGSTLEGWAAWLDNVMMQALKPYEGGR 6902 2 267 GAPPPPFSDFPROPGARFSHHSDLTFNSSALEGGAGAGGA 6903 1 149 RINOVYGGFPROPGARFSHHSDLTFNSSALEGGAGAGGA 6903 1 149 RINOVYGGFPGPTGAFSHHSDLTFNSSALEGGAGAGGA 6904 464 2092 WERSLEVSLCYLACGDVEKFPTIFNFVQATIOKKGGRPDLLLC VGMPFGSTQDAEWERVKGUT KKAPJOTYVLGANNOETVXYFQAA 6904 464 2092 WERSLEVSLSCYLACGDVEKFPTIFNFVQATIOKKGGRPDLLLC VGMPFGSTQDAEWERVKGUT KKAPJOTYVLGANNOETVXYPQAA MINNERDERGRAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	ł		OCELICIA DE CONTROL DE LA PROCESTA DEL PROCESTA DE LA PROCESTA DE LA PROCESTA DEL PROCESTA DE LA PROCESTA DEL PROCESTA DE LA PROCESTA DE LA PROCESTA DE LA PROCESTA DE LA PROCESTA DEL PROCESTA DE LA PROCESTA DEL PROCESTA DE LA PROCESTA DE LA PROCESTA DE LA PROCESTA DE LA PROCESTA DEL PROCESTA DE LA PROCESTA DE LA PROCESTA DE LA PROCEST
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RINOVYRGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI HIILK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKGGNPDLLLC VGMFFGSTQDAEMEEYKTGIKKAPIQTYVLGANQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVFGYFF SPKDVSSLRMMLCTTSGYFKGVDILLTSPMPKCVGNFGNSSGEVD TKKCGSALVSSLANGLKPRYHFAALEKTYYERLPYRNHIILQEN AOHATRFIALANVGNPEKKKYLYAPSIVPMKLMDAAELUKQPPD VTENPYRKSGQBASIGKQILAPVEESACCFFFDLNEKQGRKRSS TGRDSKSSPHPKQPKPPOPPGPCMFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKKATL RRFFKSGKKCVVFERNYKSHHLQLQVIFVPISCSSTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFFLQFGREVLASEAILNVPLXVBWRQCQISKEDEBTLARR FRKDFEFYDFTLDD 6906 3 611 SYDDHNGHTDFTTAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNNFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHKKDFFTLLDFINAVKEKYGIE PTWVQGVKMLYVFWBGHARKIKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVFVWAAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDFSLFLLYMRAGEDLRVRRRGT GGSESRASGLVGRKATEDFLGSSGYSEDDVYGYSDVDQQSS SSRRSAVSRAGSLLWWATSPGRLFFLLYMAGEDLRVRRRGT GGSESRASGLVGRKATEDFLGSSGYSEDVYGYSDVDQQSS SSRRRSAVSRAGSLLWWATSPGRLFFLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNNQKEARENDESHFQAEQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQDDSE DLFKKIVRASQESEARIQQLKSEWGSMTQESPGSSVKELRRLE DQLAAGLQQELAALAKKOSVREWGELUPOOTOAWEDDWSORDA	1	-	267	GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGQAGAQGA
6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKGGNPDLLLC VGNFFGSTQDABWEEYKTGIKKAPIQTYVLGANQETVKYPQDA DGCELABNITYLGRKGIFTGSSGQQIVVLSGTRESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKFRYHFBALEKTYYERLPYRRHILLQEN AOCHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSQGBASIGKQILAPVEESACQFFFDLNEKQGKKRSS TGRDSKSSPHPKQPKPPQPPDGVFGCLASPBVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSUVELSAEVUEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQIQVIPVPISCSTTDDIKDAF ITQAGEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFFLGFGREVLASEAILNVPDKSDWRQCQISKEDEBTLARR FRKDPEPYDFTLDD 6905 1 226 VSKTGEAETTTSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAT VAGLVQTVLYCDFFYLYLITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAT ATTTATVSGLVALEMIKVTGGYPFEAYXNNEINLAIPIVVPTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTHVVQGVKMLVYVVMPGHARKIKLITHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDD LEGVPVWAAGAFRFSSGEETSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSFLRTLKRRSSMKRLSPAPQLGPSS DAHTSYYSESLVHESWPPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDVYGYSDVDQQSS SSRLRSAVSRAGSLUWANTSPGRLPFILLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGUBEARDSSHFFQAEQRVMSRVHSL ERRLBALAAEFSSNNQKEARRDESHERDAEQRGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKVPRASQESEARIQQLKSEWGSMTQESPGSSVKELRRLE DQLAAGLQQELAALAKUSSREVBELUHDOOTOAWEDDVGSORDA	6903	1	140	SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLFENN
MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC VGMFFGSTQDABWEEYKTGIKKAPIQTYVLGANNQETVKYPQDA DGCELAEMITYLGRKGIFTGSSGLQIVYLSGTESLMEPVRGYSF SPKDVSSLRMMLCTTSQPKSVDLLTSPWPKCVGMFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYRRLPYRNHILQEN ACHATRIFALANVGMPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENFYRKSGQBASIGKQILAPVEESACQFFFDLMEKQGKKRSS TGRDSKSSPHPKQPRKPPQDPBCWFCLASPEVEKHLVVMIGTH CYIALAAKGLSDDHVLILPJGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVJPVBISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIACPGAAYPYVELDTGEKLFHR IKMNFPLDGFGREVLASEAILNVPDKSDWRCQISKEDESTLARR FRKDPEFYDFTLDD SYDDHMGHLDFITAASNLRAKMYSIEPADAFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTWVVQGVKMLYVVPWPGHARKLKUTMYKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD SSSGGSSVAGSQSTLFKDSPLRTLKKKSSMKKLSPAPQLGPSS DAHTSYYSESLVHESWPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGSUVGKAATEDFILGSSSGYSSEDDVVGYSDVDQQSS SSGRIKSAVSRASSLUMWATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADGSWEARDSSPHFQAEQRYMSRVHSL ERRLBALAAEFSSNWQKAMRLERLELRGGAPGGGGGLHED TLALLEGLUVSRRAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKLVPASQESEARIQQLKSWQSMCPSFGSSSVKLRRLE DQLAGLQQELANLALKOSSVAEEWGLLPQLOGSGSSCKLRRLE DQLAGLQQELANLALKOSSVAEEWGLLPQLOGOGGGGCABA		_	149	RINOVYROGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI
VGNFFGSTQDAEWESYKTOIKKAPIQTYVLGANNOETVKYPQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSGYRGYDTLLITSFWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYRELPYRNHILQEN AOHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENFYRKSGQRASIGKQILABPVESACQFFFDLMEKQGRKRSS TGRDSKSSPHPKQPPKPPOPPGCCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILFIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKMCVVERNYKSHHLQLQVIPVESCSTTDDIKDAF- ITQAGEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRCCQISKEDEBTLARR FRKDFBFYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLVCDFFYLYLTKVLKGKKLSLPA ATTTATVSGLVALEMIKVTGGYFFENYKNMFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKSDFTLLDTINAVKEKYGIE PTWVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGEDLPGPPVRYYSHDTD SSGGSSVAGSQSTLFKDSPLRTLKRKSSMMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRAGGVGTLFKDSPLRTLKRKSSMMKRLSPAPQLGPSS SSRLRSAVSRAGSLTMWATSPGRLFRLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLXTFLWFLLPLLLLCTTGAWYFPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRGGAPGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKLVRASQESEARIQQLKSWQSMYGESFQESSVKERRLE DQLAGLQQELANLALKOSSWAEWGLLPOOLOGPDSSVKELRRLE	6904	464	2092	
SPENDYSSLRMMLCTTSQPKGVDILLTSPWRCYGNFGNSSGSVD TKKCGSALVSSLATGLKPRYHFAALEKTYJERLEYRNHIILQEN TKKCGSALVSSLATGLKPRYHFAALEKTYJERLEYRNHIILQEN AOHATRFIALANVGNPEKKKYLYAPSI VPMKLMDAAELVKQPPD VTENPYRKSGQBASIGKQILAPVEESACQFFFDLMEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPGCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF IYQAQEQQIELLEIPHSDIKQIAQPGAAYFYVSLDTGEKLPHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDESTLARR FRKDFBPYDFTLDD 4 VSKTGRETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHMGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKITPAI ATTTATVSGLVALEMIKTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISTTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTWVQGVKNLYVPWPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 5907 2 2228 LRGVPVWAAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSMMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANMGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDCQSS SRRLRSAVSRAGSLLWMVATSPGRLFRLLYWMAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSPHFQAEQGVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQCAPGCGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKLVRASQESEARIQLLSEWGSMYTGESFGESSVKELRRLE DQLAGLQQELAALAKGSSVABEVGLLPQOLOGAWDDVESGEPBA	1 1		2032	WENEFGETODA EMERYWARD WARD TO THE PROPERTY OF
SPROVSSLRMMLCTTSQPRGVDILLTSPMPKCVGNFGNSSGEVD TKKGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHILQEN ACHATRFIALANVGNPEKKKYLYAFSI VPMKLMDAAELUKQPPD VTENPYRKSGQBASIGKQILAPVEESACQFFFDLNEKQGKKSS TGRDSKSSPHPKQPRKPPQPPGPGPGCWFGLASPEVEKHLVVNIGTH CYLALAKGGLSDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLBIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEALLNVPDKSDWRQCQISKEDEBTLARR FRKDFSPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPARFRTKRIAGKITPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKYKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKNLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYSHDTD 2228 LRGVPVWAAGAFRFSSGEETSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSBWQSMTQESFCBSVKKERRLE DQLAGLQQELAALALKOSSVAEEVGILPOOLOAWBDWESOEPA]			DGCELAENITYLGEVGIETGCCCCI OTHER COMPONING
TRRCGSALVSSLÄTGIKERTHFRALEKTYTERLEYRNHIILQEN AOHATRFIALANVGNPEKKKYLYAFSI VPMKLMDAELUKQPPD VTENPYRKSGGRASIGKQILAPVEESACOFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILIPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKOAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEBTLARR FRKDFSPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKITFAI ATTTATVSGLVALEMIKVTGGYPFERYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTWVVQGVKMLYVPVWPGHAKRLKUTWHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 2228 LRGVFVWAAGAFRFSSGEESTSHLTWSRGGDDDGS SSSGGSSVAGGQSTLFKDSPLRTLKKKSSMMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSLKTFLWFLLPLLLLTCLTYGAWYFFYPGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRWMSVHSL ERRLBALAAEFSSNWQKEAMRLERLERQGAPGGGGGLSHRD TLALLEGLVSRREAALKEDFRRTTAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFGESSVKELRRLE DQLAGLQQELAALALKOSSVAEFEGLLPOOLOAWRDUSSCOPPA				SPKDVSSLRMMLCTTSOPKGVDTLLTSPWDVGVGVEGVG
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SSRIRSAVSRAGSLIMMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKOSSVAEEVGLLPQOTOAVRDDVESORDA	l l		1	GGSESSRASGLVGRKATEDFLGSSSGYSSRDDYVGVSDVDCOSC
SLEDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKOSSVAEEVGLLPQOIOAVRDDVESGEDA				SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYDI.TTAA
TFFPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHRD TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKOSSVAEEVGLLPQOTOAVRDDVESARDA	ſ			SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWVFVDVGLO
ERRIBALAAEFSSNWQKEAMRIBERLELRQGAPGQGGGGLSHBD TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKOSSVABEVGLIPQOTOAVRDDVESABDA]			TFHPALVSWWAAKDSRRADEGWEARDSSPHFOAEORVMSRVHST.
TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKOSSVAEEVGLLPOOTOAVRDDVESORDA		ļ	1.	ERRLEALAAEFSSNWQKEAMRLERLELROGAPGOGGGGGLSHRD
DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKOSSVAEEVGLLPOOTOAVRODVESOEDA	ŀ	[[,	TLALLEGLVSRREAALKEDFRRETAARIOEELSALRAEHOODSE
DQLAGLQQELAALALKOSSVAEEVGLLPOOIOAVRDDVESOFDA	1	1	11	DLFKKIVRASQESEARIQOLKSEWOSMTOESFORSSVKELRRIE
WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGKS	1		1.	DQLAGLQQELAALALKOSSVAEEVGLLPOOIOAVRDDVESORDA
				WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGKS

SEQ	Predicted	Predicted end	Amino sold second contains signal mark/
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine.
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	· -	\=possible nucleotide insertion)
			AREAAASLSLTLQKEGVIGVTEEQVHHIVKQALORYSEDRIGLA
1			DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
			LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
			NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGEPIQTFHF
1	}		QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLOGCFGAARLLYPRFOSRG
I			PQGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
	1		QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV
1			GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSQLPPLT
1	1		AFILPSGGKISSALHFCRAVCRRAERRVVPLVOMGETDANVAKF
1			LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATEVSNSLLPEKAFSDIP
Į			SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
			LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
1			PAC
6910	1.	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
1			LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
			LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
1			LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
			LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
			NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
Į		-	RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK
			KSGG
6911	1184	966	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
L			PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
1	, i		SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
			GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
			YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
			DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
			SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS
6913	1642	1,55	NPETLDLYRDIPELQGF
6913	1643	1558	KKSHEESHKEELSYGAQASLPLPCSDFR
0 2 4.4	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDI
			CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
1			ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
			QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
6915	254	652	CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
			GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT ALILTELLMVALTVRTWHWLMVVABFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
	-52	- J_E	l
))	']		ALILTELLMVALTVRTWHWLMVVABFLSLGCYVSSLAFLNEYFD VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	
/	404	532	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
	ļ		VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPOWLPGGGGGOVSSCS
5525	20	267	
	i		DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
			VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
	ļ		LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGE
	Ì		VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
	J		LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC
			******* ******************************

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6919	850	41	QGRRELSGSVFCPFIQQEPKEMLTLSEYHERVRSQGQQLQQLQA
1			ELDKLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG
1	}		ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEPHVFPG
1			NCWAFEGDQGQVVIQLPGRVQLSDITLQHPPPSVEHTGGANSAP
1			RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEIQTFHL
Ì	1		QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS
<u> </u>			AQGPH
6920	1418	591	EAQGPSKVHLTLKKKK
6921	2	1711	MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI
i			PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV
			QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP
			SNCLGIRSFGDAQGCTELLNVAHKYTMEHFIEVIKNQEFLLLPA
			NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
			YIRLPLLPPQLLADLETSSMFTGDLECQKLLMEAMKYHLLPERR
			SMMQSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL
1			HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK
			IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMBY
			FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC
1 1			SRLSDCVERYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG
<u></u>			YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP
6922	1075	369	LTPPAGIRHEVRDRBREREREREREKFPLDSTGSELKQNIHSIT
1 1			GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA
			VNTPKDAAQQDAKAEENKKEPLCRQKQHRKVLDKGKPEDVMPSV
1 1			KGAQERLPTVPLSGMYNKSGGKVRLTFKLEODOLWIGTKERTEK
1 1			LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY
6923	2469		VDAIKDTVLGKWQYF
""	2403	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ
}]	J		LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV
1 1]		VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY
]	1		SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK
l i	1		QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP
1			EIIFYT
6924	2210	1235	PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP
1			KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP
1	į	l	ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE
1 1	l		HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF
1 1	1		HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG
1			ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI
1 1			DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ
6925			SPLESTLMGLEVQSFPV
0325	2	1653	RGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL
	.		SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF
			DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP
]	Ì	1	EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
	1	j	ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI
		ļ	IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG
		l	LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
	i		TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV
	ľ	ļ	WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC
Ī		1	GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP
			RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL
		ł	NVPPSAQNETRSPSRTYTYISR
6926	1.		SGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL
			TARY TAREST THOSE TIME TURBOUT KNOOD TOWARD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ar	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
		 	DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
1			YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGS
ı			PGAGGGRGFQMQPQHQHQHQHQHQHPGPGQPTPPPEALPCRDGT
			DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
1	1	i	SHGAISSVVSDASSAVYYCNYPDV
6927	2	1484	LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS
	_		CQGFAWATDLSTDLESQLSVSCKCYEAANEILQFRDLKSQNPEH
			VVOVI. KOMENT DIE TOURS OND DAY OCH THE TOUR DESCRIPTION OF THE TOUR DESCRIPTI
			YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQLW KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
	i		GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
į.			WELSTTVETMANI OCHVARI CRIVA CROTTERINGEN
1	[WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
1	1		VDSVSARQPLCQYRAATIHHRLASMYHSCLRNQVGDEHLRKQHR VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFQMTSQNS
1	}		WIGHT WILL COAT DIVIDING HOLD TO THE TOTAL TO THE TOTAL TOTA
			NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
			ADASPSLNREEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN
1			IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGQLAA GSAASSNAVO
6928	1086	777	
1	2000	///	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
1	l		IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE
6929	1749	607	ETEMKALGERVSIL
1	1 113	607	RDQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
			NLHQHDPQDLRHNGNVVVAGRPSCSRGPRRAIQKPQPAGGRRSG
			RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
1			QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGPGIYTSC
	1		SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD
1 .	İ		TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM
1	1		ALAMAKPMAKMQVEVEKQNRKKSPVADLLPHMPHISECLMKRSL
1 1			KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE
6930	131	545	QDAMLVDIEDLTRHAESQQKHMAEKMPAK
	-52	343	FKDTANVFVSLFQMRNNFRHYFIEPSQLKLFYDVITWIVTQVAI
1 1	í		SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTQR
1 1			RKNTHENIQLSQSKKFDEGENSLGQNSFSTTNNVCNQNQEIASR HSSLKO
6931	2	659	
	-	523	FVERLPNRPACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
, 1			PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAL LIPSCPGALTDLASSGSLARILQHFHSESKPICAVGHGVAALCC
1			ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG
	j	j	ACFSASEPDAVHVVLDRHLVTGQNASSTVPAVQNLLFLCGSRK
6932	2	1131	FVDSPGQGEQAEEEEGGIQMNSRMRAHSPAEGASVESSSPGPKK
	-		SDMCRCCESI.AACUBCUTCUDVETT TITTETT TO STATE OF THE STATE
!			SDMCEGCRSLAAGHPGYISHDKETSIKYVSHQHPSHPQLFSIVR
	1		QACVRSLSCEVCPGREGPIFFGDEQHGFVFSHTFFIKDSLARGF
[İ	ſ	QRWYSIITIMMDRIYLINSWPFLLGKVRGIIDELQGKALKVFEA
			EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACL
	1		HTSFAWLLKACGSRLTEKLLEGAPTEDTLVQMEKLADLEEBSES
	!		WDNSEAEEEKAPVLPESTEGRELTQGPAESSSLSGCGSWQPRK
			LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
6933	1431	890	KTLQEVTDSLLGGWLMAQGVGGII
		030	SLNLHCTLPPPPHQYPAGYPSDKEGKKPKGQSKKQPSGTTKRPI
1		!	SDDDCPSASKVYKASDSAEAIEAFQLTPQQQHLIREDCQNQKLW
l			DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK
ľ			DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFFGY
6934	3030		SKGR
0334	3030	2588	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
	1		CWTPFFFVQMWSVWDANAPKRASAFIIVMLLASLNSCCNPWIYM
j	1		LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
			HRSSSQRSCSQPSTA
		.	CWTPFFFVQMWSVWDANAPKEASAFIIVMLLASLNSCCNPWIYM LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	5544655	\=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVBRYSPKAGAWESVAPMNIRRSTHDL
Į.			VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
	ĺ		VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
	1	30,	TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
ì			MEADI OEYOLAALEANODADECAADDATOONALDATA
1			MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
ł			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
			NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL
6937	1	727	AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
1 055,	-	121	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
			DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
			PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA
			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMQYLREG
1			YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
6938	3	719	TWKKVRRVDQCSCPAVHSFIFI
	.	,13	NSRKLELAERVDTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
			EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
			AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS
			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
			ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
'	•	0.0	GYESL DDDGPAMGGA GCA DDGWGEGGAA GDGA DDGWGGGS
ĺĺ			GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
			EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
1			LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
1			EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
] !			EVDV
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
			VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
	,		LADSVHLAWDLSRSLGAVVFSRVTNNVVLKAPFLVGIEGSLKGS
1 }			TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
1 1	1	Í	KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
] }			EVTPDQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
l I			VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL
	İ		HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQGSG
			RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
1			AWYTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
1	ļ		MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
[[Í		QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6943	. 1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
1			HSPAGGSITETLVQGDKTEYLLTALEPKPTY11CMVTMETTNAY
[VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
		1	VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
	1	1	TKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
[į	ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
i I			LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYOKY
[1		NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
		į	FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYO
	• 1	1	SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVIGPLTSA
	Į.		VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLL
	İ		LWAN CONTROL OF THE TARGET AND THE T
	·		

1	SEQ	Predicted	Predicted end	Amino paid comme
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
-		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ		sequence		\=possible nucleotide insertion)
- 1	6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
ı		Ì		HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLQLGIHGL
- 1		Į.	1	IPPCFLSQDVQLLRIMRYYBRQQSDLDKYIILMTLQDRNEKLFY
- 1				RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
- [HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGTPVGKT.A
				LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHOPVHGK
		[ĺ	AYDDLLDEFMQAVTDKFGINCLIOFEDFANANAFRIINKVONKV
]		CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFOGAGFAAM
- [}		G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLTVOGPDU
-				LNHEKEMFAQD\HPEVNSLEEVVRLVKPTATIGVAATARA\ FTR
				QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGR
- [FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWOT.GVHCDC
1				GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
- [NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKTPGSYTDD
H	6946	133	0.551	YDSFYT/VDSYIWAQGKAMNVQTV
		4,53	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR
1				NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC
				NF\EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE
1				AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG
				C\TNILLLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR
1	1			F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
		ļ		WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS
1	ŀ	1		YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
1		ļ		IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLFDIARIE
1	1			RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE
ŀ	1			QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF
				QYRRVNELLLS ILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
1	1	i		VGKMGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD
	1	1		NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL
	- 1			RPQLMTSQFISVFSNLLESKADGIEVSYNACGVISHIMEDGDED
	j	j		WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPTI.RLI.PO
)			GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDTTKM
⊢	6947			ATARQETKEMARKVIEHCSNFKEENMDTSR
1	422/	2	1682	TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRARGRGLKMLNUD
1	- 1	1		SQSFPAPRSQQRVASGGRSKVPLKOGRSLMDWIRLTKSGKDI.TG
ı				LKGRLIEVTEBELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
				DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLK
ŀ	1	ļ		DYREEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVTI
l	İ	-		/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A
l	1			MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSL
				IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
				IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLLA
	}			AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE
			ſ	KLAPKOKRLOVEFVLSAPISEWNGKQGHISPALLSEFLKRNLOK
			l	SKYLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
1	6948	1.04	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSR
		1	1	CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY
	J	1	ļ	AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
	1	ļ	[DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDQI
	1	į		APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK
		ſ	ļ	TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT
				QETVE
E	949	152	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
				QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	\n-n1quine, C=CVSCeine, D-lenartic lain =
i	location	corresponding	Julianic Acia, F=Phenylalanina C_Cl
į.	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
- I			SCSTDTSEVPRWPENKEDHLVYADERSSNITDCBITTBERAUGIVE
f			BEFOLISTASI \IPDVLTRVST.VPSHT.NFCMI.FCDATTICO.DOMO
			SAFFIGSSGFSLVKEIKDSTSOHDDDNISTTSGEGGDAGDVDTM
}		İ	VOICE TO THE PLANSPEACE SHISLSOHTATSSEVED A THE CARCON CO.
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-			I FVRRQMARQUSAOSYGVTSSTARRII.OSI.EVMCCDI ADAVDITA
l			1 21 122 FINS PLUKSGIDITDFOAKREKVOGOV POVODI MEDVENI
		1	SIMINKSVIEKPSLTPSGEFRKTNORTDKKCCTGVEVARKEDGON
			REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
ı	1		LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS OALTNKVOMTSPSSTCSPMEKPOSST
			QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTAELSGSSSTLEPIISSSAHHVITVNSTNCKKTPPEDC
i		ĺ	EGPFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY
ſ		ĺ	TREATSSESSEIGEGESLKAGSSWOCDTCLIONERTONEOUT OF THE
1			WAALISPRUTAKOTGIETPNKSGKTTI.GASGTCECDVEVELTER
1			MUCUICLIVONKPEAIKCVACETPKPGTCVKPALTI mårgegarm
			MIASSSCIVITGILGFGDKFKRPIGSWEGSUCGUGARIA PRIMA
1	1		VOCHSERFGSSVPTSSSSTVPVSI.PSGGGIGI.PVPVVDPGTVPG
			ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS
1	1		SFKFGVSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP
	1 1		MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR
1			VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA
			I AGGE SEGNVEPASLPSASVEVI GRIEFKOODDVITCTOF LIBERT
ł	1		ADIMACIAC QUIVESFGEFOROTKOFMSSKSTERSKTKDARKE
1	Į J		SECRACAT PARGACITATIADOGA KPDI SVI AINSCOCCOUDA MO
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	1		SQSEDI SQUSKEATTSSTGTAVTPFVFGPGASSNMTTTGGTGTG
l			ALLISSSAGSSEVEGTGPSAPSASPAFGANOTPTEGGGGGGGGGG
	1		NPPGFGSISSTALFPTGSQPAPPTFGTVSSSSQPPVFGQQPSQ
			SAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTP
6950			AASAQPSGSGGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK TAVRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDELHYQDTDS
1	İ	j	DV PEQRUSKCKVKWTHEEDEOLRAL VROFGOODWYFL A CURPAIN
1 1			1DDCCD1KWLKVLNPDLVKGPWTKFEDOKVIFIJVVVCmvorm
			TANTLAGRUGKUCRBRWHNHLNPEVKKSCWTFFFFDTTTCFATTOR
1			DURKMALIAKMUPGRTDNAVKNHWNSTIKPKVDTGGET GEGOOG
1 1	,	1	AFFVILLEDEDEDEDEDEROGENTATION [
1 1		;	SEELINAATISKEQEPIGTDLDAVRTPRPI.EEFDKPFDOFCORD
1 1		1.	ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
1 !		1	DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRQRK
1 1	1) :	RRVALSPYTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF
	l	1	WNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
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	Í	, .	CARPEKAAVAQKPRSHFTTPAPMSSAWKTVACCCTPDOLEWOR
6951	1940		MARQUIGRIKPSHTSRTLILS
			AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL
		1 5	2VLPSGTPPGTMVTAPHSSTRHTSVVMI.TDMDDGDDGGAAADMA
	1	, 1	TTPRAEGHPPT\TPSPPSLRO*PPPTT.KAD/GGTGDDDAAMDU
' I	ĺ	ءً ا	SSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP
			PGSSRKGAGNSSRPVPPAPGGHSRSKEGORGRNPSSTPLGOKRP GKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQTVAAT
			TAVATOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO

SEC	Predicted	Drodieta	
ID		Predicted end	
NO	nucleotide	nucleotide	
	location	location	
į.		corresponding	
ĺ	corresponding	to first	Delicate, Mamethionine Nanagara
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan V-Tryptophan
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<u> </u>	sequence	1 -	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
İ	İ		TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
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- 1	1	1	TORE DO LOOG OF TAATGOTDAN PROTEGOR DECOTTOOLS COM-
	1		1 *** OKYSES I I SCAKELIVA / DSD*DTCCDIT CDOVIVDOSS
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ſ	ĺ	1	TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP
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			PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT
6953	1512	349	THE REPORT OF THE PROPERTY OF
- 1	ļ	1	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES
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i	1		AIETPEKRQARLIREREAKRLKRRLEKMDMMLRAQFGQDPSAMA
			ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH
6954	819	1	PPPPFTTPSUPPFACEANTE
1			PPPPFITPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQN
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6955	1968	782	
	1	/82	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD
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	1 1	ł	ACCUMENTAL PRODUCTION OF THE P
1	1		/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG
1	f i	1	LTLSDLPLHMLNNILYRPSDGWDIITLGQVTPTLYMLSEDRQLW
	1	1	KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQY
1	1 1	1	GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
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		1 -	RVRGRGREPRVKITELLNKTDNRPI, KKI, PAODOT NIDDOVA
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· /	1	l R	CAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKAD
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ļ	j	9	CQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSEI
i	l	[*	LTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQKAAV
j	1	1 **	AT DARKED NGSILLINEIDKTLESMSSVDVNVWTVECDI DD]
1	i] V.	MAKELGKSEVEMEGPEECLGRRRSSDIMFUTTCCMTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
1	ļ	1 44	AVFORKGRRUGEVUATASSTPELEROTEVI.CVDOX EEDVESSE
1	ſ	3	SQUIDRAVSLGQURYRRRYWVI,PVI,ACTEUP/GPBCMT 1/07
		K	etdslkvaahaslnpalfsmkmelagsnttassparargrprk
			- ACHORPER

			
SE		Predicted end	Amino acid segment containing signal peptide
NO		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO		location	1 Ordinate Acto, Febrery alanina C. G.
	location	corresponding	d=nistidine, l=Isoleucine v=Ivcine
	corresponding	to first	Debeucine, Memethionine National Control of the C
ł	to first amino acid	amino acid	P=Proline, Q=Glutamine P-Arginine
ì	residue of	residue of	S=Serine, T=Threonine, V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tvrosine Y-IInknown + a
- 1	sequence	sequence	Codon, /=possible nucleofide delonies
			\=possible nucleotide insertion\
į.	1		TKPGSMQPRHLKSPVRGODSEQPOAGLOPFAGLUADAGE
1	1	i	Deposit of DECESPLESEOSOHDISOSAFI CHI COTOCHESE
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	ı		I TAX TOUR TO LOUTHOP VPPEMCS CWWWT DDDDMT DAMT WATER TO
	•		TOTAL CAMERALINATION OF THE DESTROY OF THE POPULATION OF THE POPUL
1	- 1	İ	SWSPKEKTYETDLAVLQWVEELEQRVIMSDLQIRGWTCPSPDST
i			REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
1	J		AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS YEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT
- 1			CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
- 1		ļ	CLAQQVEGEFTQKFGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
}	1		OKESPANGERISEEGLSPSKRRRI, SMDNUUGDI DDODT TI ADVILL
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1	1		IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR
-	1		SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN TKP5EYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
	l .		VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
1	1		CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
1			EDITOICGERVELECEVSEDDAOVKWFKNGEETTI.UOTBVBTDV.
i i	1 1		BONNELDITEGATKADAADYSVMTTGGGGSAKT.GIMT.VDT VTT 1
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1	1		GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD
l) [LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVVKE IIEPPKTHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
	1		GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
			TASIDIRIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
}	1 1		GYTIQKADKKSMEWLRVIEHIIBPVPHTELVIGNEYYFRVFSEN
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ł	1 1	i	VNRLCHSGYMATLNCSVRGNPKPKTTWMVNWWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
6958	274		"20 TO THE TRAPSPIDGGTY CCKAVNDI GTVETE CRT. PRIVATE A COLOR
	2/9		FALSAVALEGSQGSSAMDFSVKVDTEKEVTCPTCLELLTEDT CT
		1.	DCGAST COACITAKIKESVIISRGESSCOVCOTORODONI DDND
	1	, .	THAT VERVEEVENS POEGOKROVCERHOKKTOT POKEDOWITC
		1 1	WVCELSQEHQGHQTFRINEVVKECORKI.OVAT.ODI.TVENORARY
•		ļ -	DEDDIRQUERIAWKNYIOIBROKII.KGFNEMDUTI.DNEEODELOG
	1	, ,	DEEGE VN VLDNLAAATDOLVOORODASTI.TSDI.OPPI.POGGIJEM
			DO A TO AUTUSES MILKK PKS ASKKI'K SALEDA DIT COM OUT AND
		[4	JIDVQI IWVDVMLNPGSATSNVA I SVDOPOVKTVPTOT PROTOSTON
	i	1 5	DESARGUEGCQIESSGKYYWEVDVSCKTAWTI.CVII.CVTCCTAW
		(•	KSSGFAFDPSVNYSKYYSRYRPQYGYWVIGLQNTCEYNAFEDS SSDPKVLTLFMAV\LPVVLGFS
6959	1	1469 S	LVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS
			THE FILL FOR THE COURT CSVTQAGVQWCDHSS

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion
<u> </u>	ocdence	<u> </u>	\=possible nucleotide insertion)
ł	1		LQPQTPGLNQSSHLSLLSSRDYRMLSSFNEWFWODEFWLDDNUT
l l			WIEDEDROGRVYPHPQDLLAALPLALVLLAMRLAFERFICEDIC
i	1	1	RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEDOLSLIAAOOGI
-	1		TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLPVLSSFUCCLSU
1		1	LYHESWLWAPVMCWDRYPNOLTLSCPAADSEA\SLVWWYLLELG
į.			FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DEKEOUTH
1	1		HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYTTRACKMUNYMO
1	1		YQQVCDALFLIFSFVFFYTRLVLFPTOILYTTYYESISNEGBEE
}	1		GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDV
ı			EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN
L			RHTTAT
6960	387	2068	AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
1	1		HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT
j.			PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTHP
1	1		KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGK
1	1		TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN
1	1		KGTKSLKESEQESEEEILAQKKEQREEEVEEEEKEEDEEKGDWK
1			PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG
1	1		DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA
			KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS
1	}		SPKGPTPGGGGGGCGDEAKGGKAGGGPQGERKNRSSKKS
i			SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR
1	į		ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR
L	i i		ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGB LYRRTLDSDEERPRFAPPDWSHMRGIISSDGESN
6961	340	1646	PRICED MEDICAL DE DE DE DE DE DE DE DE DE DE DE DE DE
			RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
		:	LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
1 .	1		SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
1	1		ADVVLLCGDLNMHPEDLGCCLLXEWTGLHDAYLETRDFKGSEEG
	' l		NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
	l		TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
1 1	1		PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
	1		LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
			LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6962	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
1 1	1		NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
]	}		LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
1 }		Ì	SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
l j	i		ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
1 1	ł.		NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
		į	TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
	i	1	PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
		1	LALLCYLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
	1	ľ	LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6963	374	2618	RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF
			EAVI.SPORALTHERMOLANDRA TOPOGSSAKPGLPCLNF
			EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN
1	1		LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS
]	1		PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA
	İ	Ī	LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG
	1	1	TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE
ſ	1	1.	RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL
İ		1.	STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
1			ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV
İ		1	EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPOTNOLETGASSDE
-		1 1	RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPI,PSTOT.VI,P
·			QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK

SEQ	Predicted	Predicted end	Amino agid company
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- [location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- {	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPLASSAGH
ĺ			STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI
ļ)		CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNKRFTQKSSLNVHM
ŀ			RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTPPAGTPP
			GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMRMHVSDG
6964	1	178	SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
			Q1F1G\NCSMFVLVI
6965	757	208	NVFIEPRIQGFMKTSAHPGOKHPDFSMGLLEPLLAALEVCSCGG
1			SGSLGYNLPQNH\GLLGRNTLVLLGOMPRISPFI.CLVDPCDEDE
ŀ	Ì		PQEKVEVSQLQXA\QAMSFLYDVLOOVFNFSHKAIJ\\CCMFHDI
1	1		PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGOWVIEGSTIALDDV
6966	820		FQESISTLE
1	020	1867	IITALGVRGMPGCPCPGCGMAGPRLLFLTALALELLGRAGGSQP
			ALRSRGTATACRLDNKESESWGALLSGERLDTWICSLIGST.MCC
			LSGVFPLLVIPLEMGTMLRSEAGAWRLKQLLSFALGGLLGNVFL
j			HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVIAGILTFLALEK
1	1 '		/HVPGQQGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR
1			GP\DIKVSGYLNLLANTIDNFTHGLAVAASFLVSKKIGLLTTMA
			ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA ICTQSPKGVEETAAWVLPFTSGGFLYIALVNVLPDLLEBEDPW
6967	162	633	GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEEGSELNGFEG
l			TDMKDMRLEAEAVVNDVLFAVNNMFVSKSLRCADDVAYINVETK
1		•	ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\
			SPAYREAFGKR\LLQRLEALKRDGOS
6968	1	2265	RGGGGGGGGGARERERPGEPERTMEAAAGGRGCFODHDGLOKT
1	1		LEQFHLSSMSSLGGPAAFSARWAOEAYKKESAKEAGAAAVDADU
1	1 1		PAATEPPPVLHLPAIOPPPPVLPGPFFMPSDRSTERCETVLEGE
ľ	1		TISCFVVGGEKRLCLPQILNSVLRDFSLOGINAVCDELHIVCSP
1	1		CTADQLEILKVMGILPFSAPSCGLITKTDAERICNALLVGGAVD
	1		PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS
1	1 1		SPSAACIQCLD\CRLMYPPHKFVVHSHKALENRTCHWGF\DSA\
f	}		NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP
	j		RVSSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS
ł			LGCVHPRQRLSAFRPWSPAVSASEKELSPHLPALIRDSFYSYKS
i	i í		PETAVAPNVALAPPAQQKVVSSPPCAAAVSRAPEPLATCTQPRK RKLTVDTPGAPETLAPVAAPEEDKDSEAEVEVESREEFTSSLSS
Į.	1		LSSPSFTSSSSAKDLGSPGARALPSAVPDAAAPADAPSGLEAEL
ľ	i i		EHLRQALEGGLDTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS
1			LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKMKEA
	1		NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL
1]		QHAEADREQLRADLLREREAREHLEK\VVK\FI.OROT.WDDADDD
6969	3055		AAGSEG\AAELEP
6565	1855	118	AGTMHGRLKVKTSEEOAEAKRLEREOKLKTVOSATOATEOVOON
			GELDESVLELTSQILGANPDFATLWNCRREVLOOTETOKSDEDT.
		1	AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRI, PEDNUTDEL
		İ	ELCARFLEVDERNFHCWDYRRFVATOAAVPPAEELAFTDGLTTD
	1	ł	NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF
			SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP
	1	f	AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE
			QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM
	İ	1	RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS
ŀ	1	1	VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL
ľ	ſ	1.	PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL
		1	PSVSSVLT

SEQ	Predicted	Predicted end	Amino agid goment
Œ	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6970	3	1528	SFPPLLSSPSAVGEGKVAVAAPCPGRSECAPAKMAVTOLEDINE
			GFLSRISGLLLCRWTCRHCCOKCYESSCCOSSEDEUETLGDEDA
1			QTPPWLMASRSSDKDGDSVHTASEVPI.TPRTNSprcppscente
ı			KSTYSLTRRISSLESRRPSSPLIDIKPTEFGVI.SAKKERTORSV
1	ľ	1	LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEETLSKVOLGM
Į.	1		LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRODMAHSNDVV
ľ	1		KICLLPDQKNSKQTGVKRKTOKPVFEERYTFEIPFI.RAOPRTI.I.
ļ	}		LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALTPSSONE
[[VELGELLLSLNYLPSAGRLNVDVIRAKOLLOTDVSOGSDDEVKT
l			QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPORELENASIA
	1		FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
6971	37	3700	AVEQWHSLRSRAECDRVSPASLEVT
) "	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
			SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
1			RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
			RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
			AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
1			EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
i i			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL
			LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV
i i			LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV EEGLTYKFHAAWSSVLQLLCVFFEACGRQAHPVMRKCLQSLCDL
) j	l J		RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
1			FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
1			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLARTLGMAI
1 1	ł		SERPDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
1 1	1		LYGOPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
1 1			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
		·	AHGVQKKAYRVLEEVCASPOGPGALFVOSHIEDIKKTIIDELBE
ſĺ	İ		TSSPAKRPRLKCLLHIVRKLSAEHKEFITALTPEVILCTKPVSV
1 1			GARKNAFALLVEMGHAFLRFGSNOEEALOCYLVI,TVDGI,VGAVT
1		ļ	MVSCSILALTHLLFEFKGLMGTSTVEOLLENVCLLLASPTDDVA/
1 1			KSALGFI KVAVTVMDVAHLAKHVOLVMEA I GKI SDDMPDUEDMV
i i	İ		LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVI,VNIPKARADAV
			RHRALSQAAVBEEEEEEEEEEPAQGKGDSIBEILADSEDEEDNE
1			EEERSRGKEORKLARORSRAWLKEGGGDEPLNFLDPKVAORVLA
1	i i	}	TQPGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
i	į.	l	EEMADPMEDVIIRNKKHQKLKHQKEABEEELEIPPQYQAGGSGI HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
<u> </u>	j		RKKMKLQGQFKGLVKAAQRGSQVGHKNRRKDRRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
		I	PAEAGGATRSPPPRPARPPGPSAPPLLRSDAGPGATVSAAA
! !			AAATERARRGATMGAQLSTLGHMVLFPVWFLYSLLMKLFQRSTP
		1	AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG
	j]	QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
			FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
1	1	1	SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
1	1	i i	ANQTEKDILLRPELEELRNKHSARFKLWYTLDRAPEAWDVGOG\
	ĺ	į	FVNBEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH
6075			PTERCFVF
6973	1	1964	LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
ı			SPRRQEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKO
1	}		KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKODAV
ł	1	1:	RMLSRFE/SGREHSVFTGVAIVHCSSKDHOLDTRVSEFYEETKV
1]]	RFSELSEELLWEYVHSGEPMDKAGGYGIOALGGMLVESVHGDFL
		1	NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFBDL
		-	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:		location	I I' PICHTILLE, CECVECEINE Delonoveia lais e
í	location	corresponding	Gradule Acid, F=Phenylalanine C-classic
ı	corresponding	to first	nemistidine, leisoléudine K-lucine
·	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=PIOLINE, Q=Glutamine, R=Arginine
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- }	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence) Codon, /=possible nucleotide deletion
			\=possible nucleotide insertion)
	ſ	İ	SDVEGGGSEPTQRDAGSRDEKAEAGEAGQATAEAECHRTRETLP
ſ	1	1	FFFIRDLEDIEGFMLSKGLLTACKLKVFDLJ.KDFADOKAADIAC
j]	Ì	AVDASACGMERLLDI CAAMGLLEKTEOGYSNTETAMIVI ACDOR
- 1	į		1 SURGETMENNULTWALFTYLEFAIREGTNOHHDALGEVARDIR
1	į		QUALT QSPETRLRFMRAMHGMTKLTACOVATA FNIT CD BCCA CDIT
1			GGCIGALARELAREYPRMOVTVFDLPDTIELAAHROPDCDONG
ľ			I TO TAGE TROPE PROPERTY LEGISTICS TO THE PROPERTY OF THE PROP
- 1	, i	1	RPGAGLLLVETLLDEEKRVAORALMOSI,NMI,VOTEGVEDEL CEV
6974	3082	22.75	QUILLELEGE HOVOVVHLGGVLDATI. \ DDKWDDEAOAAGE
	3002	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATEAGCALCAMIC
1	-1		I DIMAREGUETKYQATMVYKTLFAT,CTT.TAGWDVOGT.DDCADI.CT
1	j		SEPINIVPPTTIWTSSPONTDADTASPSNGTHNINGUT DIME CAR
			ISLEPANISIESREEEITSPGSNWEGTNTDPSPSGESSTECCIR!
1			I I I I LEERS LG TPEAGVAATI, SOSAAE PPTT, TSPOADA SCREET
j			SISPENISASVITNHSSTVTSTOPTGAPTAPTCPTTPTCCCOUR
6975	2	500	FISHATAEPVPQEKTPPTTVSGKVMCELTDMET\ pppppc
	_	300	REPRETVHCCKWALKLETAMETI.TNVEHAUSCKECDVVVI SKURT
]	}	A REDUCTELSGFLDVKELML*ATEALKTREEA*VCDITOGGGGGG
j	1		SUPPARQUELY LSAVPFP IHI PLITT, DPOACKDVD AUDIT MARKET
6976	1216	970	BLDENGUGEVDFQEYVVLVAALTVACNNFFWENG
	1]	GCQL*VAYGTTENSPVTFAHPPEDTVEQKAESVGRIMPHTEARI
1	ł		PHINEAGILAXLNTPGELCIRGYCVMI.GVWGEDOKTEDA VDODVA
İ	1		IWIGDVATMNEQGFCKIVGRSKDMTTRGGFNTVDAFTEDFELLIM:
	í		PKVQEVQVVGVKDDRMGEEICACIRLKDGRETTVEEIKAFCKGK
1			ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ
6977	1298	588	ACTORIA
	1	300	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
1	1		ANKKSKHHVNGNRTVEPFPEGTOMAVFGMGCFWGAERKFWVLKG
1	1		VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
	1		ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
L	1		KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK
6978	3	242	SEDEDEDECOCKOCK
L	-		SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ
6979	3917	1146	FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
Į.	1		DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE AGPGSGATPGARAMDURDI KANDE
İ	1		AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE
1	1	J	RLOAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT
	}		AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
ļ		1	NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
ł	1	J	DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHEKVARDRSSCAND TITLE
]	į	DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
	ļ	i i	GEEPFSYGYGGTGKKETNER FENGGEGER TREE
} i	1		GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAPDIOWELL
]	}	DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
		ľ	GLPAAGKTTWAIKHAASNPSKKYNILGTVAIMDKMRVMGLRRQR
	1 }	ļ	NYAGRWDULLOOATOGI NEL TOTA A DISSONAL MORROR
		1	NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
		1	EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
ľ		1	PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG
}		i i	SIGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA
		1	POOOPPPOOPPPOOPPPOOPPPOOR
İ] -	POOOPPPOOPPPOOPPPOOPPPPSYSPARNPPGASTYNKNSNI
]	ļ	17	PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ
		1,	GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
6980	1.	420	NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ FTRGRKTGRVAAPSTRRRTGNMQKLQTRSPAMSLSDPGLGYHPT
			Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z

SEQ	Predicted	Predicted end	Amino acid compat
ID	beginning	nucleotide	
NO:	nucleotide	location	I IG-GAGNING, CECVSTOING DENGELLE 1.11
l	location		Caucamac Acid, Pephensilalanian a Al
i	corresponding	corresponding	**~***OLLUINE, IBISOIPNOIDD V.T!
		to first	L=Leucine, M=Methionine N=Aconscient
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Trantonher v m
- (amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	requence	COGOII, /=possible nucleotide del
	1 2 2		\=POSSIDIE nucleofide insertion\
)	1	1	CWTLRWPPLCSLHALHVFHCLESSPICTDVCDDI MMDDVCCCC
1	1	1	GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
		1	SEKCSCCA
6981	10	1054	
Í	ł	1	PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
1		ŀ	AFRICEPQGVESLEPPPPGPWPNMTI.TKAOVDDTAOOT TOTTO
1	1	ł	AVSURALA QREPSOSOATILISTESOEVORUT VDEUD VIIII TORES
l l		ĺ	1 2 1 1 VK 1 DNG V V KNGAAP VL L DLANE (MV V V V V V V V V V V V V V V V V V V
ì	İ		EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
1	}	ļ	VDCIKHAIGHEHBVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF
1	1		TLOUDING THE THE TRANSPORT OF THE TRANSP
L	1		ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
6982	153	1005	FGDVIIWIGFIUELDCNRERGII.I.KACEDTMITUTT CHOIS
1]	1285	FPQQUCSAPAAPGLAGSEPRRI.PAVPDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
	1		T T D D C C T C C C C C C C C C C C C C
1	j l		1 OD 1 VELDMARY INAPLICAS ISCTESTILEODY BY I WHEN ONE A
1	1		PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
1	1		VEGIL VELVOVEL BOUDDENT TO THE SELECTIVE WERE SELECTIVE TO THE SELECTIVE T
1			YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
1			AIRIESGRIGYESIYAALRSTYHGEGUDGT.EGGT mamt + nna
1)		1 SOLITIME INCLKNIVPHOOVDATILT DITTMECOCIED CT. 2 CT.
1	1 1		VEADVIKINGLYPLKFOWIGOAVTITERNYGI.PGEEGGGTERS
6983	<u> </u>		LRRTLMAAMAWTVYEEMMAKMGLKS
6983	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQK
1 1	[AALEVLEDIDI KITTERSATIGAGALGAAALALLLANTDVFLSKPQK
	i i		AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
1 :			CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
1 1	j		I PUDEKKE YGPORRKMMFMGFTRI.GIMIVNIPEDAWNICGEGGHT
1 1			GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNIJ.GVI.FARVAY
6984			RPUTLASERK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
1 1	1		KCSTPEETKKPKAUTEGICARRIAGGVQVADEVCRIFYDMKVR
1 1			KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
1 1	- 1		DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELA
1 1			FUNDAMI IASSKUALKKKFOGIKHECOANGDEDINDAGTARVIG
6985	1887		GSDIVAFEGCPV
1	1007	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
1	l l	•	"VALAGERESMPLIGARILFHGVFVAGGERATHVVT TOVERSON
]	ĺ		I I LAMY EQUOSITE EAGE AT GOOD INTHIVITY I TO DESCRIPTION OF THE PARTY
1	į		IPVSGSKSEGLLYVHSSPGGPEODER TO THE TOTAL TO
I			IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK LSGENGDEVKKE
6986	642	1350	DOGETIODEANY
	1	2000	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDPKMYIAF
1 1	Ī		VFACAAAASALFEVSEVIPVMTNNVFFNTIVCUDGGVGT 7007
	1		ELLERDY VOLHAPRYOSMRRDVTCCTORMDETT WDDAWD TOUTTON
	į		LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
1 1	1		VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
<u> </u>			AVGTIEDHLRPYMPE
6987	1623	341	TERRITORIES INFE
] [-		LEAAEKASRAFKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
1	ł		FLGELEVGLYTIOILOLTPFFHKENET CKKUMTORI COLUMN
	ſ	ľ	DERINECT LALISKETSHLKNLOSDI KRCEDPETDVMII I IZADAMO
	I	1	KEIABIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQBENC
	1	1	RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLQQNS
	Į.	!	KKPMTNEKONGTI ANTTI GOVERNOOMS
	ĺ	[KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
]	l		VGLIGHQI PGPY FLACLLEWPENORI, DODGKI, TEX VICE I ND COD
1	ļ	1	GQI KKMCKSKQASTLFYLGKRKGI,NSTVHKAKTEOVEDKA ONTOK
' 1	1		SUMMSGDVWKKNEVKDLLRRLTGOAEGKI.TQUEVCTEDVZVZDI.
			ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
6988	3	689	TOTA DEPAY PUCCES ACCURAGE STREET OF THE STR
	i		TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
1	1		DVKGLGAASTAAPODAOTGPOPMPRADCIMPHI DVBCBCOTTD-
J	ļ	1	FUNCTION OF THE PERSON OF THE
			KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL
			TOOLING VALUE I

SEQ	Predicted	1 Dun 21 - 1 - 3	
ID	beginning	Predicted end	
NO:	nucleotide	location	A=Alanine, C=Cvsteine
	location	corresponding	Grucamic Acid, F=Phenvlalanine G-Cl.
ļ	corresponding	to first	H=H1Stidine, I=Isoleucine K-lycine
į	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline. O=Glutamine D-Arginine
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide delotion
	1	ļ	\=possible nucleotide insertion)
1	1		RPEKNFDSLESLISAIQGDIEEAKKRLELPEHLKIKEDNFFQVS
6989	2	1118	KSKIMNGH
1	_	1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
İ			KDQLIYNLLKEEOTPONKITVVGVGAVGMACATCII MVDI ADDI
j	1		ALVOVIEDKLKGEMMDLOHGSI,FI,RTPKTVSGKDVMUTANGUTTI
i .			1 1 1 AGARQQEGESRLNLVORNVNTFKFTTDMM/VVCDMGVLT TIV
1			>NPVDIDTYVAWKISGFPKNRVIGSGCNI.DSADEDVI MCEDI GI
			TPUSCHGWVLGEHGDSSVPVWSGMMVAGVGI.PTT. HDD1 CTDVD1
1			PUNABURAQVVESAYEVIKLKGYTSWATCI,SVADI,ARCTMVNT D
	!		RVHPVSTM1KGLYG1KDDVFLSVPCT1.CONGTED1.VVVIDT DCDD
6990	719	258	EARLKKSADTLWGIQKELQF
1		230	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
1	}		ANLIGERSEGRROGIKKMEGHYVHAGNTIATOPHEDWHDGALTIGT
1	ļ .		GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
6991	169	451	KTFVHVVPAKPEGTFKLVAML
ĺ		427	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKTAYLL
1	1		SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF CGRHVH
6992	944	510	
1	1	010	RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY
1			RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPQGY
			PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLWDMLT
6993	1	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
[DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
			VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
}		•	RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
1 1			SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS
l 1			PGQVQTFLLWGAGALVVYWLLSLLGLVLALLGRILWGLKLVIF
	1		LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL
			EAKVRGLERQVEELRWRQRRAAKGARSVEEE
6995	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
			LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
			BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS
1	ĺ		EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG
i	į		GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL
1	į.		RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
			HIYGLPTGEYPGLMKVSYHHGNHADDEEDDCDTADTDTCDUCT
i	- 1		SSFVRDHLPDLKPEPAVIESCMYTNTPDEOPTI.DPHDEVDNITT
1	1	1	GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
6996	543		KAHL
0,00	543	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
ì	}		MULTIKY YSEWKGGRKNTNEFYKTI PPRVVPT. DARNEUT I OVI B
I		j	EESKAVFLOKKSRELLDNEELONI,WFI,I,DKHOTDDMTCEEAMTN
1	İ	l l	1ENFLKVGEKAGAKCKQFFTAKVFAKIJHTDSVGPTSTMOFENV
ŀ			VMRRVWLHQTRIGLSLYDVAGOGYLRESDI.ENVTI.ELTD71 DOZ
1		Į.	DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIODILACGELDD
	1	i	LLEURDEELSKESQETNWFSAPSALRVYGOYI.NI.DKDUNGMI.CV
i		4	EBUSKYGTATMINVFLDRVFOECLTYDGEMDVKTVI.DEVI.AT DAY
f	1	1.	KKEPAALQYIFKLLDIENKGYINVFSINVFFDATOFIMETIGOD
ļ	1	- 1	FAR ADDARDET LOWAK DESTRUCTION TO THE FOR THE TOTAL TO
6997	370		NGFWITENREALVANDSENSADLDDT
/	3/0	1104	AMELTIFILRLAIYILTPPLYLINFLGLWSWICKKWEDVELUDE
1			IVI INEQMASKKRELFSNLOEFAGPSGKT.SLI.EVGCGTG2NEVE
			YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH

SEQ	Predicted	Predicted end	Dining and an artist and a second
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glucamic Acid, Paphenvialanine Cacingina
ĺ	location	corresponding	H=H1Stidine, I=Isoleucine, K=Iveine
	corresponding	to first	L=LCucine, M=Methionine N-Asparagine
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-C+on
	sequence	sequence	Codon, /=possible nucleotide deletion
	1140000	 	\=possible nucleotide insertion)
1			QVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH
	1		VAAECSTWNYFWQQVLDPAWHLLFDGCNLTRESWKALERASFSK
6998	2	616	LKLQHIQAPLSWELVRPHIYGYAVK FVSRALLRVRSRRHPAEERAAPGRPEDAPIECPGATNCPEPLWC
[[1	SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK
i	i		APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
1	ļ	1	LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN
		1	FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRLIMQYLKENSLHRALATLQE
			ETTVSLNTVDSIESFVADINSGHWDTVLOATOSI.KI.DDVTT TOT
			YEQVVLELIELRELGAARSLLROTDPMIMLKOTOPEDVIULENT
			LARSYFDPREAYPDGSSKEKRRAAIAOALAGRUSUUDDGDIMAI
1	ļ	ĺ	LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTOLGDU
			LKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKTPKDI.
			KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAODGKTKWKTOSG
	1		QCLRRFERAHSKGVTCLSFSKDSSOILSASFDOTTRIHGLEGG
			TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS
1			NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
			GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
7000	2	827	TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
		V2 ,	GPGVVFLELMESEGPPESERSEFFSQREEENEEEEAQEPEETGP
}			KNPLLQPALTGDVEGLQKIFEDPENPHHEQAMOLLLEEDIVGRN LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL
			ETLKALVELDVDIEALNFREERARDVAARYSQTECVEFLDWADA
1 1			RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
, [ETHTEASINELFEQROQLEDIVTPIFTKMTTPCQVKSAKSVTSH
7001			DQKRSQDDTSN
/001	2056	844	RRCLIIAFLKGCFIFIYPIFIFETEFLSCCPGWSAVAQSRLIAN
	İ		FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGD
1 1			TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPTT
1 [VSPAIVSPTQDSRPNMSRPLITRSPASPLNNOGTPTPAOLTKON
1 1	ĺ		APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ
			HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL
1			QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK
1 1			SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLMSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI
	•	•	RIKQEPLD
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRFTTGTCT*TAAPGPTVRWWP
1]		TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS
} [SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV
[]	•	ļ	PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA
7003	- 016		RGAEVC
7003	818	61	QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP
	ļ	1	GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA
]		i	GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIDSEND
		į	LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRTIDKDE
	İ	ľ	FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLOFFUMFAM
7004	121	2205	GIKETR\NTRRSIGIEPGAEOLLPNFCPSLEG
1		2285	FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK
	İ		G\PKRTLKTQLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE
1	1	1	GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH
ŀ	1	İ	GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF
ļ			QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ
	İ	ŀ	VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL
			EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL
			TANA TIMA KOSA SASA FAT KUVQAPUDADGDNVL

SEQ	Predicted	Predicted end	I amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
- [location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion}
ı			QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINGSI.MT
J			LRTCMDVLRENQMYGTNKMVPYRDSKLTHLFKNYFDGEGKVPMT
- [VCVNPKAEDYEENLOVMRFAEVTOEVEVARPUDKATCGT.TDGPP
			YRNQPRGP\IGNEPLVTDVVLOSFPPLPSCEILDINDEOTIDEI.
ł			IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQ
	1		GKLNEKEKMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEED
1	-		KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
			ERRVAAKQLEMQNKLWVKDEKLKQLKAIVTEPKTEKPERPSRER DREKVTQRSVSPSPVPVSYL
7005	63	876	PNMAT.VODWDCt DLOOLOXCDXVIII
ļ		-,-	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
1			ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
1			FWHSSTHVLGAAABQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
ļ	1		GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
			IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
7006			LWRSSG
/006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
	}		VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
1	1		LNITWYLKSADCYNEIYNFKAEEVELYLEKIKEKRGI.SGKYOTS
i	1	•	SKLFQNCSELFKTQTFSGDFMHRLPLLGEKOEAKENGTNTTFTG
1			DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
1	1		VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
7007	2	1001	DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
1]	2002	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
	ſ		DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
			LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
1		ļ	QNLVVLAREDAGAEKIFRSNGVQLLQRLLDMGETDLMLAALRTL
			VGICSEHQSRTVATLSILGTRRVVSILGVESOAVSLAACHLLOV
1 1		j	MFDALKEGVKKGFRGKEGAIIVGEWKOVWGLLDVTVMEGMGLSO
7008	70		PGQFFGDQTCSCRLFGIRFGDIILL
7000	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
1			SPPPLAGPGQKMVQKKPAELQGFHRSFKGONPFELAFSLDOPDH
1 1	1	ì	GDSDFGLQCSARPDMPASOPIDIPDAKKRGKKKRGRATDSFSC
1 [1	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
1 1			IRSRVFREVEMLYQCQGHRNVLELIEFFREEDRFYLVFEKMRGG
1 (1		SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
1 1	Į.		NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
l i	[RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA
i l	1		KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
			WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
7009	1	626	ARQLENSWVDDFVAAPLIPLSOOIPTGNSLYESYVKOVDPAYTG
		- 1	RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKOGFYVA
		į	LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAFAH
		i i	WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKT.DI.DUT.
7010	79		GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
, 510	19	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
		1,	GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEOSSEDIWAACC
1	İ		VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKOFHPLPVNOEGDS
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DEMTSGRAACFDIISGOQTOKOVI EIRBRITJOHNONPKIOL TFEATLQQLEAPYNSDTVLJHRVHSYLERHGLINEGIYKRIKDI PYKKTGKYI IIGGGVGALAARQLQSFLERHRTJOHLONPKIOL TFEATLQQLEAPYNSDTVLJHRVHSYLERHGLINEGIYKRIKDI PYKKTGKYI IIGGGVGALAARQLQSFUSUVTLLEARDRVGOV ATFRKGRYVADLGAMVVTGLGGNPMAVVSKOVMMELAKIKQKCP LYPANGQAVFKKDEWWEDEFRRILENSVLSHQLDFNVLNNKY VSLOQALEVVIQLGKHVKDGGIEHWKKIVKTQELKELINGVV NLKEKIKHBHQOYKEASEVKPPRDITAEFIVKSKHRDLTALCKE YDELAFTQGKLEKLGELEANPESDVISGRPQILDWHFANLE FANATPLSTILSHMDQDDDPFTGSHLTVRNGYSCVPVALAEG LDIKLMTAVRQVEYTASGGEVIAVNTSGTPFIVKCDAVLGTL PLGVIKQDPAVOFVPPLEHKTSAVQRMSGGNINKVALGFDRV FWDPSVNIFGGVGSTTARGGEVIAVNTSGTPFIVKCDAVLGTL PLGVIKQDPAVOFVPPLEHKTSAVQRMSGGNINKVALGFDRV FWDPSVNIFGGVGSTTARGGEVIAVNTSGTPFIVKCDAVLGTL PLGVIKQDPAVOFVPPLEHKTSAVQRMSGGNINKVALGFDRV FWDPSVNIFGGVGSTTARGGEVIAVNTSGTPFIVKCDAVLGTL PLGVIKQDPAVAGVSPDALAGEL HTTRNYPATVVGGLASGEVIAVPTGAPOPTPELFFAGE HTTRNYPATVVGGALLAGGIFGGSAVPOPKSTTVSBWRADPHA RGSYSVAAGSGRNDVDHAQPITGFBAPOPTPELFFAGE HTTRNYPATVVGGALLAGGFGAGPTVVVGGATTME TGLAETPGOVRRTSRRKRAKVEVTRMDESLANLSEDEYTSEERE NAKASKEKLPPPRASPFGGLAEPPGSAGFGAGPTVVVGGATTME TGLAETPGOVRRTSRRKRAKVEVTRMDESLANLSEDEYTSEERE NAKASKEKLPPPRASPFGGLAEPPGSAGFGAGPTVVVGGATTME TGLAETPGOVRRTSRRKRAKVEVTRMDESLANLSEDEYTSEERE NAKASKEKLPPPRASPFGGLAEPPGSAGFGAGPTVVVGGATTME TGLAETPGOVRRTSRRKRAKVEVTRMDESLANLSEDEYTSEERE NAKASKEKLPPPRASPFGGLAEPPGSAGFGAGPTVVVGGARTME TGLAETPGOVRRTSRRKRAKVEVTRMDESLANLSEGFARVGGRV AFFKRGRVIJLGRAFTGVTHRYBGGTALLNTGTJVKTKPL PTKKTGKVIIIGSGVGLAAARGLGSFGMUTLLEARDRVGGRV AFFKRGRVVADLGAMVTGGGMPAAVTLSRGRVGRV AFFKRGRVVADLGAMVTGGGMPAAVTLSRGRVGRV NIKKRIKELHQQYKRAGEVVPPRDITAEFTLYKSKHRLINGIV NIKKRIKELHQQYKRAGEVVPPRDITAEFTLYKSKHRLINGIV NIKKRIKELHQQYKRAGEVVPPRDITAEFTLYKSKHRLINGIV PEADGAQUFGKEKLQGLEARPPSIDVISGRRGRGTLKVVLCTGBL PANATPLSTISLKHRDQDDDFFTGSHLTVKNGMPCTLLKVCDL PEDDFSVNLFGHTGSTTASKGELFLEWNIYAGDILLALVGGAAG JMENISDVIVGCLALLKGIFGSSAUTVGGREFTNAKVRDPAV RGSTSVVANGSSGRATHAGGGRGTATHVANTLSTGOTFITKCOAVTLCTDAV PETDPSVNLFGHTGSTTASKGELFLEWNIYAGDILLALVGGHP PANGGIVMEAATTSGCDGSTDLDSKLTQCPKTVVSRRADDPA PANGGIVMEAATTSGCDGSTDLDSKLTQCPKTVVSRRADDPA PCTPWSTSPHLLVDQNLKRAPP		ľ	į.		(*OZAGI FEG \KKISKKKRAKVEYREMDESI.AMI CEDEVVODEN
TPEATLQQLEAP YNSDTYLJHEWHSYLERRGLINEGYYKRIKDL TPEATLQQLEAP YNSDTYLJHEWHSYLERRGLINEGYYKRIKDL PPKKTGKYI I IGSGYSGLARARQLGSFGMDVTLLEARDRYGGRY ATFRKGRYYADLGAMVYTGLGGNPMACKGYMMELAKI KICKCY LYEANGQAYPKEKDEWWEGEFRRILEATSYLSHQLDPNYLNNKP VSLOQALEWYTQLGEKRYKOEGIEHWKKIVKTGELKELLINKGY NLKEKIKBLHQQYKEASEVKPPROITAFFLVKSKIRDLTALCKE YDELAETOGKLEKKLGELEANPPSDVYLSSRRQILDWHFANLE PANATELSTLSLKHWODDDDFFFTGSHLTWRGYSCYVYALAGG LDI KLWTAWRQVKTASGGEVIAVATESTGGTYTKCDAVLCTL PLOVIKQGPAVOVENPJDEWKTSAVGFRINKGVALGFDRY FWDPSVNLFGIVGSTTARGGELFJFWNLYKAFILLALVAGEAAG IMENIEDDYIVGRCLALKGIFGSSAVGFRINKGVALGFDRY FWDPSVNLFGIVGSTTARGGELFJFWNLYKAFILLALVAGEAAG IMENIEDDYIVGRCLALKGIFGSSAVGPAGLAGFARPVAR RGSYSVAAGSSGNDYDLMAQPITPGFSIFGAPQFTFRLFFAGE HTIRNYPATVWGALLSGIFGSAVGFAGNAYTHVGRATFOV AQOSPSM 7013 1 2661 RRAGSVKRGEARLFGFTERQSERPLRPSARRFPMLSGKKAAAA AARAAAATATTVAGALLSGLEGGAGGAGGAGAGFAGAFGAV VGERTFRKKIPPRASPFGGLAEPPGSARGFAGAGGAGAGAFGAA AARAAAAATTCAGGVKRGEGARGAGGAGAGAGAGAGAGAGAAA AARAAAAAAATTCAGGVATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		J		1	MAKAGARALPPPPPQAPPEEENESEPEEDSCUPCA A FOCAL DIE
PIKATGKVI I TOSGOVSGLAAARQLOS TOLDRYLLEARDRYGEV ATFRKGNYJALGANVTOLGGNPMAVVSKOVMBLAKIKOKCP LYEANGGAVPKEKDEWUGDENRILEAVISHOLDPNYLJNNRY VSLGQALGVVIQLGEKHVIDEGJERMEKTVKTOGELKELLINGV NLKEKIKEHQOYKERSEWKOPROITASUKHKUKTOGELKELLINGV NLKEKIKEHQOYKERSEKVEPROITASUKSHRIDLTALCKE YDELAETGGKLEEKLOBLEANPPSDVYLSRORGILDWHFANLE FANATELSILSKIHUDDDDEF FOSHLIVRGWSCVPVALAEG LDIKLWTAVRQVRYTASGCEVIAVNTSTGGFTYKCDAVLCTL PLGYLKQOPPAVLGTE HTTRYPATVGGALLEGIFGSGRAPOPETYVSERARDPMA RGSYSVLAGASSONDYLDAGPITGPGAPOPTEPLFAGE HTTRYPATVGGALLEGIFGSGRAPOPETTAGATTORGAPOPTAGE HTTRYPATVGGALLGGAPAVLTURANGSEVALAFEDALGGKKAAAA AAAAAAATATCEAGOPTAAGGENDS EVAAPGALGGAPEVVVGGAPTME TGLATPEGA RETGREKRAKUPLREDGELANISEDEYYSEERE NARAKKEKLPPPPQAP PEERESSPEGGAFGAPOPTVVGGAPTME TGLATPEGA RETGREKRAKUPLREDGELANISEDEYYSEERE NARAKKEKLPPPPQAP PEERESSPEGGAFGAPOPTVVGGAPTME TGLATPEGA RETGREKRAKUPLREDGELANISEDEYYSEERE NARAKKEKLPPPPQAP PEERESSPEGGAFGAPOPTVVGGAPAV AGARAGE VILLEARDRYSOVLYRONGELAKIKOKCP PTRKTGKVII IGSGVGLAAARGLOSFGMUTLLEARDRVGGRV AFFKGGAVVALLGAGNITURHVGGAPATVKGAPALACK VELGALLEVVILOLGSKHVKDEOLGEINKTVCGBELKELLAKOM NLKEKIKELHQOYKBASCVLPRGTTAGHTTAGTIVKSKHRDLTALCKE VELLAETGGCGCGEVLAVATGGGAPATVLGECHLANDEN VELGALLEVVILOLGSKHVKDEOLGEINKTVCGBELKELLAKOM NLKEKIKELHQOYKBASCVLPRGTTAGHTTAGTIVKSKHRDLTALCKE PANATPLSTISLKHDODDDFFTTGSHITORGCVTVARRADDPA RGSYSVAAGSSGROTLLANGPTTTGPSIGGAPOPTRVE FANATPLSTISLKHVDODDFFTTGSHITORGCPTRVVGRARADDPA RGSYSVAAGSSGROTLANGPTTTGPSIGGAPOPTRVF PLGYLKGOPPAVGTTTGSSLITEGAPATLAGATGSHP PLGYDESVALFERGESLARITEGAPATLAGYCGSHP PLGYDESVALFERGESLARITEGARATAGOTTAGAPPATVLPRGATGSHP PCTPVSTSPHLLUDONLKRAPPLUVRPSSLATTLAGAPTLAVAGSHP PCTPVSTS		i		}	DIGITS VERACE PULLS GPOOTOKVFI, FIRND TI.OT MIT DADKETON
ATPERKGNYVADLGAMVVTGLGGFMAVLKENGKCP LYPANGGAVYEKDEMVEGGFNELLERTSYLSHOLDENVLINKEV VSLOQALEVVIQLGEKHVKDGOLTEKKIVKTOTEDELKELLINKEV VSLOQALEVVIQLGEKHVKDGOLTEKKIVKTOTEDELKELLINKEV NILKEKIKBLHQOYKBABEVKPPRDITAEFLVKSKHRDLTALCKE YDELAFTOCKLEEKLOELEANPPSDVIJSBRORILDMHFANLE PANATPLSTLSLKHWDQDDFPFTYGHSTRORILDMHFANLE PANATPLSTLSLKHWDQDDFPFTYGHSTRORILDMHFANLE PANATPLSTLSLKHWDQDDFPTYGHSTRORICHVKVLCFDRV FWDPSVNLFGFWGSTTASRGEFJEWNIJKAPILLALVAGEBAG IMENISDDVIVGGCLALIKGIFGSAVOPMCFGWINKVLCFDRV FWDPSVNLFGFWGSTTASRGEFJEWNIJKAPILLALVAGEBAG IMENISDDVIVGGCLALIKGIFGSAVOPMCFGWINKVLCFDRV FWDPSVNLFGFWGSTTASRGEFJEWPSAVOPMCFGWINKVLCFDRV FWDSVNLFGFWGSTTASRGEFJEWPSAVOPMCFGWINKVLCFDRV FWDSVNLFGFWGSTTASRGEFJEWPSAVOPMCFGWINKAPILLALVAGEBAG IMENISDDVIVGGCLALIKGIFGSIPOLTOPMTHERAGE FATTRYPATVKGALLSGLREAGRIADOPLIGMYTTPRCATFGVV ACGSPSM RGSSYSVAAGSSGNDYLMAQPITGPSIPOLAOPPTPLFFAGE HTTRNYPATVKGALLSGLREAGRIADOPLIGMYTTPRCATFGVV AAAAAAAAATCTEAGPTTAGSSENGSEVAAQPAGLSGPAEVGFGA VGERTPRKKEPPRASPPGGLABFPGSAGFQAGSTVAFGBAFFME TGIASTPGGLAAFFDISGSENGSEVAAQPAGLSGPAEVGFGA VGERTPRKKEPPRASPPGGLABFPGSAGFQAGSTVAFFME TGIASTPGGLAAFFDISGSCAMAFACOGENVALLEARDRVGGRV AAFRKGNVADLGAMVUTGLGGNPAVVSKQVMMSLAKIKKLE PRIKTGKVI IIGGSVAGAAGROGGENDALLEARDRVGGRV AAFRKGNVADLGAMVUTGLGGNPAVVSKQVMMSLAKIKKCCP VSLGQALEVVI QLQEKHVKDDCIEHMKKIVKTOGELKELINKMV NLKEKIKELHQQYKEASSVKPRDITAEFLVKSHRDLTALCKE TOELABFTQGKLEKLQQYKEASSVKPRDITAEFLVKSHRDLTALCKE TOELABFTQGKLEKLQQYKEASSVKPRDITAEFLVKSHRDLTALCKE TOELABFTQGKLEKLQQYKEAUSPTVSKRRADHVAN RGSYSYVAAGSSGNYTUMAQGCVIATKAPILLALAGGAAG MMENISDDVIVGRCLALLKGIFGSSAVPQPKETVVSKRRADHVA RGSYSYVAAGSSGNYTUMAQGCVIATKAPILLALAGGAAG MMENISDDVIVGRCLALLKGIFGSSAVPQPKETVVSKRRADHVA RGSYSYVAAGSSGNYTUMAQGSKITGGMYTLPRAGATEGD PLATAPVORVTTABGCEVIATKAPTLKAPILLALAGEAAG MMENISDDVIVGRCLALLKGIFTGSSAVPQPKETVVSKRRADHVA RGSYSYVAAGSSGNYTUMAGCSVLATKAPILLALAGVARGPARTEGD DFEVGDRYKHLATLEDGMLEGSIKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARTPETSLDCLENTTGAUTGSVYSIEBERLEBEPD CTIMPATOPHLANASYTKIKHTSVVSISERLEBERLEMPG PLATARPHOLASSTRADHASSYTKHTSVVSISERLEBERLEMPG PLATARPTOMBLEBERLEBERGDHMENSVVSISERLEMPG PLATARPTOMBLEBE					1 PART DOUBLE INSUTVIVIENT TO THE TWO TWO
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VGERTPRKKEPPRASPPGGLAEP PGSAGPQAGPTVVPGSATFME TGIAETPEG\RTSRKRAKVEYREMDESLANLSEDETYSEERR NAKAEKEKKLPPPPPQAPPEERNSEPEEPSGVEGAAFQSRLPH DRMTSGEAACPPDIISGPQQTQKVFLFIRNRTLQIMLDNPKIQL TFEATLQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEAMQQAVDKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLINKMV NLKEKIKELHQQYKEASSVKPPRDITAEFLVKSKHRDLTALCKE YDELABTQCKLEEKLQELEANPPSDVYLSSRDRQILDMHFANLE FANATPLSTLSLKHWDQDDDFFTGSHLTVENGYSCVPVALAEG LDIKLNTAVRQVKYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLIGVLKQOPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKRPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDVDLMAQPITTGPSIFGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGMYTLPRQATFGVP AQQSPSM 7014 3 3950 DFFVGDKKRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLIGVEEQRIETSDHEAEREPD CIISEAPTSPLGHLTSEYDTDRNSVQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVLNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLETLAGKSCHAPPPRR HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHTTSSVYSISBRLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRDSRPAPLIPPSAQQRTNNAV SPKLLSRHRPTCETLEKEGPGHMRPSLDOTSBOPLUV BU LEMM	۱	7013	1	2661	
TGIAETTEG\RTSERKRAKUEYREMDESLANLSEDETYSEEER NAKAEKKKLPPPPPQAPPEEENESEPEBSGVEGAAFQSRIPH DRMTSGEAACPPDIISGPQOTQKVFLFIRNTIQLWIDNPKIQL TFEATLQCLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL PTKKTGKVIIIGSGVSGLAAARGLQSFGMDVTLLEARDRVGGRV ATFRKGNYVADLGAMVVTLGGNPMAVVSKQVMMELAKIKQKCP LYFANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLMNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTYGELKELINKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQUELEANPPSDVYLISRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFFFTGSHLTVKNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEMKTSAVQRMGFGNLMKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQFKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITFGPSIFGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATFGVP AQQSPSM 7014 3 3950 DFFVGDKTRILATLEDGWLEGSLKGRTGIFFYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEBPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVFFHNLQKSQYYSTVGGSHP HEBQYPDLLPLEARTRDVASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRXVKPRQSSPQLHNLASYTKKHTTSSVYSISBRLEMKPG PQAQGLVMEAATHSQGDSTDLDSKLTQQLIFFKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERKALRPPPPR PCTPVSTSPHLLVDQNLKPBPPLVVNRSRPAPLIPPSAQGRTNAV SPKLLSRHRPTCETLEKEGPGHMGSLDOTSBOPLLVI MILBEMY	ł				HAMAMAAATGTEAGPGTAGGSENGSEVAAODAGI CODABUGAGA
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DRMISCBACEPDI ISGPOQTOKVFLFIRMTLOLMIDMPKIQL TPEATLQQLEAPYMSDTVLVHRVHSYLERHGLINFGIYKRIKPL PTKKTCKVII IGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV ATFRKGMYVADLGAMVVTGLGGMPMAVVSKQVMMELAKIKQKCP LYEAMCQAVPKEKDEMVEQEFMRLLEATSYLSHQLDFMYLIMKPV VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLIMKMV MLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQPKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQPEAMPPSDVYLSSRDRQILDMHFAMLE FANATPLSTISJKHMDQDDDFEFTGSHLTVRMGYSCVEVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVIKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITFGPSIFGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATFGVP AQQSPSM AQQSPSM DFEVGDKTRILATLEDGWLEGSLKGRTGIFFYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAREPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSTSDFTEVVNGISSQPQVFFHPNLQKSQYYSTVGGSHP HSGQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVNPSRPAPLPPSAQQRTNAV SPKLLSRHRFTCETLEKEGDGHMGBSLDOTEGDI WINDENDAN	l	j	j		I IGIAETPEG\RRTSRRKRAKVEVPEMDEGLANT GERENNERS
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PLATISPTEDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV SPKLLSRHRPTCETLEKEGPGHMGPSIDOTSPCDLYMDLERMY		- 1		1	CITSEAPTSPLGHLTSEYDTDRNSVODEDTAGGDDDGDGTGTGT
SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV SPKLLSRHRPTCETLEKEGPGHMGPSIDOTSPQDIVLYDIEFEND				f .	PLATUSPISDPIEVVNGISSOPOVPFHPNIOKSOVVETUCCOUR
PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTMAV SPKLLSRHRPTCETLEKEGPGHMGPSLDOTSPCDLVLVBLERM				1 :	ASEQ1PULLPLEARTRDYASLPPKRMYSOLKTLOKPUT DI VDGG
POAGEVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRIMAV SPKLLSRHRPTCETLEKEGPGHMGPSIDOTSPCDLVLVDLEDAV		1	1	1.	SVSASKVVKPRQSSPQLHNLASYTKKHHTSSVVSTCERLEMVRC
PCTPVSTSPHILVDQNLKPAPPLVVRPSRPAPLPPSAQQRTMAV SPKLLSRHRPTCETLEKEGPGHMGPSLDOTSPCDLVLWDIEPHY		1	İ	1 -	*VAVGDVMEAATHSQGDGSTDLDSKT.TOOLTEERKSLAGBCTER
SPKLLSRHRPTCETLEKEGPGHMGRSJDOTSDCDLYLYDDDWG SPKLLSRHRPTCETLEKEGPGHMGRSJDOTSDCDLYLYDDDWG		Ì	ļ	1.	DAILKHFSIMDFNSEKDIVRGSSKLITEOELDERDENALDBRODD
RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN		- 1		1.	PCTPVSTSPHLLVDONLKPAPPLVVRPSPDADI.DDSAGODUMATE
A STANCE ELIN MILEEKODES SRAETLEDLK FCESNIES LN	_			1 2	PALLSRHRPTCETLEKEGPGHMGRSI, DOTSDCDI, VI VD TEDWO
					THE TANKE BUNDMILE EKODES SRAET LEDLKFCE SNIESLN

SEQ	Predicted	Predicted end	Drive said second
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
-	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	• • • • • • • • • • • • • • • • • • • •	\=possible nucleotide insertion)
			MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
	1	ĺ	ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
İ			IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
			LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
1	1		VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
1			YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
1			LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES
i			ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
}) i		TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
į	[DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCVHGY
İ			AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVIO
1]		QLQVFTFFPESLPATKKPFERKTIDROSARKPLLGLPSYMLOSR
			ELRASLLARYPPEKLFQAERNFNAAODLDVSLLEGDLVGVIKKK
1			DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
]		TESENGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCOKOPO
1	1	1	DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSOPRSGD
1]		SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
1]		CARTAQAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
7015	1842	513	NQKLKILEFKOVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
1		213	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL
}			GFORRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS
	}		SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
			KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN
	1	ļ	QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG
			VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
	İ		FKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
1	}		EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL
j j			LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV
			KLLK
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST
]			AFROKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEVLS
	1	i	LVARLIIHFRDIHNKKSQASVSDPMNALOSLTGGPAAGAAGTGM
1 1	İ		PPRGPGQSLGGMGSLGAMGQPMSLSGOPPPGTSGMAPHSMAVVS
1	1	1	TATPOTOLOLOGVAAAAAATARSSSSSSRRRYSSSSSSSSSSS
1	1	1	FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQQQQQHLIKLHHQNQQ
i i			QIQQQQQLQRIAQLQLQQQQQQQQQQQQQQQQALQAQPPIQQP
1)	j		PMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQ
1			LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP
	i		QVQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
]		1	QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPF \QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY
		1	LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
! [SKRCPLKTLQKCBIALEKLKNDMAVPTPPPPPVPPTKQQYLCQP
		1	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
			RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC
		į	KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV
			HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
7017	1	1785	INLGNTCYMNSVI*ALFMATDFRROVLSINLNGCNSLMKKTOHI.
1		1:	FAFLAHTQREAYAPRIFFEASRPPWFTPRSOODCSEYLRFLLDR
- 1	ļ	1:	LHEEEKILKVQASHKPSEILECSETSLOEVASKAAVLTETPRTS
1	1	[]	DGEKTLIEKMFGGKLRTHIRCLNCRSTSOKAEAFTDLSLAFWPS
		[]	YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF
ł	ļ) :	ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPOKPG
		(GETTPSVTDLLNYFLAPEILTGDNQYYCENCASLONAEKTMOIT
		E	SEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS

SEO	1 8		
. ~	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Truntonham V Devaline,
ı	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	1 1 1	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
ı	1		FSSLSESWSVDVDFTDLSENLAKKLKPSGTDBASCTKLVPYLLS
- [1		TO A AUGUST SOURCE IN A SAN LACALLICATION OF THE SAN LACALLICATION OF T
			SHELLGRUSPSAVFEODLENKEMSKEWFLFNDSDVÆREMORAGIVAL
Ì	1		I I SKEPKUTAYVLLYKKOHSTNGI SCHNOTEGI WINGBODT OVE
i	i	1	DIDALIKONKLYLQEOELNARARALOAASASCSERRNGERRNING
7018	484	1000	FOSCGPTGGGGGGFNTVGRI,VF
	101	1066	SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGTERIRAPEIIFQ
ļ	1		PSDIGECAGIAETLOYILDRYPKDVOEMIJONTIET TOCOMMUNICA
1	1	1	GARAGUERE PRESERVOLAS NOVI. DALIVOR DELLA TARIA
- [i		DDNEAMITEKETEEKGGEYLKEHCASNIVVDIDI DVOX CDCCD
7019			QASSAGGAGGGAGEOA
/019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTT GVDWGTTT
j	•	l	RMRHIPLAFGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
i			SSGALRGVCSCVEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA
1	1	l	GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR
ĺ	1		SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK
			ARESASAKIKEERAAKD
7020	1	2154	FADSKRKGVI I DVI VOVI OVIDA
1			FADSKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR
			NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE
1	ł		DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC
ſ			NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF
Ì]		MANALLALLYRQLDMSPDPKASOHFARVAVVOUADERCUDATA
			I MER VAVERSLIDIGSKEKLVDET, SPCMTOT, OCTOBAT COR TITUE
1	1		ENVERSAPHERDLKIVVLMLTGEVPEOOLEEDORVILORVOVOL
1	! !		Production of the production
1]		FGRDDPSFVSSENAFYLSPDIRKOCDWFOGDODWDHI INCOUNTED
1	1 1		ANALIMATOOLIZULALIKEAAAAAKDIAAAAAAAAAAAAAA
1	1		I THOUSANDARAKPASAKSAAKSAAKAATATATATATATATATATATATATATA
i	1 1		FVAARPAAVRIPAAAAAKPVATKPEVDDDOAAFDAATIDAATIVAA
1	f i		MANUSKEVQVFEITENSAKLHWERPEDDGDVBVDI WWWGAIDOG
[i	l l	í	TATE OF THE PARTY OF THE PART
1 3	! !	}	TAKSQUEEFQEAKSASSSTINTMVQTEDIALTERATOR TAKE
1 .	i l		1 CRDF 1 LAWYIDPNIKS CARFWYGGCGGNENKFGSOKECEKUON
7021	2		EATHER PORT SAMO.I.
	- 1	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG
1	1	Ì	115 VAF SASGRULLAGYDDFNCNVWDTLKGDRAGVLAGUDNDVG
7022			CLGVIDLGMAVAIGSWDSFLRIWN
	2	856	VYIGSFWSHPLLIPDNRKLFEAFEODLEDDYOGLDDWAATOWY
1 !	. [Í	DLIARAKLAKVHAYIISSLKKEMPSVFGKTNKKVELIADNI A TITIL
			GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD
!!	1	1	DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG
i i	ł		EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM
1	i	1	VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH
			ELPNELPAHLLPPSKRKVAE
7023	2	748	AMURCCUUDUUDOVODIDIDIO
i i	i i	i '	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
	1		WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
- 1	1	1	TAADS KDEEVKVAPRRSFLDFDPHHFWOWSSFSDVXOOGG A DOG
i	1	1	VAGIITILSIDSALFVETLGFLAVI.TEAMI.GVDOT.VDMUDUOOM
1		1.	EGISTAMVLMWTSGDAFKTAYFLLKGAPLOFSVCGLLOVIT VDI A
7024	1207		LLGUATAFARHPUKPAPHAVHPTGTKAI,
	1201	190	RTGVTGVVAQVWMFGGGGVLSSGROLOMPVKPFPGLCDCDCWLV
- 1	j	1 2	SSKKGSPGTVLGLPFWLLTPVLVSRSTPSMIJI TPCDTPMUIDIG
i		, ,	2LKPPVLPGTLGGQALHLRSWLLSROGPAFTGGOGOPOGPGT Pm
- 1		1 1	CLLITGUEGAGLGGAWLALRAEKERI.OOOKPTEAT.DOAAKOOOD
- 1		1 E	FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV
		l v	RQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL

SEQ	Predicted	Predicted end	l Draine and
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Water tanks and the same of th
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence		Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
1			TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
7025	232	832	LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
1			ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF
1	1		KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG
j	Į.		SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
1			ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS
7026	328	1146	VHKRIHTGEKSYECKECGKAFSCG
		1140	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
(1		LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
1			SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
1	ł		HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
1	!		LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
			EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
7027	43	954	QDEQPHIFG
	1	234	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
Į,			YYQELKIYPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
			KNKYFKELEDLEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK
1			SPHLEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
1 .			MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
L			QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
7028	189	608	CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
1 1			SRPPPEPERTMVEKGSDSSSEKGGVPGTPSTQSLGSKNFIRNS
1	l		KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR
			EILLOGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA KLIPNAIO
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
1 1	j		PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
1	1		SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
1			RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
! !	1		TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG
j .			R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGFGTDNS\
1 1	1		AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
	ŀ		VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
	1		PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPLPL
!			PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG
7030			T I
/030	2	521	FVCFSAPGSGQGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
			EYLVKWKGWSQKYSTWEPEENILDARIJAAFERDEDEMEI VODY
i i	1	J	KKGPKPKTFLLKAOAKAKAKTYEFRSDSAPGIPIPVPCPCPCPC
l l	<u>. </u>		ASTSRAREGIEN \RVCPRORAAPAPAAD\ DDDCDCCDCDDDC+C
7031	000		PGLHF PGPGGPSKHGFVPASEOHOHOOHI, PRRCDSCDGDDDC
,031	960	39	HCSVPGAEWPRKPPAOICPOLTSRPHI.SSPPSI.SPCCCHSPGDG
į	j	į.	/CKPS/RHCDELHEGPSRTAALPCGKPOPKHGVRECG/BCDC/A
İ			PRRUIE PPAUTVSPVGRAAPSGAL*PSGRACSACSHDIADDAAT
1			SAAAPRPSLGSGONASGLPAASLPPODSSOPHKTUDGDADGUDD
		f .	LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGDDVDCDTDcm
1	J	1	SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFFVT.TAAAGAAA
7032	1302		ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHDet.
7552	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNI.HI.API.*OGDI DV
- !	1	1 3	SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFI.*DCCct
1	1	1 2	EPWMKRQFGRLHSLFWKSWOKMNSFLLTPKLDTSIMSGUPVDOB
1		1.	bPKLHTFLKKSLQMASELAPPLPTPAPLAGGLDDDDCDDDT r Dy
i	i	1,2	PLA*LSRSGILVPPNSGFSLSC\PLGDH+GSSGEVRGSCGSPPP
7033	600		HCMATAAAA.TTTAAK
,,,,,	689	815 J	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA
	-		THE POPOSA

SEO	Predicted	Dyodiata	
ID	beginning	Predicted end	
NO:	nucleotide		A=ALanine, C=Cvsteine, D=Aspartic Acid P
1	location	location	Glutamic Acid, F=Phenylalanine, G-Glucine
	corresponding	corresponding	H=H1St1dine, I=Isoleucine, K=T,veine
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of	S=Serine, T=Threonine, V=Valine
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-c+
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\~possible nucleotide insertion)
ł			LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
1		į	GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
1	ł	1	AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
i	1	İ	WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
!	1		SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREBALQDPR
			NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
	1		KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
	1	İ	TLL TLEVEOU CANCERDATED CONTROL OF CONTROL O
	I		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
1	ł	Ì	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1			FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1	j		TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
			IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
			YLWVQMYKGTVSMPVFQSLEAYWPGLOSLIGDIDNAMPTFLNVV
1	1.		TVWKQFGGLPEFYNIFQGYTVEKREGYPLRPELIESAMVI.VDA#
1	1		GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKIDNDMFOR
į.			FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECIIGAGGYI
į			FNTEAHPIDPAALHCCORLKEEOWEVEDI.MREEVSI.KDSDSVEO
1			KNTVSSGPWEPPARPGTLFSPENHDOARERKPAKOKUPLLSCRE
1]		QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
2032			K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
1			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
1) ·		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
	1		RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1			FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1 1	!		TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
1	1		IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW.
1 1		,	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1 1	ŀ		TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
i :	ĺ		GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
i l	ļ		FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1 1			FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREPYSLKRSRSKFQ
l l	1		KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
1 1			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
	1		K K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
	[RNW*ERKAGGGORG (PAGGYUGE DEGYGE)
			RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRRPPRNRRPG
7037	442	761	CLADI BOCKOTTI
			CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	Į	i	RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
7038	155	891	PPPPPPPPPRRPPRNRRPG
		031	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
	1		QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
		į	LQEMAQLKIKHQEELTELHKKRGELAO\RVIDINNOMOPKDPPM (
	j	I	QMMEAKIAECLQTISDLETECLDLRTKLCDLERANOTIKDEVDA
ŀ	1	!	LQITFTALEGKLRKTTEENOELVTRWMAEKAOFANRINADE**VP
7030			LUEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEOLBERDRIOROAFFFTTT
l l	ŀ		QYNKLLEXSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
1	1	İ	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
į.		1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1	ļ	l	LOITFTALEGKI, RKTTEENOET INDENARY OF THE TOTAL BY
			LQITFTALEGKLRKTTEENQELVTRWMABKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KTTDDDD DUOCS COUCAD DOSSAGE
1			KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS
···		 L	GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN

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ID		Predicted end	
NO:	nucleotide	nucleotide location	
ļ	location	location	I Charle Mild. Papapanulalanian o ol
1	corresponding	corresponding to first	(************************************
1	to first	amino acid	Debeucine, Memethionine, Nananasia
- }	amino acid	residue of	F=FLO11De, O=Glutamine D_hwainine
- 1	residue of	amino acid	S=Serine, T=Threoning U_U_U_U_
	amino acid	sequence	Welryptophan, Yerorgine Vulture
ı	sequence	Seductice	// /-possible micleofide 3-1
		 	\=possible nucleotide insertion\
1	j	}	PGSQRRRLIPALSLDTSSPVRKPDNSTGUMUDGD
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1	1 - 1	2170	ARGMAARDSDSEBDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD
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j	1		
	<u> </u>		KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEEHAPELSAN
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-	1	. = •	EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS
1	1 1		FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG
	<u> </u>	J	EPTDEETTGDISDSMDFVILNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV
7045	3	513	I GEVMENT CON CONTROL
]		1	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
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L-54			THE VOICE FULL KNAS IS IVE TWENTY TO THE TAKE AND THE TAK
7046	3	513	ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG LGFKMEALSPACAEMST AND ACCOUNTS TO THE TOTAL CONTROL OF THE TOTAL CHRISTIAN ADDITION OF
		1	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
j 1		1	KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLBFOLHEPFLLVDNASI SINGTUNGEN
		}	DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
7047	103	486	ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
1 1	1	1	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN
			IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY
7048	92		TO THE OWNER OF THE PROPERTY O
1	ĺ		FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKOPAENTOEEN DERSCHEEEANY
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7049	393		
1 1			RTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
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j		1.	**************************************
H-705		, ~	GGVLDVIVYASAADKMKNRGLRLRGVREPFRGCHWLGRKLIAWX
7050	393		
			RTGSASYGGPPPGLGGPATXASVAGRCSSVGKI PARRCYEDEL

SEO	Predicted				
ID	beginning	Predicted end			
NO:	nucleotide	nucleotide			
	location	location			
- 1	corresponding	corresponding			
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ı	amino acid	amino acid			
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7051	119	036			
1		816	KKMNLABICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS		
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			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL		
7056	2	527			
1			DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP EYHYLHOMIG/ALCUSPACACE		
}	}				
			SOKVPSRTTRLLDKSRTFHITCGATICIPSGVHVAAHLVNALN FSVNYSEDFVRINA ARVEDEDDDDVA		
7057)	FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL		
7057	1368	431			
		İ	GIYLHVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA SGEVPSQASLRGFFTEDEPGCFGEGENLPEALQNIQDEGTGEQL SPOER ISEKOLGOULBNEWGGGGGGEGENLPEALQNIQDEGTGEQL		
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7060	90	1 1 1 1	VNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ RFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS		

SEQ	Predicted	Predicted end	Amino agid goment contain
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	WaTmatonhan Value
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	1 1 1 1 1 1 1 1 1	\=possible nucleotide insertion)
			LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
			OOFI DI PUNUI CNUDGGEGGET I GILL BOGGET DI COLLINI DE C
1			QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
İ	1		LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
1	Í		RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
1			VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
1			TAEEICESSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
Ì]		SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
ŀ		•	QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
1	[,		SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	APMOCRICONCI DIMPROMETRICO
1		, 20	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
1]		RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
			EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
1			QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD
L			PGQLLG
7062	71.	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
1			TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL
1 :	' I		YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAA
			TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKD
1	j		FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
·			MEHH
7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
i i			LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
)]			FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
			EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS
			HKGFLLRLDM .
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
1			SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC
1 1	1		SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVDAD
!!!			CRCPAARTGAPAAATWLRRRLSGLRAFALGRRRSPGPSPKSAAP
7065			PLLTPLGAGRAGGSRANS
/065	1	555	ATTTHSARRSGRGAAAEAAASAAGGRQKGPDRKAWEGRRTTPGG
1	,		RSQSEPKAPPPQKRSEAAFASMAHSPVAVOVPGMONNTADPERT.
ļ j	1		PTKLERIGKGSFGEVFKGIDNRTQOVVAIKIIDLEEARDEIEDI
1 1		i	QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
7066	75.		RAGPFDEFQ
1 '''	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT
j l	ľ		YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
7067	150		VGVEVGGSGGCLEERTPP
1 ,00,	152	973	KENITMATEIGSPPRFFHMPRFQHQAPROLFYKRPDFAQQQAMQ
	İ	!	QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWORDORDMRATO
	•		PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
(l	İ	}	TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH
	ł	[NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNID
		i	FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
7068	222		HSPFCWAPF
, , , ,	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
		İ	DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
]		VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
l			GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
7069	7747		AELRIHENKVKKIQKDTFKKK
.003	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEESQAQENRDETLAKQ
1	1		TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
			TLLQSNVPVLQPPLPLEMPPPPPPPPPPESPPPPPPPPPPPAPKMPPP

SEQ	Predicted	Predicted end	1 Amino
ID	beginning	nucleotide	
NO:	nucleotide	location	
ı	location	Tocalion	
ĺ	corresponding	corresponding	**=**+********** ==180{@110196
- 1	to first	to first	L-Leucine, M-Methionine N-Asparation
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	Warrantonhan W. m.
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	sequence	1 4	COCOU, /=possible nucleofide deleti-
	T	 	\=Possible nucleotide incertion\
1	į	1	EKTKKGRKDKAKKSKTKMPSIJVKKWOSTOPELDEEDNIGGE
7070		<u> </u>	RVSTAQKRIEEWKQQQLVSGMAERNANFEA
1 /0/0	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
i	1	ļ	LEDEKHUGAGAAI ONUKGODDU
İ	1	1	LEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLI
- 1	· F	1	DELL'ARROY ARCHARASHED DE DE ET TREDITO DE DES TENTES DE L'ARROY D
1	1	1	**************************************
7071	2		INTARE
1		921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1	1	}	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
i	1	ļ	FODPRIOTPERUPOVEOUS PROTECTION OF THE PROTECTION
i		İ	FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
			PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
			1 TOGETAPVIDSKIWRPPMYORDDITTDENET DDMDtagragaria
1	1		THE PROPERTY OF THE PROPERTY O
7072	2		TARREDOWAY I HTUKAPL VSSTI DVATOCOTODOM STORES
1	1 4 1	921	ARGILRALETAKKVGKVGANGOKAAGDSADSVERSVERS
1	}		VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
			FORPETOT PERUPONDO TO THE PROPERTOR OF TH
1	!		FODPRTQIPFRUPQYPQTGYYPPPPTUPAGVAPCVPRFVRSNNV
1	Į į		1 2 DO DIFFROMFIADHYSTES DRODMING COVORDAD CONTROL
1]		1 TOGHTMEVIDSKKIWKPPMYORDDTTDCMCTDDMDIDGGGGGGGGG
1	1 1		TOWNS THE PROPERTY OF THE PROPERTY AND T
7073	50		TANKEDYNAVIHIOKAPLYSSTI.PVATOSDTDDCmt vinches
1	1 30	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAMP
) !		LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI
	1		VTIGKDEFHILIT VDTAGODDISCT
	<u> </u>		VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL HSFQVIESLYQKLHEGHGK
7074	263	1003	VODE COMPANY OF THE CHECK
1 1		2003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
1 1	i .		I VOUS AN AMOUNT DVCKY I LIGHT GENS DVCK MVDCVT DVCC AND
} }	1		CHARLES CONTRACT CONTRACTOR DE
1 1	1		I TOTHUNGNIFULFVKSWSTNTSGT.DTTTT CONT TENDENDED
1 1	1		MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
1 2000			AGVFFDRTELDRKEKLTFTESTHVEI
7075	598	1005	NALMERBARADAMON
1 1	J	· · · · · ·	NYINFFFRKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESESQ
1 1	į.		I VALUE ARRAY OUR RICCAT TO THE TOTAL OF THE PROPERTY OF THE P

7076	279		****
1 1		1049	LQSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK
1 1	1	ļ	OF DIGITAL PROPERTY OF THE PRO
1 1	į.	j	KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKGKSH
1 1	ļ	ſ	RQDAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL
1 1	į.	ŀ	ROLEKSMMETERDINGALOGUERAN
	į.	f	RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
7077	3	1119	PARTIE TOROVETSSEASMOLDRYCETDTIMETERS
1 1	1	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR
	!		PHARTING SHADAWLSKRFOKVKI PCPKCI DCCI DA WALLOUS
		1	SKELLEONPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA
	1	1	RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ
1		f.	AFWCI VOTCDKYL DCYYGAGI HA TOT DCGAQAPYAAVLLMHMPAEQ
	l	. 1	AFWCLVQICDKYLPGYYSAGLEAIQLDGEIFFALLRRASPLAHR
	ļ	·	HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
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1		1,	VYVFGELLELANVORLARGANAAVIOLISCOLEARG
		1.	VYVFGELLELANVQELAEGANAAYLQLLNLPAYGTYPDYIANKE SLPELY
7079	2		206801
		•	SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
			MQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	
ł	location	corresponding	I Victorial Actor Pappential and a comme
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Turceine v_U
j	amino acid	sequence	(COUCH) /=possible nucleotide deleti-
 	sequence	<u> </u>	\=POSSIDIE nucleotide insertion\
7080	200		ABVLOMTVDHLKMLHATGGTGTHALLEOAGELOOTS
1 .000	200	595	VQLPLEAPCLSLLSCRDHSGGNPDI SPRUNDGRIVGGREE
ĺ			DIMPLEADOV VSVGRLOIRALATPRUTORULIOT I DORDUTORO
7081	213		COF SCHOOL DSGCGEFPRKREE! GPRCPPDID A AMYDIA
1		506	AVIESEMILINGLESLCYHNKI, TI, A PMURUGTI, DMRI I AI DUGE SE
ì	į		VICEEDIDERMIQCKRVVNEVLSTVDFVAPDDRVVFRTCERFON
7082	3	1137	KAALOMGIS
İ		113/	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL
			CCRSSPRUDRUGEREHEAAORKADGAFCCDCI DI GTODTOMOS
	}		SSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSEDPSMLS
1			QAQSATEVEERHVSPSCSTSRERPFQAGELILAETGEGETKFKK
	}		LFRLNNFGLINSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRP
1			ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH
1			VEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVF
7083			1 ************************************
, , , ,	115	541	RSNAVQLTRMEYAMKSLSLLVPKSLSPHVCVPTCVPTCVPTCVPTCVPTCVPTCVPTCVPTCVPTCVP
			SPAAPRARPCRVSTADRSVRKGTMAVCT.PDI.I.I. VIIDDMI.I.E
1			TIPE VEEEDGITVETEEYFOALAGDTVFMVI.OKGOVWORDSBOOK
7084	3	522	THEFTSHAR
1		322	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK
, ,	j		VKNKAPAEVQITAEQLLREAKERELELLPPPPPQQKITDEEELND
			YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTI.
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC
}			ABLVSFKHPHVANPRLQMASPEEKCQQVLEPPYDEMFAAHLRCT
1 1	1		YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
1 1			DER VEANNADOOLVKKGKSKVGDMI.EKAARI.I.MCCERUGA GROOP
1 1			OGTEDSKAMGMLFLVNOLFKTYFKTNKI.HI.CVDI.TD3.TDCCCCCC
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			ATTICUS DUAL LVALKEMOVEDVD TDEVOCTE ANT TIMOTOTICS
7086	256	525	Prigray ASKON PED PRINCIP.
} }	×.		ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCP SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR
			EF EF
7087	166	723	LSGSSAGKVAAPCVPFSNHELVPITTENAPKNVVDKGEGASRGG
			"TANGUEDINGSTRVTPSVOPHI OPTDNMSVCDTMDDOOM D
1	1	Į.	VIERTIAVSEPSTANEENERSNI, REVIDOMI, VEVUCCINUT, TOTAL
			ERREDITALHAKVLEFGWPDLHTPALEKICSICKAMPTMI MALIN
7088	104		INCK V DRIVAG
1		759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
l			
l		ı	ARMAN LABEEDUDSSTASDSDVI.IPDNVEDAEVDD II GUODDGO
		• 1	FREE LIDRY BMG QMASMFFNKVGVNI. FVECT TVVT VARY S TV-
7089	33	1775	AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
1	ĺ		SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYLPNTKVEC
			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFWWSSVPESTTDG
J			SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
1		[6	DLKLQLEGQVTELRSRVQBLERALATARQEHTELMEQYKGISRS
}	1	1 -	GET LESKULLSKOOGDHVAR ILELEDD LOTT CEVER TOVERING D
		1 -	WALL VANDIREOEKLEGOUKEVOADKEOGERELOWA COMMISSION
		N	ILDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	In-nighted C-Cysteine D-Accepti- a-13 m
i	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, Tathreonine V-Valine
١,	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y-Unbnorm + Gb-
1	amino acid	sequence	COGON, /=possible nucleatide deleti-
	sequence		\=Possible nucleotide insertion)
- 1			LKEQLRGAQELAASSOOKATI LGEELAGAAAADDDTTAELEDGE
			1 15 VAEVNGKLAELGLHLKREKCOWSKEDAGLI OSVEDBYDYSKEL W
1			1 12ABILKUEKAVOEERTONOVEKTELAPEKTEELUOL CECKPES
ì		1	I TEDROAURVLOKEKEOLOEEKORI.I.EVMORT ENDT EVITA DEVITA
	1		EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ ASLLLGLE
7090	33	1775	
			SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
ĺ		1	HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
			PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
-			QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
Į.	1		HGETTEERDILSROOGDHVARILELEDDIOTTCRVIT TVD
1			RURDIVKALTREOEKLIGOLKEVOADKEOSEAET OVA COEMILIT
1			THE TAKE AND WEEDS AOAORLKDKVAOMKDTI GOAOOPUN BY BD
1			LABQUAGAQELAASSQOKATLLGEELASAAAADDDTTAELUBGD
-	[DEVAEVNGKLAELGLHLKEEKCOWSKERAGTLOGVEREVDVITV
1			LISASIANLEKAVQEERTONOVFKTELAREKDOGIJJOLOGOVDET
-			1 LUKSAUKVLOKEKEOLOEEKORI,I, EVMOKI, DADI, DEVIA DEVIA DEVIA
1	1		EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETO
7091	186	1076	ASLLIGLE
1		2070	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
1			EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEEGDDDHPD
1			SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
1			WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
i i			HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVCDVGT CVCDV
7092	- 500		ISVNVPIQDGIQDEKYYOICERYEPPAPNDCI.
1032	522	809	KQGINEDQEESOKPRIGEGCEPISKROMYKITKOYOMPEODELD
1 1			NORREERRERERE COMEPNSDGHDRKRVRRDVVHSTLRLTT
7093	454	#FF	DESPUALM
	.51	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
7094	2	508	ECPQLCVCEIRPWFTPQSTYREA
1		300	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
1 1	i		DIIAFPLODYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
			LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSFFCLKMETYLRM ADLFYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
1 1			SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
1 1	1		TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
7096			KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRSSRISFAGALFLTRFLLQELLLNNFC
1			SAMSPAPDAAPAPASISLFDLSADAPVFOGI,SI,VSHADGEALAD
		•	APRISCSGSGERESPERKLLOGPMDISEKT.ECCTCDOMPONIOR
			UKEHYKLDWHRFNLKORLKDKPLLSALDFEKOSSTCDLSSTCCC
		1	EUSUSASEEDLOTLDRERATFEKI,SR PDGEVDUDVI PONAGGOD
		į	LYAYRCVLGPHODPPEEAELLLONLOSKGPPDCVVII MAAAGUPA
	1	1	GAIFQGKEVVTHKTFHRYTVRAKRGTAOGLEDARGGDGUGACAN
1	j	ļ	LRKYNEATLYKDVRDLLAGPSWAKALEEAGTIIJRAPPSGPSI.P
1			FGGKGAPLQRGDPRLWDIPLATRRPTFOELORVI,HKT.TTT.WVVP
1		Ť	EDPREAVRIHSPOTHWKTVREERKKPTEEETRKICPDEKEALCO
			NEES PKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
ĺ		1	RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
			LDEAKAPGOPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
7097	256	1228	LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADFTVQCQDH
			IRTKSAATWEAWFQCGREGSRIITEPCEANAGSRQELQTERISS FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA

SEQ	Predicted	Predicted en	2 12 12 12 12 12 12 12 12 12 12 12 12 12
ID	beginning	nucleotide	
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}	location	corresponding	I VANCOUNTE ACIO. PEUNENVISIANIA A A.
	corresponding	to first	
	to first	amino acid	D=Deucine, M=Methionine N-hamana
J	amino acid	residue of	F-F-O-Line, O=Glucamine, D-Aini
!	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
			SNSFSDIUGENANDERVOOR
ļ			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSHDTMTYC
- }	1		LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQALDVTEQ
İ	1		LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISE WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG
- 1		1	EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYWWGNRVK
7777			TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSEQSLFSTLEBPRDKEIDNYCVMRLQT
ł		i	EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
ł	1	ļ	LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
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1	332	210	LFRLAPGFLRSLAROGYHOTWAFDFT.DCCATATHOLAS
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		012	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
1			* *** OF FEQUUIPLEAFPVFKKYDDNGT.NGFTDGWDGGG
			DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWYLIAWEN SSVPVAFSHFRFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1			VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP
			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
7102			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
1 102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVPAGGGPPPPP
1 1	1		VALUE VGEPK VGKTSLIMSLVSKREDERVEDDD DEFTUYDD DAWN
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			GOGVIVNALHPGVARTELGRUTCTUCQTDI OUTDI VILLING
	j		AGERGMENTAPAUHNTLAVARELA VIGGEVERGI VOVA DA DOS
7105	765	143	**************************************
j			GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA
i	Į.		LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST
1			SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
		İ	MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT
1	ļ	1	YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF
- 1			GAEFVEVIKOSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
1		ĺ	TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF
1]	PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
			AKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKL
1	1	1	RECEREFIMECGEAVERNERLITADOREYOOFI.KKUVNELEDNI
7107	1145		RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS
	11.13	591	*I*WLQTGKKK

S	Q Predicted	1 21 .	
I		Predicted end	
NC	3	nucleotide location	I M-Miduille, CECVSERINA D-Xamami:
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ĺ	correspond	corresponding ing to first	n=nistidine, l=Isolengine v=Ivg:
	to first	amino acid	L=Leucine, M=Methionine N-Densys-
1	amino acid	residue of	P=Proline, Q=Glutamine P-broining
- 1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	sequence		Cocon, /=possible nucleofide deleti-
710	08 1	942	\=possible nucleotide insertion)
ł			VKVALLITNLEQPRIESEWENSFILKMFLFQFVNLNSSTFYIAF
			FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
	ľ	1	OTWINIFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
- 1		1	QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
ł	}	1	RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
l l	1	1	AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
			DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF WHVLAW
710	9 964	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
1	1		TOPPPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
	1		SEKLATOTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
		•	VIAKELFIGKKDHECSECGKTFIVNSHIJINDOBINGCOPKOVIA
		1	SDCGKTFKQSSNLGOHORIHTGEKPFECNECGVA PRINCEY I I I I I I I I I I I I I I I I I I I
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''	36	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKOMLTRACITTUT
1			1 SESTARREQUIDEST LEGETAHFFEET KEEREDGUMT CORT COME
1		İ	ATAVQVQSSLKNSESDVEENOEKI,AT.DT.DT.QQQDAAGMDDT TOO
ļ	1		LWARRAEKKKLRKTLREFEEAFYOONGRNAOKEDBURG ERING
7111	. 2		INVINATOR
	· -	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
1		<u>†</u>	DIVISUES IN THE REPORT LEGISLAND TO THE PROPERTY
1		Į.	MESHNI VHQARFFRRQTDSSGKEWWVTNNTYWRI RAEDGYGNMD
7112	103	495	GAVLW
}		****	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
L	.]	į.	TAMBUDIQUESERFSVKVEOAKYVSMTIKCUTEEDECVVGTSTV.
7113	1	824	KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
}			KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
l		- [LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
			ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
1		1 1	QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
ļ			DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
7114	- 		SSGPLNLPRR
/114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKICRKI
	}		TILMIDIVSVKQRLPKYYSWERCSKHHINKI.CONPEYSDERVED
			CAMINAVCLHYNLHKAOPAERFFDPNORGKATHOKONI BYGORG
		1	QIGERLIKCTECGKVFIOKANLVVHORTHTGERDVECCEGA VA D
		1 1	SONS IDIAHOR THIS EXPYECS ECCKTPION OF TAU OF THE PROPERTY OF
•		[]	AFF VCDACPRAPKSSYHLIRHEKTHIROAFVKGIKCTTCGI TVA
	İ	1	ALTISEAPQCSEHGKASDEKPSPTKHWRTHTKFNTVFCCVCCVC
	1	1	FRGASHUSVHORIHTGEKPYECSTCGKTFSGKSHI SIZIKIDINING
			EXPIBERREGRAFGERSTLIVHORMHTGERPYKENEGERARGER
		1	SPLIANORIHIGERPYECTDCKKAFSRKSTLIKHOD TUTCEVEN
			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI KHQRSHTGDKVL
7115	1		
		1	NAAHGYNWGLWCMYIIPPODWLDRGDESAPIRTPAMIGCSPVVD
	1	1	REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
	1	- []	HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHYYMAWNIPM SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
	1		YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
	1	_	LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
		-	FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
7117			WIKHARH
7116	866		RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
	L		PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR
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- 1	amino acid	amino acid	W=Tryptophan, Y=Turosine v_Unlance
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i	}		ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTGT AUGT TOTAL
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7119	49	1863	FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
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	1		ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
	1 1		LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
Į.	1	İ	NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
1			YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
1	1 1	J	MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
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-		- 6	AYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL

SEQ	Predicted	Predicted end	
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NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
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1	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
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İ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
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1	1	1	LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAY SVPLTLAETVASLWPALOPLATON
1	1	1	SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVE GAYFNVLINLRDITDE EKDOLHUNGE
		1	GAYFNVLINLRDITDRAFKDQIHHRVSSLLQEAKTQAALVLDCI
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7125	166	1127	KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
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l			FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS LPESCLLT\RDTVIRSVLGAVLWWWW.
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1	1	1	PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC WRGGRIASAFASST#TDGGGDDAGGGRIASAFASST#TDGGGDDAGGGRIASAFASST#TDGGGDDAGGGRIASAFASST#TDGGGDDAGGGRIASAFASST#TDGGGDDAGGGRIASAFASGGGRIASAFASGGGRIASAFASGGRIASAFASGGGRIASAFASGGGRIASAFASGGGRIASAFASGGGRIASAFASGGGRIASAFASGGGRIASAFASGGGRIASAFAGGGGRIASAFAGGGGRIASAFAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
7127	1311		
	1		GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF
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		AI SI CE RA RQ	LASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA RVLADPSLPBLFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL LLVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
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		AI SI CE RA RQ TI DC KV	LASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA RVLADPSLPBLFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL LLVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR

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- 1	1 1		ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA
	1		EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK
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7129			PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR
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7140	1401	1957 R	ASSLQVLKANGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF MNVSLBKQLRPSQPWPRGKCRKTPGWEEARPKAQDLRGDLGKT		

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \-possible nucleotide insertion) QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ
7141	124	1073	ADFMTNQCG LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHBUPESCURVANNAGESSVPP
7142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDETVKSLSLIJA
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNGSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDACTLDALDHDALGHUNGS
7144	1		HSVVFHSTVSILLFFQIKYKTLOKNISTIISKSLKI FRVNMQDGGFSPAEHSKAEESAGMEARFLGLPDAAGSSGFTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- An antibody directed against the polypeptide of claim 10.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

A. CL	A COLEY CA THON OR COMPANY		FC17U30U/342	263					
IPC(7) US CL	ASSIFICATION OF SUBJECT MATTER : C07H 21/04; C12N 15/11, 15/63, 15/70, 1 : 536/23.1; 435/320.1, 455, 468, 530/300, 3	5/82, 15/85	; C07K 14/00						
According to International Patent Classification (IPC) or to both national classification and IPC									
B. FIELDS SEARCHED									
Minimum documentation searched (classification system followed by classification symbols)									
U.S. :	U.S.: 536/23.1; 435/320.1, 455, 468, 530/300, 350								
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched									
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) MEDLINE, EAST									
C. DOC Category *	UMENTS CONSIDERED TO BE RELEVANT								
A	Citation of document, with indication, wher	e appropriat	e, of the relevant passages	Relevant to claim No.					
	hydroxysteroid dehydrogenase of chickens. Gene.	expression of an ovary-specific 17beta- 1999, Vol.233, pages 75-82		1-11, 13-16, and 19-26					
A	US 5,175,095 A (MARTINEAU et al) 29 Decem columns 3-18.	per 1992 (29.12.1992), see especially		1-11, 13-16, and 19-26					
A	Database PubMed, ID No. 2393392, FREUDENS inhibitor of metalloproteinase: sequence and expre Biophys. Res. Commun. August 1990. Vol.171. I	ripp propries stance D1 1	1-11, 13-16, and 19-26						
A,P Database PubMed, ID No. 10919256, HENNEBO generation and characterization of an ovary-selectifibrary. Endocrinology. August 2000. Vol.141. No.			Ovary-selective genes I: the	1-11, 13-16, and 19-26					
A	Database PubMed, ID No. 2760883, BEIL et al. 9	2760883, BEIL et al. Synthesis of polypeptides by the cervix of J. Reprod. Fertil. July 1989, Vol.86. No.2. pages 535-544, see							
A,P	Database PubMed, ID No. 10830289, HINSHELV upstream of the human CYP19 (aromatase) gene m transgenic mice. Endocrinology. June 2000. Vol. 1	1-11, 13-16, and 19-26							
	documents are listed in the continuation of Box C.		See patent family annex.						
• Sp	ecial categories of cited documents:	-T"	later document published after the inte	reational filing data as a incini					
"A" document defining the general state of the art which is not considered to be of particular relevance			date and not in conflict with the applic principle or theory underlying the inve	ation but cited to undecound the					
'E" earlier application or patent published on or after the international filing date		"X"	document of particular relevance; the considered novel or cannot be conside when the document is taken alone	claimed invention cannot be red to involve an inventive step					
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		-Y-	1						
O" document referring to an oral disclosure, use, exhibition or other means			combined with one or more other such being obvious ') a person skilled in the	documents such combination					
P" document published prior to the international filing date but later than the priority date claimed		"&" document member of the same patent family							
Date of the actual completion of the international search			Date of mailing of the international search report						
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Box PC Washir	CT 1800n, D.C. 20231 (703)305-3230	Michael Woodward							
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Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one

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